

## PATENT COOPERATION TREATY

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## NOTIFICATION OF ELECTION

(PCT Rule 61.2)

From the INTERNATIONAL BUREAU

To:

United States Patent and Trademark  
Office  
(Box PCT)  
Crystal Plaza 2  
Washington, DC 20231  
ÉTATS-UNIS D'AMÉRIQUE

in its capacity as elected Office

Date of mailing (day/month/year) 10 March 1999 (10.03.99)	Applicant's or agent's file reference PB481PCT
International application No. PCT/US98/12718	Priority date (day/month/year) 20 June 1997 (20.06.97)
International filing date (day/month/year) 18 June 1998 (18.06.98)	
Applicant CHOI, Gil, H. et al	

1. The designated Office is hereby notified of its election made:

☒ in the demand filed with the International Preliminary Examining Authority on:

19 January 1999 (19.01.99)
☐ in a notice effecting later election filed with the International Bureau on:

2. The election ☒ was  
☐ was not

made before the expiration of 19 months from the priority date or, where Rule 32 applies, within the time limit under Rule 32.2(b).

The International Bureau of WIPO  
34, chemin des Colombettes  
1211 Geneva 20, Switzerland

Facsimile No.: (41-22) 740.14.35

Form PCT/IB/331 (July 1992)

Authorized officer

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2516325

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12718

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/68

US CL : 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 5,466,577 A (WEISBURG) 14 November 1995, Abstract and claim 7.	19
X	US 5,582,990 A (BERGSTROM ET AL.) 10 December 1996, Abstract and claim 12.	19

☐

Further documents are listed in the continuation of Box C.

☐

See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*E* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*g* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

02 SEPTEMBER 1998

Date of mailing of the international search report

OCT 13 1998

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
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Authorized officer

JAMES MARTINELL

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**INTERNATIONAL SEARCH REPORT**

International application No.

PCT/US98/12718

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1-18, 20, and 21  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims refer to tables of nucleotide and amino acid sequences. No sequence data were submitted in computer readable form in the instant application. Accordingly, no meaningful search can be performed for claims 1-18, 20, and 21.

3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

**Remark on Protest**

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12718

## B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, STN Online

borrel?, burgdorffii, afzelii, garinii, andersonii, anserina, japonica, coriaceae, lyme(w)disease, sensu, lato, stricto, pcr,  
polymerase(w)chain(w)reaction#



## PATENT COOPERATION TREATY

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## INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

REC'D 01 NOV 1999

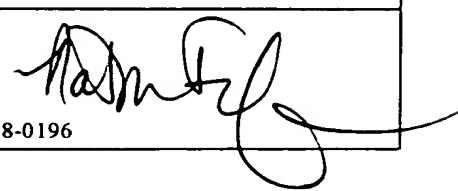
WIPO PCT

Applicant's or agent's file reference PB481PCT	<b>FOR FURTHER ACTION</b> See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/US98/12718	International filing date (day/month/year) 18 JUNE 1998	Priority date (day/month/year) 20 JUNE 1997
International Patent Classification (IPC) or national classification and IPC IPC(6): C12Q 1/68 and US Cl.: 435/6		
Applicant HUMAN GENOME SCIENCES, INC.		

- This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.
- This REPORT consists of a total of 4 sheets.  
☐ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority. (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).  
 These annexes consist of a total of 0 sheets.

## 3. This report contains indications relating to the following items:

- I ☒ Basis of the report
- II ☐ Priority
- III ☒ Non-establishment of report with regard to novelty, inventive step or industrial applicability
- IV ☐ Lack of unity of invention
- V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
- VI ☐ Certain documents cited
- VII ☐ Certain defects in the international application
- VIII ☐ Certain observations on the international application

Date of submission of the demand  19 JANUARY 1999	Date of completion of this report  14 OCTOBER 1999
Name and mailing address of the IPEA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer  JAMES MARTINELL 
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**I. Basis of the report**

1. This report has been drawn on the basis of *(Substitute sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to the report since they do not contain amendments):*

- ☒ the international application as originally filed.
- ☒ the description, pages 1-267 , as originally filed.  
pages NONE , filed with the demand.  
pages NONE , filed with the letter of \_\_\_\_\_  
pages \_\_\_\_\_ , filed with the letter of \_\_\_\_\_
- ☒ the claims, Nos. 1-21 , as originally filed.  
Nos. NONE , as amended under Article 19.  
Nos. NONE , filed with the demand.  
Nos. NONE , filed with the letter of \_\_\_\_\_  
Nos. \_\_\_\_\_ , filed with the letter of \_\_\_\_\_
- ☒ the drawings, sheets/~~fig~~ NONE , as originally filed.  
sheets/~~fig~~ NONE , filed with the demand.  
sheets/~~fig~~ NONE , filed with the letter of \_\_\_\_\_  
sheets/~~fig~~ \_\_\_\_\_ , filed with the letter of \_\_\_\_\_

2. The amendments have resulted in the cancellation of:

- ☒ the description, pages NONE
- ☒ the claims, Nos. NONE
- ☒ the drawings, sheets/~~fig~~ NONE

3. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the ~~Supplemental Box~~ Additional observations below (Rule 70.2(c)).

4. Additional observations, if necessary:

NONE

**III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability**

The question whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been and will not be examined in respect of:

☐ the entire international application.

☒ claims Nos. 1-18, 20, and 21

because:

☐ the said international application, or the said claim Nos. \_ relate to the following subject matter which does not require international preliminary examination (*specify*).

☐ the description, claims or drawings (*indicate particular elements below*) or said claims Nos. \_ are so unclear that no meaningful opinion could be formed (*specify*).

☐ the claims, or said claims Nos. \_ are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for said claims Nos. 1-18, 20, and 21.

**V. Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement****1. STATEMENT**

Novelty (N)	Claims	<u>NONE</u>	YES
	Claims	<u>19</u>	NO
Inventive Step (IS)	Claims	<u>NONE</u>	YES
	Claims	<u>19</u>	NO
Industrial Applicability (IA)	Claims	<u>19</u>	YES
	Claims	<u>NONE</u>	NO

**2. CITATIONS AND EXPLANATIONS**

Claim 19 lacks novelty under PCT Article 33(2) as being anticipated by either one of Weisburg (U.S. 5,466,577) or Bergstrom et al (U.S. 5,582,990). Weisburg et al discloses a method for detection of *Borrelia* DNA using PCR amplification (e.g., see the abstract). Bergstrom et al discloses a method for detection of *Borrelia* DNA using PCR amplification (e.g., see claim 12).

Claim 19 meets the criteria set out in PCT Article 33(4), for industrial applicability.

----- NEW CITATIONS -----

NONE

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WORLD INTELLECTUAL PROPERTY ORGANIZATION



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :

C12Q 1/68

A1

(11) International

(43) International Publication Date

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60/057,483	3 September 1997 (03.09.97)	US

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(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

With international search report.

(54) Title: LYME DISEASE VACCINES

(57) Abstract

The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of *Borrelia burgdorferi*. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Borrelia* gene expression.

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## Lyme Disease Vaccines

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### Field of the Invention

The present invention relates to novel vaccines for the prevention or attenuation of Lyme disease. The invention further relates to isolated nucleic acid molecules encoding antigenic polypeptides of *Borrelia burgdorferi*. Antigenic polypeptides are also provided, as are vectors, host cells and recombinant methods for producing the same. The invention additionally relates to diagnostic methods for detecting *Borrelia* gene expression.

### 15 Background of the Invention

Lyme disease (Steere, A.C., *Proc. Natl. Acad. Sci. USA* 91:2378-2383 (1991)), or Lyme borreliosis, is presently the most common human disease in the United States transmitted by an arthropod vector (Center for Disease Control, *Morbid. Mortal. Weekly Rep.* 46(23):531-535 (1997)). Further, infection of house-hold pets, such as dogs, is a considerable problem.

While initial symptoms often include a rash at the infection point, Lyme disease is a multisystemic disorder that may include arthritic, carditic, and neurological manifestations. While antibiotics are currently used to treat active cases of Lyme disease, *B. burgdorferi* persists even after prolonged antibiotic treatment. Further, *B. burgdorferi* can persist for years in a mammalian host in the presence of an active immune response (Straubinger, R. *et al.*, *J. Clin. Microbiol.* 35:111-116 (1997); Steere, A., *N. Engl. J. Med.* 321:586-596 (1989)).

Lyme disease is caused by the related tick-borne spirochetes classified as *Borrelia burgdorferi* sensu lato (including *B. burgdorferi* sensu stricto, *B. afzelii*, *B. garinii*). Although substantial progress has been made in the biochemical, ultrastructural, and genetic characterization of the organism, the spirochetal factors responsible for infectivity, immune evasion and disease pathogenesis remain largely obscure.

A number of antigenic *B. burgdorferi* cell surface proteins have been identified. These include the outer membrane surface proteins (Osp) OspA, OspB, OspC and OspD. OspA and OspB are encoded by tightly linked tandem genes which are transcribed as a single transcriptional unit (Brusca, J. *et al.*, *J. Bacteriol.* 173:8004-8008 (1991)). The most-studied *B. burgdorferi* membrane protein is OspA, a lipoprotein antigen expressed by borreliae in resting ticks and the most abundant protein expressed *in vitro* by most borrelial isolates (Barbour, A.G., *et al.*, *Infection & Immunity* 41:795-804 (1983); Howe, T.R., *et al.*, *Science* 227:645 (1985)).

A number of different types of Lyme disease vaccines have been shown to induce immunological responses. Whole-cell *B. burgdorferi* vaccines, for example, have been shown to induce both immunological responses and protective immunity in several animal models (Reviewed in Wormser, G., *Clin. Infect. Dis.* 21:1267-1274 (1995)). Further, passive immunity has been demonstrated in both humans and other animals using *B. burgdorferi* specific antisera.

While whole-cell Lyme disease vaccines confer protective immunity in animal models, use of such vaccines presents the risk that responsive antibodies will produce an autoimmune response (Reviewed in Wormser, G., *supra*). This problem is at least partly the result of the production of *B. burgdorferi* specific antibodies which cross-react with hepatocytes and both muscle and nerve cells. *B. burgdorferi* heat shock proteins and the 41-kd flagellin subunit are believed to contain antigens which elicit production of these cross-reactive antibodies.

Single protein subunit vaccines for Lyme disease have also been tested. The cell surface proteins of *B. burgdorferi* are potential candidates for use in such vaccines and several have been shown to elicit protective immune responses in mammals (Probert, W. *et al.*, *Vaccine* 15:15-19 (1997); Fikrig, E. *et al.*, *Infect. Immun.* 63:1658-1662 (1995); Langerman S. *et al.*, *Nature* 372:552-556 (1994); Fikrig, E. *et al.*, *J. Immunol.* 148:2256-2260 (1992)). Experimental OspA vaccines, for example, have demonstrated efficacy in several animal models (Fikrig, E., *et al.*, *Proc. Natl. Acad. Sci. USA* 89:5418-5421 (1992); Johnson, B.J., *et al.*, *Vaccine* 13:1086-1094 (1996); Fikrig, E., *et al.*, *Infect. Immun.* 60:657-661 (1992); Chang, Y.F., *et al.*, *Infection & Immunity* 63:3543-3549 (1995)), and OspA vaccines for human use are under clinical evaluation (Keller, D., *et al.*, *J. Am. Med. Assoc.* 271:1764-1768 (1994); Van Hoecke, C., *et al.*, *Vaccine* 14:1620-1626 (1996)). Passive immunity is also conferred by antisera containing antibodies specific for the full-length OspA protein. Further, vaccination with plasmid DNA encoding OspA has been demonstrated to elicit protective immune responses in mice (Luke, C. *et al.*, *J. Infect. Dis.* 175:91-97 (1997); Zhong, W. *et al.*, *Eur. J. Immunol.* 26:2749-2757 (1996)).

Recent immunofluorescence assay observations indicate that during tick engorgement the expression of OspA by borreliae diminishes (deSilva, A.M., *et al.*, *J. Exp. Med.* 183:271-275 (1996)) while expression of other proteins, exemplified by OspC, increases (Schwan, T.G., *et al.*, *Proc. Natl. Acad. Sci. USA* 92:2909-2913 (1985)). By the time of transmission to hosts, spirochetes in the tick salivary glands express little or no OspA. This down-modulation of OspA appears to explain the difficulties in demonstrating immune responses to this antigen early in infection following tick bites (Kalish, R.A., *et al.*, *Infect. Immun.* 63:2228-2235 (1995); Gem, L., *et al.*, *J. Infect. Dis.* 167:971-975 (1993); Schiabile, U.E., *et al.*, *Immunol. Lett.* 36:219-226 (1993)) or following challenge with limiting doses of cultured borreliae (Schiabile, U.E., *et al.*, *Immunol. Lett.* 36:219-226 (1993); Barthold, S.W. and Bockenstedt, L.K., *Infect. Immun.* 61:4696-4702 (1993)).

Furthermore, OspA-specific antibodies are ineffective if administered after a borreliac challenge delivered by syringe (Schiabile, U.E., *et al.*, *Proc. Natl. Acad. Sci. USA* 87:3768-3772 (1990)) or tick bite (deSilva, A.M., *et al.*, *J. Exp. Med.* 183:271-275 (1996)). To be efficacious,



OspA vaccines must elicit protective levels of antibody which are maintained throughout periods of tick exposure in order to block borrelia transmission from the arthropod vector.

Vaccines in current use against other pathogens include *in vivo*-expressed antigens which could boost anamnestic responses upon infection, potentiate the action of immune effector cells and complement, and inhibit key virulence mechanisms. OspC is both expressed during infection (Montgomery, R.R., *et al.*, *J. Exp. Med.* 183:261-269 (1996)) and a target for protective immunity (Gilmore, R.D., *et al.*, *Infect. Immun.* 64:2234-2239 (1996); Probert, W.S. and LeFebvre, R.B., *Infect. Immun.* 62:1920-1926 (1994); Preac-Mursic, V., *et al.*, *Infection* 20:342-349 (1992)), but mice immunized with this protein were only protected against challenge with the homologous borrelial isolate (Probert, W.S., *et al.*, *J. Infect. Dis.* 175:400-405 (1997)). Identification of *in vivo*-expressed, and broadly protective, antigens of *B. burgdorferi* has remained elusive.

### Summary of the Invention

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding the *B. burgdorferi* peptides having the amino acid sequences shown in Table 1. Thus, one aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) a nucleotide sequence encoding any of the amino acid sequences of the truncated polypeptides shown in Table 1; and (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), or (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b), (c), or (d) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b), (c), or (d) above. This polynucleotide which hybridizes does not hybridize under stringent hybridization conditions to a polynucleotide having a nucleotide sequence consisting of only A residues or of only T residues. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of epitope-bearing portions of a *B. burgdorferi* polypeptide having an amino acid sequence in (a), (b), or (c) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using these vectors for the production of *B. burgdorferi* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *B. burgdorferi* polypeptides having an amino acid

sequence selected from the group consisting of: (a) an amino acid sequence of any of the full-length polypeptides shown in Table 1; (b) an amino acid sequence of any of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) an amino acid sequence of any of the truncated polypeptides shown in Table 1; and (d) an amino acid sequence of an epitope-bearing portion of any one of the polypeptides of (a), (b), or (c).

The polypeptides of the present invention also include polypeptides having an amino acid sequence with at least 70% similarity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% similarity to those described in (a), (b), (c), or (d) above, as well as polypeptides having an amino acid sequence at least 70% identical, more preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those above; as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides a vaccine, preferably a multi-component vaccine comprising one or more of the *B. burgdorferi* polypeptides shown in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *B. burgdorferi* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Borrelia* genus in an animal. The *B. burgdorferi* polypeptides of the present invention may further be combined with one or more immunogens of one or more other borrelial or non-borrelial organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Borrelia* genus and, optionally, one or more non-borrelial organisms.

The vaccines of the present invention can be administered in a DNA form, *e.g.*, "naked" DNA, wherein the DNA encodes one or more borrelial polypeptides and, optionally, one or more polypeptides of a non-borrelial organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed fusion proteins.

The vaccines of the present invention may also be administered as a component of a genetically engineered organism. Thus, a genetically engineered organism which expresses one or more *B. burgdorferi* polypeptides may be administered to an animal. For example, such a genetically engineered organism may contain one or more *B. burgdorferi* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such a genetically engineered organism may secrete one or more *B. burgdorferi* polypeptides.

The vaccines of the present invention may be co-administered to an animal with an immune system modulator (*e.g.*, CD86 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Borrelia* genus, *e.g.*, *B. burgdorferi* sensu stricto, *B. afzelii*, and *B. garinii*, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent or attenuate an infection by members of the *Borrelia* genus, comprising administering to the animal a composition comprising one or more of the polypeptides shown in Table 1, or fragments thereof. Further, these polypeptides, or fragments thereof, may

be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the administration of one or more *B. burgdorferi* polypeptides of the present invention.

The invention also provides diagnostic methods for detecting the expression of genes of members of the *Borrelia* genus in an animal. One such method involves assaying for the expression of a gene encoding *Borrelia* peptides in a sample from an animal. This expression may be assayed either directly (*e.g.*, by assaying polypeptide levels using antibodies elicited in response to amino acid sequences shown in Table 1) or indirectly (*e.g.*, by assaying for antibodies having specificity for amino acid sequences shown in Table 1). An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Borrelia* nucleic acid sequences.

The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence shown in Table 1 which are capable of hybridizing under stringent conditions to *Borrelia* nucleic acids. The invention further relates to a method of detecting one or more *Borrelia* nucleic acids in a biological sample obtained from an animal, said one or more nucleic acids encoding *Borrelia* polypeptides, comprising:

- a) contacting the sample with one or more of the above-described nucleic acid probes, under conditions such that hybridization occurs, and
- b) detecting hybridization of said one or more probes to the *Borrelia* nucleic acid present in the biological sample.

### Detailed Description

The present invention relates to recombinant antigenic *B. burgdorferi* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological protection to disease caused by members of the genus *Borrelia*. The invention further relates to nucleic acid sequences which encode antigenic *B. burgdorferi* polypeptides and to methods for detecting *Borrelia* nucleic acids and polypeptides in biological samples. The invention also relates to *Borrelia* specific antibodies and methods for detecting such antibodies produced in a host animal.

### Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (*e.g.*, a secondary infection). Further included are species and strains of the genus *Borrelia* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Borrelia*" means any species or strain of bacteria which is members of the genus *Borrelia*. Included within this definition are *Borrelia burgdorferi* sensu lato (including *B. burgdorferi* sensu stricto, *B. afzelii*, *B. garinii*), *B. andersonii*, *B. anserina*, *B. japonica*, *B. coriaceae*, and other members of the genus *Borrelia* regardless of whether they are known pathogenic agents.

As used herein, the phrase "one or more *B. burgdorferi* polypeptides of the present invention" means the amino acid sequence of one or more of the *B. burgdorferi* polypeptides disclosed in Table 1. These polypeptides may be expressed as fusion proteins wherein the *B. burgdorferi* polypeptides of the present invention are linked to additional amino acid sequences which may be of borrelial or non-borrelial origin. This phrase further includes fragments of the *B. burgdorferi* polypeptides of the present invention.

As used herein, the phrase "full-length amino acid sequence" and "full-length polypeptide" refer to an amino acid sequence or polypeptide encoded by a full-length open reading frame (ORF). An ORF may be defined as a nucleotide sequence bounded by stop codons which encodes a putative polypeptide. An ORF may also be defined as a nucleotide sequence within a stop codon bounded sequence which contains an initiation codon (*e.g.*, a methionine or valine codon) on the 5' end and a stop codon on the 3' end.

As used herein, the phrase "truncated amino acid sequence" and "truncated polypeptide" refer to a sub-sequence of a full-length amino acid sequence or polypeptide. Several criteria may also be used to define the truncated amino acid sequence or polypeptide. For example, a truncated polypeptide may be defined as a mature polypeptide (*e.g.*, a polypeptide which lacks a leader sequence). A truncated polypeptide may also be defined as an amino acid sequence which is a portion of a longer sequence that has been selected for ease of expression in a heterologous system but retains regions which render the polypeptide useful for use in vaccines (*e.g.*, antigenic regions which are expected to elicit a protective immune response).

Additional definitions are provided throughout the specification.

#### ***Explanation of Table 1***

Table 1 lists *B. burgdorferi* nucleotide and amino acid sequences of the present invention. The nomenclature used therein is as follows:

"nt" refers to nucleotide sequences;

"aa" refers to amino acid sequences;

"f" refers to full-length nucleotide or amino acid sequences; and

"t" refers to truncated nucleotide or amino acid sequences.

Thus, for example, the designation "f101.aa" refers to the full-length amino acid sequence of *B. burgdorferi* polypeptide number 101. Further, "f101.nt" refers to the full-length nucleotide sequence encoding the full-length amino acid sequence of *B. burgdorferi* polypeptide number 101.

***Explanation of Table 2***

Table 2 lists accession numbers for the closest matching sequences between the polypeptides of the present invention and those available through GenBank and GeneSeq databases. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familiar with their denominations. The descriptions of the nomenclature for GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or GeneSeq databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and GeneSeq are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and GeneSeq are represented more than once.

***Explanation of Table 3.***

The *B. burgdorferi* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

***Explanation of Table 4***

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full length *B. burgdorferi* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *B. burgdorferi* polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

### ***Selection of Nucleic Acid Sequences Encoding Antigenic B. burgdorferi Polypeptides***

The present invention provides a select number of ORFs from those presented in the fragments of the *Borrelia burgdorferi* genome which may prove useful for the generation of a protective immune response. The sequenced *B. burgdorferi* genomic DNA was obtained from a sub-cultured isolate of ATCC Deposit No. 35210. The sub-cultured isolate was deposited on August 8, 1997 at the American Type Culture Collection, 12301 Park Lawn Drive, Rockville, Maryland 20852, and given accession number 202012.

Some ORFs contained in the subset of fragments of the *B. burgdorferi* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are generally bounded at the amino terminus by a methionine residue and at the carboxy terminus by a stop codon.

Many of the selected sequences do not consist of complete ORFs. Although a polypeptide representing a complete ORF may be the closest approximation of a protein native to an organism, it is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for *in vitro* expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening all theoretical *Borrelia burgdorferi* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence*: An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol.* 13:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence*: The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed

above. Although functionally related, the type IV<sup>9</sup> signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoprotein*: Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C., *J. Bioenerg. Biomembr.* 22:451-471 (1990)).

4. *LPXTG motif*: It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *B. burgdorferi*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A., *ASM News* 62:405-410 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.

An algorithm for selecting antigenic and immunogenic *Borrelia burgdorferi* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application 08/781,986, filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to select immunologically useful *Borrelia burgdorferi* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

### ***Nucleic Acid Molecules***

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding the *B. burgdorferi* polypeptides having the amino acid sequences shown in Table 1, which were determined by sequencing the genome of *B. burgdorferi* deposited as ATCC deposit no. 202012 and selected as putative immunogens.

Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc.), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of DNA sequences determined as

10

above. Therefore, as is known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion.

Unless otherwise indicated, each "nucleotide sequence" set forth herein is presented as a sequence of deoxyribonucleotides (abbreviated A, G, C and T). However, by "nucleotide sequence" of a nucleic acid molecule or polynucleotide is intended, for a DNA molecule or polynucleotide, a sequence of deoxyribonucleotides, and for an RNA molecule or polynucleotide, the corresponding sequence of ribonucleotides (A, G, C and U), where each thymidine deoxyribonucleotide (T) in the specified deoxyribonucleotide sequence is replaced by the ribonucleotide uridine (U). For instance, reference to an RNA molecule having a sequence of Table 1 set forth using deoxyribonucleotide abbreviations is intended to indicate an RNA molecule having a sequence in which each deoxyribonucleotide A, G or C of Table 1 has been replaced by the corresponding ribonucleotide A, G or C, and each deoxyribonucleotide T has been replaced by a ribonucleotide U.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *B. burgdorferi* polypeptides and peptides of the present invention (e.g. polypeptides of Table 1). That is, all possible DNA sequences that encode



the *B. burgdorferi* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *B. burgdorferi* in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1 at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. "At least" means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1 or of the *B. burgdorferi* nucleotide sequences of the plasmid clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *B. burgdorferi* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of

Table 1 or the plasmid clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasmid clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

Preferred nucleic acid fragments of the present invention also include nucleic acid molecules encoding epitope-bearing portions of the *B. burgdorferi* polypeptides shown in Table 1. Such nucleic acid fragments of the present invention include, for example, nucleic acid molecules encoding polypeptide fragments comprising from about the amino terminal residue to about the carboxy terminal residue of each fragment shown in Table 4. The above referred to polypeptide fragments are antigenic regions of particular *B. burgdorferi* polypeptides shown in Table 1. Methods for determining other such epitope-bearing portions for the remaining polypeptides described in Table 1 are well known in the art and are described in detail below.

In another aspect, the invention provides isolated nucleic acid molecules comprising polynucleotides which hybridize under stringent hybridization conditions to a portion of a polynucleotide in a nucleic acid molecule of the invention described above, for instance, a nucleic acid sequence shown in Table 1. By "stringent hybridization conditions" is intended overnight incubation at 42 C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 g/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 C.

By polynucleotides which hybridize to a "portion" of a polynucleotide is intended polynucleotides (either DNA or RNA) which hybridize to at least about 15 nucleotides (nt), and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably about 30-70 nt of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above and in more detail below.

Of course, polynucleotides hybridizing to a larger portion of the reference polynucleotide, for instance, a portion 50-100 nt in length, or even to the entire length of the reference polynucleotide, are also useful as probes according to the present invention, as are polynucleotides corresponding to most, if not all, of a nucleotide sequence as shown in Table 1. By a portion of a polynucleotide of "at least 20 nt in length," for example, is intended 20 or more contiguous nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., a nucleotide sequences as shown in Table 1). As noted above, such portions are useful diagnostically either as probes according to conventional DNA hybridization techniques or as primers for amplification of a target sequence by PCR, as described, for instance, in *Molecular Cloning, A Laboratory Manual*, 2nd. edition, Sambrook, J., Fritsch, E. F. and Maniatis, T., eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989), the entire disclosure of which is hereby incorporated herein by reference.

Since nucleic acid sequences encoding the *B. burgdorferi* polypeptides of the present invention are provided in Table 1, generating polynucleotides which hybridize to portions of these sequences would be routine to the skilled artisan. For example, the hybridizing polynucleotides

of the present invention could be generated synthetically according to known techniques.

As indicated, nucleic acid molecules of the present invention which encode *B. burgdorferi* polypeptides of the present invention may include, but are not limited to those encoding the amino acid sequences of the polypeptides by themselves; and additional coding sequences which code for additional amino acids, such as those which provide additional functionalities. Thus, the sequences encoding these polypeptides may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (Qiagen, Inc.), among others, many of which are commercially available. As described in Gentz *et al.*, *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the resulting fusion protein.

Thus, the present invention also includes genetic fusions wherein the *B. burgdorferi* nucleic acid sequences coding sequences provided in Table 1 are linked to additional nucleic acid sequences to produce fusion proteins. These fusion proteins may include epitopes of borrelial or non-borrelial origin designed to produce proteins having enhanced immunogenicity. Further, the fusion proteins of the present invention may contain antigenic determinants known to provide helper T-cell stimulation, peptides encoding sites for post-translational modifications which enhance immunogenicity (*e.g.*, acylation), peptides which facilitate purification (*e.g.*, histidine "tag"), or amino acid sequences which target the fusion protein to a desired location (*e.g.*, a heterologous leader sequence). For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz *et al.* (1989) *Proc. Natl. Acad. Sci.* 86:821-24. The "HA" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin protein. See Wilson *et al.* (1984) *Cell* 37:767. As discussed below, other such fusion proteins include the *B. burgdorferi* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Post-translational modification of the full-length *B. burgdorferi* OspA protein expressed in *E. coli* is believed to increase the immunogenicity of this protein. Erdile, L. *et al.*, *Infect. Immun.* 61:81-90 (1993). *B. burgdorferi* OspA when expressed in *E. coli*, for example, is post-translationally modified in at least two ways. First, a signal peptide is cleaved; second, lipid moieties are attached. The presence of these lipid moieties is believed to confer enhanced immunogenicity and results in the elicitation of a strong protective immunological response.

#### ***Variant and Mutant Polynucleotides***

The present invention thus includes nucleic acid molecules and sequences which encode fusion proteins comprising one or more *B. burgdorferi* polypeptides of the present invention fused to an amino acid sequence which allows for post-translational modification to enhance immunogenicity. This post-translational modification may occur either *in vitro* or when the fusion protein is expressed *in vivo* in a host cell. An example of such a modification is the introduction

of an amino acid sequence which results in the attachment of a lipid moiety. Such a lipid moiety attachment site of OspA, which is lipidated upon expression in *E. coli*, has been identified.

Bouchon, B. *et al.*, *Anal. Biochem.* 246:52-61 (1997).

Thus, as indicated above, the present invention includes genetic fusions wherein a *B. burgdorferi* nucleic acid sequence provided in Table 1 is linked to a nucleotide sequence encoding another amino acid sequence. These other amino acid sequences may be of borreliar origin (*e.g.*, another sequence selected from Table 1) or non-borreliar origin. An example of such a fusion protein is reported in Fikrig, E. *et al.*, *Science* 250:553-556 (1990) where an OspA-glutathione-S-transferase fusion protein was produced and shown to elicit protective immunity against Lyme disease in immune competent mice.

The present invention further relates to variants of the nucleic acid molecules of the present invention, which encode portions, analogs or derivatives of the *B. burgdorferi* polypeptides shown in Table 1. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such variants include those produced by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. These variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *B. burgdorferi* polypeptides disclosed herein or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *B. burgdorferi* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *B. burgdorferi* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *B. burgdorferi* activity include, *inter alia*, isolating an *B. burgdorferi* gene or allelic variants thereof from a DNA library, and detecting *B. burgdorferi* mRNA expression samples, environmental samples, suspected of containing *B. burgdorferi* by Northern Blot analysis.

Embodiments of the invention include isolated nucleic acid molecules comprising a polynucleotide having a nucleotide sequence at least 90% identical, and more preferably at least 95%, 96%, 97%, 98% or 99% identical to (a) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the full-length polypeptides shown in Table 1 but minus the N-terminal methionine residue, if present; (c) a nucleotide sequence encoding any of the

amino acid sequences of the truncated polypeptides shown in Table 1; and (d) a nucleotide sequence complementary to any of the nucleotide sequences in (a), (b), or (c) above.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *B. burgdorferi* protein activity. By "a polypeptide having *B. burgdorferi* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *B. burgdorferi* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *B. burgdorferi* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *B. burgdorferi* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genres, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *B. burgdorferi* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% (5 of 100) of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention)

and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) *Comp. App. Biosci.* 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's.

5 The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

10 If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query  
15 sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present  
20 invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence  
25 and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In  
30 another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are  
35 manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

### ***Vectors and Host Cells***

The present invention also relates to vectors which include the isolated DNA molecules of

the present invention, host cells which are genetically engineered with the recombinant vectors, and the production of *B. burgdorferi* polypeptides or fragments thereof by recombinant techniques.

Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line and then transduced into host cells.

Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

Expression vectors useful in the present invention include chromosomal-, episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*, *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the

above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A available from Stratagene; pET series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals, such as Davis *et al.*, *Basic Methods In Molecular Biology* (1986).

Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 bp that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of the replication origin at bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment, appropriate secretion signals may be incorporated into the expressed polypeptide. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian



counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL-5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See Bennett, D. *et al.*, *J. Molec. Recogn.* 8:52-58 (1995) and Johanson, K. *et al.*, *J. Biol. Chem.* 270 (16):9459-9471 (1995).

The *B. burgdorferi* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

### ***Polypeptides and Fragments***

The invention further provides isolated polypeptides having the amino acid sequences in Table 1, and peptides or polypeptides comprising portions of the above polypeptides. The terms "peptide" and "oligopeptide" are considered synonymous (as is commonly recognized) and each term can be used interchangeably as the context requires to indicate a chain of at least to amino acids coupled by peptidyl linkages. The word "polypeptide" is used herein for chains containing more than ten amino acid residues. All oligopeptide and polypeptide formulas or sequences herein are written from left to right and in the direction from amino terminus to carboxy terminus.

As discussed in detail below, immunization using *B. burgdorferi* sensu stricto isolate B31 decorin-binding protein elicits the production of antiserum which confers passive immunity against *Borrelia* species and strains which express divergent forms of this protein. Cassatt, D. *et al.*, *Protection of Borrelia burgdorferi Infection by Antibodies to Decorin-binding Protein*, in VACCINES97, Cold Spring Harbor Press (1997), pages 191-195. Thus, some amino acid sequences of the *B. burgdorferi* polypeptides shown in Table 1 can be varied without significantly effecting the antigenicity of the polypeptides. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the polypeptide which determine antigenicity. In general, it is possible to replace residues which do not form part of an

antigenic epitope without significantly effecting the antigenicity of a polypeptide.

### ***Variant and Mutant Polypeptides***

To improve or alter the characteristics of *B. burgdorferi* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

### ***N-Terminal and C-Terminal Deletion Mutants***

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *B. burgdorferi* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein *See, e.g.,* Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of the *B. burgdorferi* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid in length, are selected from any two integers, one of which representing a N-terminal position. The initiation codon of the polypeptides of the present inventions position 1. Every combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given amino acid sequence of Table 1 is included in the invention. At least means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in a full length amino acid sequence minus 1. Therefore, included in the invention are contiguous fragments specified by any N-terminal and C-terminal positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in

amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in a full length sequence minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

#### ***Other Mutants***

In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *B. burgdorferi* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated, it should be remembered that there will be critical areas on the protein which determine activity.

Thus, the invention further includes variations of the *B. burgdorferi* polypeptides which show substantial *B. burgdorferi* polypeptide activity or which include regions of *B. burgdorferi* protein such as the protein portions discussed below. Such mutants include deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. See, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

These studies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by Bowie *et al.* (*supra*) and the references cited

therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plasmids listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code: or (ii) one in which one or more of the amino acid residues includes a substituent group: or (iii) one in which the *B. burgdorferi* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol): or (iv) one in which the additional amino acids are fused to the above form of the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *B. burgdorferi* polypeptides of the present invention may include one or more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *B. burgdorferi* proteins of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. See, e.g., Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. See, e.g., Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *B. burgdorferi* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

The invention further provides for isolated *B. burgdorferi* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plasmids listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plasmids listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *B. burgdorferi* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *B. burgdorferi* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by the plasmids listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the

query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual corrections are to made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present

invention that do not have *B. burgdorferi* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *B. burgdorferi* protein expression or as agonists and antagonists capable of enhancing or inhibiting *B. burgdorferi* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *B. burgdorferi* protein binding proteins which are also candidate agonists and antagonists according to the present invention. *See, e.g.*, Fields et al. (1989) Nature 340:245-246.

### ***Epitope-Bearing Portions***

In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *B. burgdorferi* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. *See, e.g.*, Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002. Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other antigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. *See, e.g.*, Sutcliffe, et al., (1983) Science 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the

mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. See, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. See Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger peptides in immunoprecipitation assays. See, *e.g.*, Wilson, et al., (1984) Cell 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (*i.e.* any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used to generate an *Borrelia*-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present inventions provides for isolated and purified antigenic epitope-bearing fragments of the polypeptides of the present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a



sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4.

Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing fragments may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragments of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragments of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. 82:5131-5135 at 5134).

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. See, e.g., Sutcliffe, et al., *supra*; Wilson, et al., *supra*; and Bittle, et al. (1985) J. Gen. Virol. 66:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or

carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of  
5 anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid  
10 concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located  
15 by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide analogs of the  
20 epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which  
25 is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989), describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971  
30 to Houghten, R. A. *et al.* (1996) discloses linear C<sub>1</sub>-C<sub>7</sub>-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this  
35 section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for

chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Traunecker et al. (1988) Nature 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *B. burgdorferi* polypeptide or fragment thereof alone. See Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *B. burgdorferi* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

## 10 **Antibodies**

*B. burgdorferi* protein-specific antibodies for use in the present invention can be raised against the intact *B. burgdorferi* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

15 As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')<sub>2</sub> and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *B. burgdorferi* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')<sub>2</sub> fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')<sub>2</sub> fragments). Alternatively, *B. burgdorferi* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that,

therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *B. burgdorferi* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *B. burgdorferi* polypeptide-specific antibody can be blocked by the *B. burgdorferi* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *B. burgdorferi* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *B. burgdorferi* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above., i.e. by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies the specifically bind a particularlly discribed fragment of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Borrelia* other than *B. burgdorferi* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Borrelia*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Borrelia*, are included in the present invention.

### Diagnostic Assays

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Borrelia*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Borrelia* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, e.g., Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Borrelia* has already been made, the present invention is useful for monitoring progression or regression of the disease state

whereby patients exhibiting enhanced *Borrelia* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Borrelia* polypeptide, mRNA, or DNA.

5 Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Borrelia* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Borrelia* infections in  
10 animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Borrelia* polypeptides having sufficient  
15 homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

20 Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter  
25 is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium phosphate buffer. A *B. burgdorferi* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the <sup>32</sup>P-multiprimered DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in  
30 the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *B. burgdorferi* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate  
35 further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (i.e., mRNA encoding *Borrelia* polypeptides).

Levels of mRNA encoding *Borrelia* polypeptides are assayed, for e.g., using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial

concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Borrelia* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or *Borrelia* species including *B. burgdorferi* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm<sup>2</sup>) and low density chip arrays (<1000 oligonucleotides per cm<sup>2</sup>). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect *Borrelia* species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other *Borrelia* infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *B. burgdorferi* or other *Borrelia* infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragments, i.e., by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect *Borrelia* species, including *B. burgdorferi*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *B. burgdorferi* or other *Borrelia* species and infections thereof.

Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect *Borrelia* species, including *B. burgdorferi*, using biosensors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Borrelia* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Borrelia* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Borrelia* polypeptides for Western-blot or dot/slot assay. *See, e.g.*, Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Borrelia* polypeptide can be accomplished using an isolated *Borrelia* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Borrelia* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Borrelia* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Borrelia* polypeptide. The amount of a *Borrelia* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Borrelia* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Borrelia* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above

and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include radioisotopes, such as iodine ( $^{125}\text{I}$ ,  $^{121}\text{I}$ ), carbon ( $^{14}\text{C}$ ), sulphur ( $^{35}\text{S}$ ), tritium ( $^3\text{H}$ ), indium ( $^{112}\text{In}$ ), and technetium ( $^{99\text{m}}\text{Tc}$ ), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Borrelia* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, *Borrelia* nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include  $^3\text{H}$ ,  $^{111}\text{In}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ ,  $^{51}\text{Cr}$ ,  $^{57}\text{To}$ ,  $^{58}\text{Co}$ ,  $^{59}\text{Fe}$ ,  $^{75}\text{Se}$ ,  $^{152}\text{Eu}$ ,  $^{90}\text{Y}$ ,  $^{67}\text{Cu}$ ,  $^{217}\text{Cl}$ ,  $^{211}\text{At}$ ,  $^{212}\text{Pb}$ ,  $^{47}\text{Sc}$ ,  $^{109}\text{Pd}$ , etc.  $^{111}\text{In}$  is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the  $^{125}\text{I}$  or  $^{131}\text{I}$ -labeled monoclonal antibody by the liver. In addition, this radionucleotide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example,  $^{111}\text{In}$  coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include  $^{157}\text{Gd}$ ,  $^{55}\text{Mn}$ ,  $^{162}\text{Dy}$ ,  $^{52}\text{Tr}$ , and  $^{56}\text{Fe}$ .

Examples of suitable fluorescent labels include an  $^{152}\text{Eu}$  label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by



Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

5 In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *B. burgdorferi* infection. Such a kit may include an isolated *B. burgdorferi* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*B. burgdorferi* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific embodiments, the kit may include a  
10 recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the  
15 antibody to the *B. burgdorferi* antigen can be detected by binding of the reporter labeled antibody to the anti-*B. burgdorferi* polypeptide antibody.

In a related aspect, the invention includes a method of detecting *B. burgdorferi* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *B. burgdorferi* antigen, and examining the antigen for the presence of  
20 bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known  
25 techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in  
30 conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Borrelia species including *B. burgdorferi* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Borrelia species, including  
35 *B. burgdorferi*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Borrelia species, including *B. burgdorferi* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Borrelia species, including *B. burgdorferi*, in biological and environmental samples and to

diagnose an animal, including humans, with an *B. burgdorferi* or other Borrelia infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *B. burgdorferi* or other Borrelia infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragments, i.e., by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Borrelia species, including *B. burgdorferi*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

#### ***Treatment:***

##### ***Agonists and Antagonists - Assays and Molecules***

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *B. burgdorferi* polypeptides of the present invention. The present invention further provides where the compounds kill or slow the growth of *B. burgdorferi*. The ability of *B. burgdorferi* antagonists, including *B. burgdorferi* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. See, e.g., Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross bridge

formation. Antibodies against *B. burgdorferi* may be employed to bind to and inhibit *B. burgdorferi* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

## 5 **Vaccines**

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *B. burgdorferi* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be more effective in eliciting protective immune responses against multiple species and strains of the *Borrelia* genus than single polypeptide vaccines. Thus, as discussed in detail below, a multi-component vaccine of the present invention may contain one or more, preferably 2 to about 20, more preferably 2 to about 15, and most preferably 3 to about 8, of the *B. burgdorferi* polypeptides shown in Table 1, or fragments thereof.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. Decker, M. and Edwards, K., *J. Infect. Dis.* 174:S270-275 (1996). In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. Aristegui, J. *et al.*, *Vaccine* 15:7-9 (1997).

The present invention thus also includes multi-component vaccines. These vaccines comprise more than one polypeptide, immunogen or antigen. An example of such a multi-component vaccine would be a vaccine comprising more than one of the *B. burgdorferi* polypeptides shown in Table 1. A second example is a vaccine comprising one or more, for example 2 to 10, of the *B. burgdorferi* polypeptides shown in Table 1 and one or more, for example 2 to 10, additional polypeptides of either borreliar or non-borreliar origin. Thus, a multi-component vaccine which confers protective immunity to both a borreliar infection and infection by another pathogenic agent is also within the scope of the invention.

As indicated above, the vaccines of the present invention are expected to elicit a protective immune response against infections caused by species and strains of *Borrelia* other than *B. burgdorferi* sensu stricto isolate B31 (ATCC Accession No. 35210). Immunizations using decorin-binding protein and OspA derived from one strain of *B. burgdorferi* has been shown to elicit the production of antiserum which confers passive immunity against other strains of *B. burgdorferi*. Cassatt, D. *et al.*, *Protection of Borrelia burgdorferi Infection by Antibodies to Decorin-binding Protein*, in VACCINES97, Cold Spring Harbor Press (1997), pages 191-195. Further, the inventors have found using an *in vitro* assay that antiserum produced in response to *B. burgdorferi* decorin-binding protein will kill several species of *Borrelia*. The amino acid sequences of decorin-binding protein expressed by different strains of *B. burgdorferi* are believed to diverge by as much as 25%. Thus, antisera elicited against decorin-binding proteins confers passive immunity against *Borrelia* expressing proteins having only 75% or less amino acid sequence similarity.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *B. burgdorferi* polypeptides shown in Table 1. For example, the *B. burgdorferi* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *B. burgdorferi* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing heterologous proteins are known in the art. See, e.g., Robinson, K. *et al.*, *Nature Biotech.* 15:653-657 (1997); Sirard, J. *et al.*, *Infect. Immun.* 65:2029-2033 (1997); Chabalgoity, J. *et al.*, *Infect. Immun.* 65:2402-2412 (1997). These cells may be administered live or may be killed prior to administration. Chabalgoity, J. *et al.*, *supra*, for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *B. burgdorferi* polypeptides of the present invention, or fragments thereof, with additional non-borrelial components (e.g., diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Borrelia* genus and non-borrelial pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA vaccines are currently being developed for a number of infectious diseases. Boyer, J *et al.*, *Nat. Med.* 3:526-532 (1997); reviewed in Spier, R., *Vaccine* 14:1285-1288 (1996). Such DNA vaccines contain a nucleotide sequence encoding one or more *B. burgdorferi* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. The direct administration of plasmid DNA encoding OspA has been shown to elicit protective immunity in mice against borrelial challenge. Luke, C. *et al.*, *J. Infect. Dis.* 175:91-97 (1997).

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim, J. *et al.*, *Nature Biotech.* 15:641-646 (1997), for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves. These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to borrelial infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to borrelial infection through active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a borrelial infection. When the vaccines of the present invention are used to

confer resistance to borrelial infection through passive immunization, the vaccine is provided to a host animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Borrelia* genus.

5       The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating borrelial infections when passive immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *B. burgdorferi* polypeptides disclosed herein, or fragments thereof, as well as other *Borrelia* proteins, are labeled with toxin molecules prior to their administration to the patient. When such  
10       toxin derivatized antibodies bind to *Borrelia* cells, toxin moieties will be localized to these cells and will cause their death.

      The present invention thus concerns and provides a means for preventing or attenuating a borrelial infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a  
15       vaccine is said to prevent or attenuate a disease if its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

      The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compound(s) are  
20       provided in advance of any symptoms of borrelial infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Borrelia* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the  
25       *B. burgdorferi* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

      The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a  
30       macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow *et al.*, *Antibodies:*  
35       *A Laboratory Manual, 2nd Ed.*; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1988), the entire disclosure of which is incorporated by reference herein.

      A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered

is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *B. burgdorferi* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and incomplete), mineral salts (for example,  $\text{AlK}(\text{SO}_4)_2$ ,  $\text{AlNa}(\text{SO}_4)_2$ ,  $\text{AlNH}_4(\text{SO}_4)$ , silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*). Other substances useful as adjuvants are the saponins such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as  $\text{AlK}(\text{SO}_4)_2$ ,  $\text{AlNa}(\text{SO}_4)_2$ , and  $\text{AlNH}_4(\text{SO}_4)$ . Examples of materials suitable for use in vaccine compositions are provided in *Remington's Pharmaceutical Sciences* (Osol, A, Ed, Mack Publishing Co, Easton, PA, pp. 1324-1341 (1980), which reference is incorporated herein by reference).

The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharyngeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents

commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization of mice against *Bordetella pertussis* infection using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide) has been shown to stimulate protective immune responses. Shahin, R. *et al.*, *Infect. Immun.* 63:1195-1200 (1995). Similarly, orally administered encapsulated *Salmonella typhimurium* antigens have also been shown to elicit protective immunity in mice. Allaoui-Attarki, K. *et al.*, *Infect. Immun.* 65:853-857 (1997). Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000  $\mu\text{g/ml}$  per dose, more preferably 0.1-500  $\mu\text{g/ml}$  per dose, and most preferably 10-300  $\mu\text{g/ml}$  per dose.

Having now generally described the invention, the same will be more readily understood through reference to the following example which is provided by way of illustration, and is not intended to be limiting of the present invention, unless specified.

## Examples

### 1. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Borrelia burgdorferi* genome, such as those of Table 1, can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and

amplified DNA of this Example find use in the Examples that follow.

## 2. Isolation of a Selected DNA Clone From *B. burgdorferi*

Three approaches are used to isolate a *B. burgdorferi* clone comprising a polynucleotide of the present invention from any *B. burgdorferi* genomic DNA library. The *B. burgdorferi* strain B31PU has been deposited as a convenient source for obtaining a *B. burgdorferi* strain although a wide variety of strains *B. burgdorferi* strains can be used which are known in the art.

*B. burgdorferi* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *B. burgdorferi* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with  $^{32}\text{P}$ - $\gamma$ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN



MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *B. burgdorferi* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25  $\mu$ l of reaction mixture with 0.5  $\mu$ g of the above DNA template. A convenient reaction mixture is 1.5-5 mM  $MgCl_2$ , 0.01% (w/v) gelatin, 20  $\mu$ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

### 3(a). Expression and Purification *Borrelia* polypeptides in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression of some of the polypeptide fragments of the present invention. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Amp<sup>r</sup>") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *B. burgdorferi* protein of the present invention is amplified from *B. burgdorferi* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *B. burgdorferi* polynucleotide shown in Table 1. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *B. burgdorferi* polynucleotide sequence in Table 1. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site

followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *B. burgdorferi* DNA fragment and the vector pQE60 are digested with restriction enzymes which recognize the sites in the primers and the digested DNAs are then ligated together. The *B. burgdorferi* DNA is inserted into the restricted pQE60 vector in a manner which places the *B. burgdorferi* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing a *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity are purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *B. burgdorferi* polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over

a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

The polypeptide of the present invention are also prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture is resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm is approximately 10-20 O.D./ml. The suspension is then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells are lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample is then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant is passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction is collected.

The pre-cleared flow-through is applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant is loaded onto the column in Lysis Buffer A at 4°C, the column is first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column is washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein is eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations are used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein are analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein is then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein is stored at 4°C or frozen at -80°.

The following alternative method may be used to purify *B. burgdorferi* expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

### 3(b). *Alternative Expression and Purification Borrelia polypeptides in E.*

*coli*

The vector pQE10 is alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *B. burgdorferi* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *B. burgdorferi* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences of Table 1 encoding amino acid sequences may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

### **3(c). *Alternative Expression and Purification of Borrelia polypeptides in E. coli***

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *B. burgdorferi* amino acid sequence is amplified from an *B. burgdorferi* genomic DNA prep the deposited DNA clones

using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *B. burgdorferi* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

5 For cloning a *B. burgdorferi* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by  
10 nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

The amplified *B. burgdorferi* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *B. burgdorferi* DNA into the restricted pQE60 vector places the *B.*  
15 *burgdorferi* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance  
20 ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant  
25 colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells  
30 are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *B. burgdorferi* polypeptide, the cells are then stirred for 3-4 hours at 4°C in  
35 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease

inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *B. burgdorferi* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

5 The following alternative method may be used to purify *B. burgdorferi* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus  
10 Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer (Microfluidics,  
15 Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride  
20 (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles, the  
GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of  
25 buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared  
tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area  
30 (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

35 Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20,

Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant  $A_{280}$  monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5  $\mu$ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

### 3(d). Cloning and Expression of *B. burgdorferi* in Other Bacteria

*B. burgdorferi* polypeptides can also be produced in: *B. burgdorferi* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

### 4. Cloning and Expression in COS Cells

A *B. burgdorferi* expression plasmid is made by cloning a portion of the DNA encoding a *B. burgdorferi* polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *B. burgdorferi* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *B. burgdorferi* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for



construction of vectors for expression of *B. burgdorferi* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* DNA, a stop codon, and a convenient restriction site.

5 The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and  
10 examined by restriction analysis or other means for the presence of the fragment encoding the *B. burgdorferi* polypeptide

For expression of a recombinant *B. burgdorferi* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *B.*  
15 *burgdorferi* by the vector.

Expression of the *B. burgdorferi*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing <sup>35</sup>S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed  
20 with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

## 25 5. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *B. burgdorferi* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese  
30 hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing  
35 concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may

be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s).

Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse  
5 Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol.  
5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human  
cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter  
are the following single restriction enzyme cleavage sites that allow the integration of the genes:  
*Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and  
10 polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be  
used for the expression, e.g., the human  $\beta$ -actin promoter, the SV40 early or late promoters or the  
long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-  
On gene expression systems and similar systems can be used to express the *B. burgdorferi*  
polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci.  
15 USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human  
growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest  
integrated into the chromosomes can also be selected upon co-transfection with a selectable  
marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable  
marker in the beginning, e.g., G418 plus methotrexate.

20 The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated  
using calf intestinal phosphates by procedures known in the art. The vector is then isolated from  
a 1% agarose gel. The DNA sequence encoding the *B. burgdorferi* polypeptide is amplified using  
PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of  
the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and  
25 nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide is synthesized and used. A  
3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3'  
coding sequence of the *B. burgdorferi* polypeptides is synthesized and used. The amplified  
fragment is digested with the restriction endonucleases and then purified again on a 1% agarose  
gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase.  
30 *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the  
fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five  
 $\mu$ g of the expression plasmid pC4 is cotransfected with 0.5  $\mu$ g of the plasmid pSVneo using a  
lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE™ (LifeTechnologies  
35 Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene  
from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418.  
The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the  
cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus

MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1  $\mu$ M, 2  $\mu$ M, 5  $\mu$ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200  $\mu$ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

## 6. Immunization and Detection of Immune Responses

### 6(a). *B. burgdorferi* propagation

*B. burgdorferi* sensu stricto isolate B31 is propagated in tightly-closed containers at 34°C in modified Barbour-Stoenner-Kelly (BSKII) medium (Barbour, A.G., *Yale J. Biol. Med.* 57:521-525 (1984)) overlaid with a 5%O<sub>2</sub>/5%CO<sub>2</sub>/90%N<sub>2</sub> gas mixture. Cell densities of these cultures are determined by darkfield microscopy at 400X.

*Immunization of Mice and Challenge with B. burgdorferi.* For active immunizations BALB/cByJ mice (BALB, Jackson Laboratories) are injected intraperitoneally (i.p.) at week 0 with 20 g of recombinant borrelial protein, or phosphate-buffered saline (PBS), emulsified with complete Freund's adjuvant (CFA), given a similar booster immunization in incomplete Freund's adjuvant (IFA) at week 4, and challenged at week 6. For challenge *B. burgdorferi* are diluted in BSKII from exponentially-growing cultures and mice are injected subcutaneously (s.c.) at the base of the tail with 0.1 ml of these dilutions (typically 10<sup>3</sup>-10<sup>4</sup> borreliae; approximately 10-100 times the median infectious dose). Borreliae used for challenge are passaged fewer than six times *in vitro*. To assess infection, mice are sacrificed at 14-17 days post-challenge, and specimens derived from ear, bladder, and tibiotarsal joints are placed in BSKII plus 1.4% gelatin, 13 g/ml amphotericin B, 1.5 g/ml phosphomycin, and 15 g/ml rifampicin, and borrelia outgrowth at two or three weeks is quantified by darkfield microscopy. Batches of BSKII are qualified for infection testing by confirming that they supported the growth of 1-5 cells of isolate B31. In some instances seroconversion for protein P39 reactivity is also used to confirm infections (see below). Others have previously shown that mice elicited antibodies to P39 when inoculated with live borreliae by syringe or tick bite, but not with killed borreliae (Simpson, W.J., *et al.*, *J. Clin. Microbiol.* 29:236-243 (1991)).

### 6(b). Immunoassays

Several immunoassay formats are used to quantify levels of borrelia-specific antibodies (ELISA and immunoblot), and to evaluate the functional properties of these antibodies (growth inhibition assay). The ELISA and immunoblot assays are also used to detect and quantify antibodies elicited in response to borrelial infection that react with specific borrelial antigens. Where antibodies to certain borrelial antigens are elicited by infection this is taken as evidence that

the borrelial proteins in question are expressed *in vivo*. Absence of infection-derived antibodies (seroconversion) following borrelial challenge is evidence that infection is prevented or suppressed. The immunoblot assay is also used to ascertain whether antibodies raised against recombinant borrelial antigens recognize a protein of similar size in extracts of whole borreliae.

Where the natural protein is of similar, or identical, size in the immunoblot assay to the recombinant version of the same protein, this is taken as evidence that the recombinant protein is the product of a full-length clone of the respective gene.

**Enzyme-Linked Immunosorbant Assay (ELISA).** The ELISA is used to quantify levels of antibodies reactive with borrelial antigens elicited in response to immunization with these borrelial antigens. Wells of 96 well microtiter plates (Immunlon 4, Dynatech, Chantilly, Virginia, or equivalent) are coated with antigen by incubating 50  $\mu$ l of 1  $\mu$ g/ml protein antigen solution in a suitable buffer, typically 0.1 M sodium carbonate buffer at pH 9.6. After decanting unbound antigen, additional binding sites are blocked by incubating 100  $\mu$ l of 3% nonfat milk in wash buffer (PBS, 0.2% Tween 20, pH 7.4). After washing, duplicate serial two-fold dilutions of sera in PBS, Tween 20, 1% fetal bovine serum, are incubated for 1 hr, removed, wells are washed three times, and incubated with horseradish peroxidase-conjugated goat anti-mouse IgG. After three washes, bound antibodies are detected with  $H_2O_2$  and 2,2'-azino-di-(3-ethylbenzthiazoline sulfonate) (Schwan, T.G., *et al.*, *Proc. Natl. Acad. Sci. USA* 92:2909-2913 (1985)) (ABTS®, Kirkegaard & Perry Labs., Gaithersburg, MD) and  $A_{405}$  is quantified with a Molecular Devices, Corp. (Menlo Park, California) Vmax™ plate reader. IgG levels twice the background level in serum from naive mice are assigned the minimum titer of 1:100.

#### **6(c). *In Vitro* Growth Inhibition Assay**

Unlike other bacteria, borreliae can be killed by the binding of specific antibodies to their surface antigens. The mechanism for this *in vitro* killing or growth-inhibitory effect is not known, but can occur in the absence of serum complement, or other immune effector functions. Antibodies elicited in animals receiving immunizations with specific borrelial antigens that result in protection from borrelial challenge usually will directly kill borreliae *in vitro*. Thus, the *in vitro* growth inhibition assay also has a high predictive value for the protective potency of the borrelial antibodies, although exceptions, such as antibodies against OspC which are weak at *in vitro* growth inhibition, have been observed. Also, this assay can be used to evaluate the serologic conservation of epitope binding protective antibodies. A microwell antibody titration assay (Sadziene, A., *et al.*, *J. Infect. Dis.* 167:165-172 (1993)) is used to evaluate the growth inhibition (GI) properties of antisera against recombinant borrelial antigens against the homologous B31 isolate, and against various strains of borrelia. Briefly,  $10^5$  borrelia in 100  $\mu$ l BSKII are added to serial two-fold dilutions of sera in 100  $\mu$ l BSKII in 96-well plates, and the plates are covered and incubated at 34°C in a 5% $O_2$ /5% $CO_2$ /90% $N_2$  gas mixture for 72 h prior to quantification of borrelia growth by darkfield microscopy.

**6(d). Sodiumdodecylsulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) and Immunoblotting**

Using a single well format, total borrelial protein extracts, recombinant borrelial antigen, or recombinant P39 samples (2 g of purified protein, or more for total borrelial extracts) are boiled in SDS/2-ME sample buffer before electrophoresis through 3% acrylamide stacking gels, and resolving gels of higher acrylamide concentration, typically 10-15% acrylamide monomer. Gels are electro-blotted to nitrocellulose membranes and lanes are probed with dilutions of antibody to be tested for reactivity with specific borrelial antigens, followed by the appropriate secondary antibody-enzyme (horseradish peroxidase) conjugate. When it is desirable to confirm that the protein had transferred following electro-blotting, membranes are stained with Ponceau S. Immunoblot signals from bound antibodies are detected on x-ray film as chemiluminescence using ECL™ reagents (Amersham Corp., Arlington Heights, Illinois).

**6(e). Detection of *Borrelia* mRNA expression**

Northern blot analysis is carried out using methods described by, among others, Sambrook *et al.*, *supra*, to detect the expression of the *B. burgdorferi* nucleotide sequences of the present invention in animal tissues. A cDNA probe containing an entire nucleotide sequence shown in Table 1 is labeled with <sup>32</sup>P using the *rediprime*™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using a CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to detect the expression of *Borrelia* mRNA in an animal tissue sample.

Animal tissues, such as blood or spinal fluid, are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70 C overnight, and films developed according to standard procedures.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

Provisional Application Serial No. 60/057,483 filed 3 September 1997 is incorporated by reference herein in its entirety.

TABLE 1. Nucleotide and Amino Acid Sequences

f101.aa

MSKIFLLFNAGFFFLKIIYVFSYPEIKNFSRQDPVFSDLKIKVLKYNKKQHIPLFFYSYKVKKGDTFFKIAN KING  
WQSGIATINLLDSPAVSVGQEILIPSKKGVFVFDSDKYRFNNLLLATRDLAKAEKVKIKRNDRVYEFYFFDFVKNP  
DFGLFSGTELLFFLNANFIFPLKKFIVSSDFGFRNDPFTGNKSFHTGIDLAAPMNAEVYLLLLLE

t101.aa

SYPEIKNFSRQDPVFSDLKIKVLKYNKKQHIPLFFYSYKVKKGDTFFKIAN KINGWQSGIATINLLDSPAVSVGQE  
ILIPSKKGVFVFDSDKYRFNNLLLATRDLAKAEKVKIKRNDRVYEFYFFDFVKNPDFGLFSGTELLFFLNANFIFP  
LKKFIVSSDFGFRNDPFTGNKSFHTGIDLAAPMNAEVYLLLLLE

f101.nt

ATGAGTAAAATTTTTTTATTATTTAATGCAGGTTTCTTTTTTTTAAAAATAATTTATGTTTTTCTTATCCAGAAA  
TAAAAAATTTCTCAAGGCAAGATCCTGTTTTTTCTGATCTTAAATTAAGTTTTTAAATATAACAAAAACAACA  
TATTCCTCTGTTTTTTTACTCATATAAAGTTAAAAAGGGGATACTTTTTTTTAAATTTGCCAATAAAATAAATGGA  
TGGCAGTCCGGCATTGCTACTATTAATTTATTAGATTCTCCTGCTGTGAGTGTTGGGCAAGAGATTCTTATCCCA  
GTAAAAAAGGAGTTTTTGTTTTTGATAGTAAAGATTATAGATTTAATAATTTGCTTTTAGCAACAAGGGATCTTGC  
TAAAGCTGAAAAGGTAAAAATTAAAAGGAACGACAGAGTTTATGAATTTTATTTTTTTGATTTTGTTAAGAATCCA  
GATTTTGGACTTTTTTCAGGCACAGAATTGCTTTTTTTCTTAAATGCCAATTTTATTTTTTCCTTTAAAAAATTTA  
TTGTTAGTTCTGATTTTGGATTTAGAAATGACCCTTTCACTGGCAACAAAAGTTTCCATACAGGAATAGATCTTGC  
AGCTCCAATGAATGCTGAAGTGATCTTCTTCTTCTGGAATAG

t101.nt

TCTTATCCAGAAATAAAAAATTTCTCAAGGCAAGATCCTGTTTTTTCTGATCTTAAATTAAGTTTTTAAATATA  
ACAAAAACAACATATTCCTCTGTTTTTTTACTCATATAAAGTTAAAAAGGGGATACTTTTTTTTAAATTTGCCAA  
TAAATAAATGGATGGCAGTCCGGCATTGCTACTATTAATTTATTAGATTCTCCTGCTGTGAGTGTTGGGCAAGAG  
ATTCTTATTTCCAGTAAAAAAGGAGTTTTTGTTTTTGATAGTAAAGATTATAGATTTAATAATTTGCTTTTAGCAA  
CAAGGGATCTTGCTAAAGCTGAAAAGGTAAAAATTAAAAGGAACGACAGAGTTTATGAATTTTATTTTTTTGATTT  
TGTTAAGAATCCAGATTTTGGACTTTTTTCAGGCACAGAATTGCTTTTTTTCTTAAATGCCAATTTTATTTTTTCCT  
TTAAAAAATTTATTTGTTAGTTCTGATTTTGGATTTAGAAATGACCCTTTCACTGGCAACAAAAGTTTCCATACAG  
GAATAGATCTTGCAGCTCCAATGAATGCTGAAGTGATCTTCTTCTTCTGGAATAG

f11.aa

VKKYIKTIFLISMVYFYCCTTIKINHDYETDFKVLESPSKYINIDVIKATNEYIYIQITNNSLDVVKINWQNTSLN  
NDKIVLKKEDLTINNETGYKNKYREFFIGPKTSFKFKVYPLKIH SKNKNNSNLSSTIKYPSIFKLNITKVGIEAKK  
TINVLTITRTTKINITNK

t11.aa

CCTTIKINHDYETDFKVLESPSKYINIDVIKATNEYIYIQITNNSLDVVKINWQNTSLNNDKIVLKKEDLTINNET  
GYKNKYREFFIGPKTSFKFKVYPLKIH SKNKNNSNLSSTIKYPSIFKLNITKVGIEAKKTINVLTITRTTKINITNK

f11.nt

GTGGAAAAATTTCTTTTATTCCAGGAAATGAAAATATTGCAGATCTTGTTTTCATAAACTAAGTAGAAATATTG  
TCAAAAAATACATAAAAAACAATATTTCTGATTTCAATGGTTTATTTTTTATTGTTGTACGACAATAAAAAATAACCA  
TGATTATGAAACTGATTTTAAAGTTCTAGAATCTCCCTCTAAATACATCAATATAGATGTAATTAAAGCTACAAAT  
GAATATATTTATATTCAAATTACAAACAATAGCTTAGACGTAGTAAAAATAAATTTGGCAAAACACTAGTCTTAACA  
ACGATAAGATCGTCTTAAAAAAGAAGATCTTACAATAAACAATGAAACAGGGTATAAAAAATAAATACAGAGAGTT

TABLE 1. Nucleotide and Amino Acid Sequences

TTTTATTGGTCCTAAAACTTCATTTAAATTTAAAGTATATCCACTAAAAATTCATTCTAAAAACAAAAATAGCAAT  
AACTTAAGCTCAACTATTAAATATCCGTCTATTTTAAAGCTCAACATAACAAAAGTAGGAATTGAAGCAAAAAAAA  
CAATAAATGTTTTAATAACAAGAACTACAAAAATTAATATTACTAATAAATGA

t11.nt

TGTTGTACGACAATAAAAAATAAACCATGATTATGAAACTGATTTTAAAGTTCTAGAATCTCCCTCTAAATACATCA  
ATATAGATGTAATTAAAGCTACAAATGAATATATTTATATTCAAATTACAAACAATAGCTTAGACGTAGTAAAAAT  
AAATTGGCAAAACACTAGTCTTAACAACGATAAGATCGTCTTAAAAAAGAAGATCTTACAATAAACAATGAAACA  
GGGTATAAAAAATAAATACAGAGAGTTTTTTATTGGTCCTAAAACTTCATTTAAATTTAAAGTATATCCACTAAAAA  
TTCATTCTAAAAACAAAAATAGCAATAAAGCTCAACTATTAAATATCCGTCTATTTTAAAGCTCAACATAAC  
AAAAGTAGGAATTGAAGCAAAAAAACAATAAATGTTTTAATAACAAGAACTACAAAAATTAATATTACTAATAAA  
TGA

f12.aa

MREFLYRNVFKKSFIVFLIFLTFSNAIFAQTIDDENSKKRDKLTLSQKSYLRELELSTDEDLKKWALKEGLKETDV  
SKIRELLKKFGIDPELFIKKGKLAGSGRYKIIETADNLENFTYGLTKDESIIFEGRVNIIIVEDIKENKKHNIK  
DRIVLNKNSKKLYAIGNVEYIILDMTNEKLYFYGNEFLVDFDSQNFLLKNGILQKKMQKNQIDHILSFGGKVLKKI  
DNDVTILEQAFATTSKIPEPYYSIKASKIWALPSGDFGFLNAIFYMGRVPVFYIPFFFRPGDSLFFNPISGLNPRK  
GFSVFNTVYVLFNGKSSSEDSSFLDFDFNSVYNSGKKPYIRNGYLTFFAENLAPSVNKDYVKLIFDIYANLGFYSG  
IDFNLGNTLGHFKTLEGNFGLGFTRNVSVDGGYYPFDNRTLKQSLFSFNSLNKGDVFGFEVPPFRYLFKFKTEFL  
SDALFSVLEHYSDPYVNIDFRDRIESATFFSLNLDKDSVKEQTSISTFDWNLSFFYKRTFNDGSILDYKLNGL  
LSFKLSGYENLYVKSPLKPKDVNDPTRKWFYLERIYAPYIDLNFQKDLNNQWTFPADTKEMIMRPEIKNLEDKD  
NDKKSVEKENTKKTTELTKDLYIPPEPITLKNIDQSDSFFIRFGINPYLRNNVFFDNYGITSKDFNYEIKNYLFD  
IKNKTDIKIHADFYNRLITFENLLYLNTIEYSPLNKDFKVEDKDKKSEHSIINQINLNLPPFIRYPLFSRSTLKE  
NKATLYSFNKKYSDVKS LVNKNSSIFLSDPETFYQSLTASLIYDYDYFTTELSELKNSFEDIKASSELKLSLDF  
PYLLQEAGIGIKYKFKEDAMKNSGISAVQSPLEPQKPSSPYKNLEMSPALYKIEPRYLDYFKFSFLVAYDPLI  
NRVSELSFKLVNDFQFLFAMKDDFEYNDPLKGDGFSKIGTTTTKLVPYSLDSSYKKELYVLTFFDNKLSFTLGVDV  
GWKINLQKFTDNELRSALT LKFKYTEFLEIYFSTLSINTKTFKYFKGYMDQIGLEPVNFFVDLSKSFNFNSQDRK  
DSLFIKKKFSFGFKFNFYDWKFVGEYNLEPDLLRGSDGIYSPIWRNNFTIYISWNFFAPIKASFENNKDTNYEFI  
NRKTKK

t12.aa

IFAQTIDDENSKKRDKLTLSQKSYLRELELSTDEDLKKWALKEGLKETDVSKIRELLKKFGIDPELFIKKGKLAG  
SGRYKIIETADNLENFTYGLTKDESIIFEGRVNIIIVEDIKENKKHNIKDRIVLNKNSKKLYAIGNVEYIILDMT  
NEIKLYFYGNEFLVDFDSQNFLLKNGILQKKMQKNQIDHILSFGGKVLKKIDNDVTILEQAFATTSKIPEPYYSIK  
ASKIWALPSGDFGFLNAIFYMGRVPVFYIPFFFRPGDSLFFNPISGLNPRKGFVSFNTVYVLFNGKSSSEDSSFLDF  
DFNSVYNSGKKPYIRNGYLTFFAENLAPSVNKDYVKLIFDIYANLGFYSGIDFNLGNTLGHFKTLEGNFGLGFT  
NVYSVDGGYYPFDNRTLKQSLFSFNSLNKGDVFGFEVPPFRYLFKFKTEFLSDALFSVLEHYSDPYVNIDFRDRI  
ESATFFSLNLDKDSVKEQTSISTFDWNLSFFYKRTFNDGSILDYKLNGLSFKLSGYENLYVKSPLKPKDVND  
PTRKWFYLERIYAPYIDLNFQKDLNNQWTFPADTKEMIMRPEIKNLEDKDNDKKSVEKENTKKTTELTKDLYIPP  
EPITLKNIDQSDSFFIRFGINPYLRNNVFFDNYGITSKDFNYEIKNYLFDIKNKTDIKIHADFYNRLITFENLLY  
LNTIEYSPLNKDFKVEDKDKKSEHSIINQINLNLPPFIRYPLFSRSTLKFENKATLYSFNKKYSDVKS LVNKNSS  
IFLSDPETFYQSLTASLIYDYDYFTTELSELKNSFEDIKASSELKLSLDFPYLLQEAGIGIKYKFKEDAMKNS  
GISAVQSPLEPQKPSSPYKNLEMSPALYKIEPRYLDYFKFSFLVAYDPLINRVSELSFKLVNDFQFLFAMKDDF  
EYNDPLKGDGFSKIGTTTTKLVPYSLDSSYKKELYVLTFFDNKLSFTLGVDVGVKINLQKFTDNELRSALT LKFKYT  
EFLEIYFSTLSINTKTFKYFKGYMDQIGLEPVNFFVDLSKSFNFNSQDRKDSLFIKKKFSFGFKFNFYDWKFVGE  
YNLEPDLLRGSDGIYSPIWRNNFTIYISWNFFAPIKASFENNKDTNYEFIINRKTKK

f12.nt

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CAATTTTGGCCAGACTATAGATGATGAAAATTTCAAAAAAGGGATAAGCTAACTTTAAGTCAAAAAATCTTATTT  
AAGAGAACTTGAGCTTTCAACCGATGAGGATTTAAAAAATGGGCCTTAAAAGAGGGTTTAAAAGAAACAGATGTT

TABLE 1. Nucleotide and Amino Acid Sequences

TCAAAAATACGAGAATTGCTTTTAAAAAAGTTTGGAAATAGATCCTGAGCTTTTATCAAAGGAAAGGGACTTGCCG  
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 AAGTATTATTTTTGAAGGAAGAGTTAATATCTTGGTTGAAGATATTAAAGAAAAATAAAAAGCACAAATATTAAAGGC  
 GACAGAATAGTCCTTAATAAGAACTCTAAAAAAGTTTATGCTATTGGAATGTTGAATATATTTCTTGATATGGATA  
 CCAATGAAAAGCTTTATTTTTATGGCAATGAATTTCTTGTCGATTTTGATTCTCAAAAATTTTTTATTAAAAAATGG  
 TATTCCTTCAAAAAAATGCAAAAAAATCAAATAGATCATATTCTTTTCGTTTGGAGGAAAGGTTTTAAAAAAGATA  
 GACAATGATGTTACCATTTTGGACAAGCTTTTGCAACAACCTAGTAAAATTCAGAGCCTTACTATTCAATCAAGG  
 CTTCTAAAATATGGGCATTGCCCTCGGGAGATTTTGGGTTTTTAAATGCCATATTTTACATGGGAAGAGTTCCAGT  
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 GGTTTTTCTGTTTTTAATACCGTTTATCTTTTTTGGTAATAAATCTTCAAGTGAAGATTCTCTTTTTTGGATTG  
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 TCTTAACAAAGGAGATGATTTTGGGTTTGAAGTTCTTTTAGATATTTATTTAAATTTAAAACAGAATTTCTTTTA  
 AGTGATGCACTTTTCTCGGTTGTTTTAGAGCACTATTCTGACCCGTATGTTAATATTGATTTTAGAGATAGGATAG  
 AAAGTGCTACATTTTTTCTCTTTTAAATTTAGATAAAGATTTCGGTTAAAGAGCAAACTAGCATTAGCACTTTTGA  
 TTGGAATTTATCTTCTTTTATAAGCGAACATTTAATGACGGTTTCGATTTTAGATTATAAATTAATAATTTAGGT  
 TTAAGTTTTAAATGTGCGGCTATGAAAATCTTTATGTTAAATCTCCTTTAGAGAAACCAAAGATGTTAATGATC  
 CTACAAGAAAATGGTTTTATTTGGAGAGAATTTATGCTCCATATATTGATTTGAATTTTCAAAAAGATCTTTACAA  
 TAACCAATGGACATTTCCAGCTGATACTAAAGAAATGATAATGCGCCAGAAATTA AAAATCTAGAAGATAAAGAT  
 AATGATAAAAAGAGTGTGAAGGAGAAAAATCTAAAAAACAACAGAATTAACCAAAGATTTATATATTTCCCTCCAG  
 AACCAATTACTTTAAAAAATATTGATCAATCCGATTCTTTTTTTATTAGGTTTGGCATTAATCCTTATTTAAGAAA  
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 ATAAAAATAAAAACGGATATAAAAAATTCATGCTGATTTTTACAATCGTTAATTACTTTTGAAAATTTATTATATC  
 TTAATACTATTGAGTATAGTCCTTTAAATAAAGATTTTAAAGTTGAAGATAAAGATAAAAAAAGTGAGCACTAT  
 TATTAACCAATCTGTTTTAAACTTGCTTCCTTTTTATTAGATATCCTTTATTTTCTAGAAGTACTTTAAAGTTTGAA  
 AATAAGGCTACTTTATATTCAATTTAATAAAAAATATGATTCTGATGTAAATCTTTGGTTAATAAGAATAGTAGTA  
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 TGAGCTTTTCAGGTGAATTA AAAAATAGTTTGAAGATATTAAAGCTTCTCTGAGCTTAACTTTCTTTAGATTTT  
 CCTTATTTGCTACAAGAAGCTGGGATTGGAATTAATATTATAAAAAGTTTAAAGAAGATGCTATGAAAACTCTG  
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 AATATAATTATGATCCTTTAAAAGGAGATTTTCCAAAGATTGGTACTACAACCAAACCTGTTCATATTTCTTTAGA  
 TTCTAGTTACAAAAGGAATTGTACGTTTTAACTTTTTTTTGACAATAAGCTTTCTTTTACCTTGGGGGTAGATGTT  
 GGTGGA AAAATAAATTTGCAGAAAATTTACGGATAATGAACCTTCGATCTGCATTGACTTTGAAGTTTAAATATACAG  
 AATTTTTAGAAATTTACTTTTCTACTTTATCTATTAACTAAGACTTTTAAATATTTTAAAGGGTATATGGACCA  
 AATGGTCTAGAACCCTGTTAATTTCTTTGTGATTATCAAAATCTTTCAATTTCTTTAATCTCAAGACAGAAAA  
 GATTCACTTTTTAAATTA AAAAATTTTCATCAGGCTTTAAATTCATTTTATGATTGGAATTTGTTGGAGAAT  
 ATAATTTAGAACAGATTTATTAAGGGGATCTGATGGGATTTATTCTCCTATTTGGAGAAATAATTTTACAATTTA  
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 AATAGAAAAACA AAAAATAA

t12.nt

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 GAGAACTTGAGCTTTCAACCGATGAGGATTTAAAAAATGGGCCTTAAAGAGGGTTTAAAGAAACAGATGTTTC  
 AAAAATACGAGAATTGCTTTTAAAAAAGTTTGGAAATAGATCCTGAGCTTTTATCAAAGGAAAGGGACTTGCCGGA  
 TCTGGTAGATATAAAAATAATCATTGAACTGCAGATAATCTTGAAAATTTCACTTATGGACTTACTAAAGATGAAA  
 GTATTATTTTTGAAGGAAGAGTTAATATCTTGGTTGAAGATATTAAAGAAAAATAAAAAGCACAAATATTAAAGGCGA  
 CAGAATAGTCCTTAATAAGAACTCTAAAAAAGTTTATGCTATTGGAATGTTGAATATATTTCTTGATATGGATACC  
 AATGAAAAGCTTTATTTTTATGGCAATGAATTTCTTGTCGATTTTGATTCTCAAAAATTTTTTATTAAAAAATGGTA  
 TTCTTCAAAAAAATGCAAAAAAATCAAATAGATCATATTCTTTTCGTTTGGAGGAAAGGTTTTAAAAAAGATAGA  
 CAATGATGTTACCATTTTGGACAAGCTTTTGCAACAACCTAGTAAAATTCAGAGCCTTACTATTCAATCAAGGCT  
 TCTAAAATATGGGCATTGCCCTCGGGAGATTTTGGGTTTTTAAATGCCATATTTTACATGGGAAGAGTTCCAGTAT



TABLE 1. Nucleotide and Amino Acid Sequences

TTTATATTCCTTTTTTTTTTCAGACCGGGAGATAGTTTGTTTTTTAAATCCATCTTTAGGTCTAAATCCACGAAAAGG  
TTTTTCTGTTTTTAAATACCGTTTATCTTTTTTGGTAATAAATCTTCAAGTGAAGATTCTTCTTTTTTGGATTTTGAT  
TTCAATTCGTGTTTATAATTCGGGTAAAAAACCTTATATAAGAAATGGATATTTAACTTATTTTTTGCAGAAAATF  
TAGCACCCAGTGTTAATAAAGATTATGTTAAGCTTATTTTTTGACATTTATGCTAATCTGGGATTTTATTCTGGAAT  
TGATTTTAAATTTGGGCAATACTTTGGGGCATTTTAAAACTTTGGAAGGAAATTTTGGATTGGGTTTTACCAGGAAT  
GTTTATAGTTACGATGGAGGATATTATCCTTTTGATAATAGGACTTTAAAACAATCTCTTTTTTAGTTTTTCCAATC  
TTAACAAAGGAGATGTATTTGGGTTTGAAGTTCCTTTTAGATATTTATTTAAATTTAAAACAGAATTTCTTTTAAAG  
TGATGCACTTTTCTCGGTGTTTTAGAGCACTATTCTGACCCGTATGTTAATATTGATTTTAGAGATAGGATAGAA  
AGTGCTACATTTTTTCTCTTTTAAATTTAGATAAAGATTCGGTTAAAGAGCAAACCTAGCATTAGCACATTTTGATT  
GGAATTTATCTTCTTTTTTAAAGCAACATTTAATGACGGTTCGATTTTAGATTATAAATTAATAATTTAGGTTT  
AAGTTTTAAATTTGTCGGGTATGAAAATCTTTATGTTAAATCTCCTTTTAGAGAAACCAAAGATGTTAATGATCCT  
ACAAGAAAATGGTTTTATTTGGAGAGAATTTATGCTCCATATATTGATTTGAATTTTCAAAAAGATCTTTACAATA  
ACCAATGGACATTTCCAGCTGATACTAAAGAAATGATAATGCGCCAGAAATTAATAATCTAGAAGATAAAGATAA  
TGATAAAAAAGAGTGTGAAGGAGAAAAATACTAAAAAACAACAGAATTAACCAAAGATTTATATATTCCTCCAGAA  
CCAATTACTTTAAAAAATATTGATCAATCCGATTCTTTTTTTATTAGGTTTGGCATTAACTCTTATTTAAGAAATA  
ATGTTTTTTTTTGATAATTATGGCATAACAAGTCCAAAGGACTTTAATTATGAAATAAAAAATTATTTATTTGATAT  
AAAAAATAAAACGGATATAAAAAATTCATGCTGATTTTTACAATCGTTTAATTACTTTTGAAAATTTATTATATCTT  
AATACTATTGAGTATAGTCCTTTAAATAAAGATTTTAAAGTTGAAGATAAAGATAAAAAAAGTGAGCACTCTATTA  
TTAACCAAATAAATTTAACTTGCTTCCTTTTATTAGATATCCTTTATTTCTTAGAAGTACTTTAAAGTTTGAAAA  
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AGCTTTTCAGGTGAATTAATAAATAGTTTGAAGATATTAAAGCTTCTTCTGAGCTTAACTTTCTTTAGATTTTCC  
TTATTTGCTACAAGAAGCTGGGATTGGAATTAATATTATAAAAAAGTTTAAAGAAGATGCTATGAAAACTCTGGA  
ATTTCTGCTGTTCAAAGTCCCTTTGGAGCCTCAAAAACCATCATCGCCTTATAAAAAATTTAGAAATGTCTCCTGCTT  
TGTATTATAAAATTGAGCCGAGATATTGGATTATTTTAAATTTAGTTTTTTAGTCGCCTATGATCCTTTGATAAA  
TAGAGTTTCTGAACCTTTCTTTTAAAGCTTAATGTTTTTGATTTTCAATTTTGTGTTGCTATGAAAGACGACTTTGAA  
TATAATTATGATCCTTTTAAAGGAGATTTTTTCCAAGATTGGTACTACAACCAAACCTTGTTCCATATTCTTTAGATT  
CTAGTTACAAAAAGGAATTTGTACGTTTTTAACTTTTTTTTGACAATAAGCTTTCTTTTACCTTGGGGGTAGATGTTGG  
TTGGAATAAATAATTTGCAGAAATTTACGGATAATGAACCTTCGATCTGCATTGACTTTGAAGTTTAAATATACAGAA  
TTTTTTAGAAATTTACTTTTCTACTTTATCTATTAATACTAAGACTTTTAAATATTTTAAAGGGTATATGGACCAA  
TTGGTCTAGAACCCTGTTAATTTCTTTGTTGATTTATCAAAATCTTTCAATTTCTTTAATTTCTCAAGACAGAAAAGA  
TTCACCTTTTTTAAATTAATAAATTTTTCATCAGGCTTTAAATTCATTTTATGATTGGAAATTTGTTGGAGAATAT  
AATTTAGAACCAGATTTATTAAGGGGATCTGATGGGATTTATTTCTCCTATTTGGAGAAATAATTTTACAATTTATA  
TTTCTTGGAACCTTTTTTGCTCCTATAAAAGCGTCATTTGAAAACAACAAAGATACAAACTACGAGTTTATTATTAA  
TAGAAAAACAAAAAATAA

f129.aa

MTKKLFVRVLIFLISNNYAFKDTIKDLFFIQDILIKKEKYSEVLNNASLEGIIIEIHNGPYIKDHDSEVKLILKE  
NGYRRNFNFNLLNTSNI IKSLSLFDSRPKNIKENEI ILLETKMIKENPYKRYKDDDDFELKLSVTRKNNQIYLIL  
DFNFLFDQRKTFPSIYIKEEDVSTIINSFMKLQDSSFLSPQAS

t129.aa

KDTIKDLFFIQDILIKKEKYSEVLNNASLEGIIIEIHNGPYIKDHDSEVKLILKENGYRRNFNFNLLNTSNI IKSL  
LSLFDSPKNIKENEI ILLETKMIKENPYKRYKDDDDFELKLSVTRKNNQIYLILDFNFLFDQRKTFPSIYIKEED  
VSTIINSFMKLQDSSFLSPQAS

f129.nt

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AGGCATTATTGAAATTTGAACATAACGGACCATACATTAAAGATCAGGATTCAGAAGTTAACTTATCCTAAAAGAA  
AACGGATATAGAAGAAATTTCAACTTTTTTAAATCTTTTAAATACTAGTAATATAATCAAAAGTCTAAGCTTATTTG  
ACAGCAGACCAAAAAACATTAAAGAAAATGAAATCATATTATTAGAGACAAAAATGATTAAAGAAAATCCCTATAA  
ACGATACAAAGACGATGATGATTTTGAATTAATACTAAGTGTAACTCGAAAAAATAATCAAATTTATTTAATTTCTT

TABLE 1. Nucleotide and Amino Acid Sequences

GATTTC AATTT CCTATTTTGATCAAAGAAAAACGTTTCCATCAATTTACATCAAAGAAGAAGATGTATCAACAATAA  
TAAACAGCTTCATGAACTACAAGATTCAAGCTTTTTATCTCCTCAAGCTTCTTAA

t129.nt

AAAGACACAATCAAAGATTTGTTCTTTATACAAGATATACTAATAAAAAAGAGAAATATTCCGAGGTTCTAAATA  
ATGCAAGCCTTGAAGGCATTATTGAAATTGAACATAACGGACCATACATTAAAGATCACGATTCAGAAGTTAAACT  
TATCCTAAAAGAAAACGGATATAGAAGAAATTTCAACTTTTTTAATCTTTTAAATACTAGTAATATAATCAAAAGT  
CTAAGCTTATTTGACAGCAGACCAAAAAACATTAAAGAAAATGAAATCATATTATTAGAGACAAAAATGATTAAAG  
AAAATCCCTATAAACGATACAAAGACGATGATGATTTTGAATTTAAACTAAGTGTAACTCGAAAAAATAATCAAAAT  
TTATTTAATTTCTGATTTCAATTTCTTATTTGATCAAAGAAAAACGTTTCCATCAATTTACATCAAAGAAGAAGAT  
GTATCAACAATAATAACAGCTTCATGAACTACAAGATTCAAGCTTTTTATCTCCTCAAGCTTCTTAA

f142.aa

MDKISILYTLINIIMLILISIVYLCKRKNVSFTKRVFIALAIGIVFGMTIQYFYGTNSEITNETINWISILGDGY  
VRLMKMIIPLIITSIIISAI IKLTNSKDVGKMSLLVILTLVFTAGIAAIIIGIFTALALGLTAEG LQAGTIEILQSE  
KLQKGLEILNQTTITKKITDLIPQNI FDFAGLRKNSTIGVVIFSAIIGIAALKTSIKKPESIEFFKKIILTLQDI  
ILGVVTLILKLTPYAILALMTKITATSEIKSIIKLGEFVIAS YIAIGLTF LHMHTLIAINKLNPITFIKKIFPALS  
FAFISRSSAATIPINIEIQTKNLGVSEGIANLSSSFGTSIGQNGCAALHPAMLAIMIAPTQGINPTDISFILTLIG  
LIIITSFGAAGAGGGATTASLMVLSAMNFPVGLVGLVISVEPIIDMGR TAVNVGGSMLAGVISAKQLKQFNHNIYN  
QKELVNK

t142.aa

CKRKNVSFTKRVFIALAIGIVFGMTIQYFYGTNSEITNETINWISILGDGYVRLMKMIIPLIITSIIISAI IKLTN  
SKDVGKMSLLVILTLVFTAGIAAIIIGIFTALALGLTAEG LQAGTIEILQSEKLQKGLEILNQTTITKKITDLIPQNI  
IFEDFAGLRKNSTIGVVIFSAIIGIAALKTSIKKPESIEFFKKIILTLQDIILGVVTLILKLTPYAILALMTKITA  
TSEIKSIIKLGEFVIAS YIAIGLTF LHMHTLIAINKLNPITFIKKIFPALSFAFISRSSAATIPINIEIQTKNLGV  
SEGIANLSSSFGTSIGQNGCAALHPAMLAIMIAPTQGINPTDISFILTLIGLIIITSFGAAGAGGGATTASLMVLS  
AMNFPVGLVGLVISVEPIIDMGR TAVNVGGSMLAGVISAKQLKQFNHNIYNQKELVNK

f142.nt

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TGGAATGACCATTCAATATTTTTATGGAACAAATTCAGAAATAACAAACGAAACTATAAATTGGATAAGTATTTTG  
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AACTAACCAATAGTAAAGATGTTGGGAAAATGAGCCTACTTGTAATATTAACACTAGTATTTACAGCAGGTATTGC  
TGCCATAATTGGCATTTCCTACTGCTTTAGCATTGGGATTAACAGCCGAAGGACTACAAGCGGGAACCATCGAAATT  
TTACAAAGTGAAAAATTGCAAAAAGGCCTTGAAATATTAATCAAACAACAATCACAAAAAAATCACAGATCTTA  
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CTCCAAGACATAATATTAGGTGTAGTAACCTTGATTTTAAACTAACGCCTTATGCTATATTAGCTTTAATGACAA  
AAATTACAGCAACCAGCGAAATCAAAAGCATAATAAAGCTTGGAGAATTTGTAATTGCTTCTTACATTGCCATAGG  
TCTTACATTTCTTATGCATATGACATTAATTGCAATAAATAAATTAACCCCAATTACTTTTTATAAAAAAAATATTC  
CCAGCACTATCATTTGCATTTCATATCTAGGTGAGTGCTGCAACCATACCCATTAAATATAGAAATTCAAAC TAAAA  
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ACTACACCCCGCTATGCTTGCAATAATGATAGCACCAACTCAGGGAATAAACCCACAGATATTTCAATTTATACTC  
ACACTTATTGGATTAATAATAAATAACTTCATTTGGAGCTGCTGGCGCTGGTGGAGGCGCAACAACAGCCTCACTAA  
TGGTGCTCTCAGCAATGAAC TTTCCAGTGGGATTGGTAGGACTTGTAATATCTGTTGAGCCTATAATTGACATGGG  
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AATATATACAACCAAAAAGAGCTTGTAACAATAA

t142.nt

TABLE 1. Nucleotide and Amino Acid Sequences

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 GCATTTTCACTGCTTTAGCATTTGGGATTAACAGCCGAAGGACTACAAGCGGGAACCATCGAAATTTTACAAAGTGA  
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 TTATGCATATGACATTAATTGCAATAAATAAATTAAACCAATTACTTTTATAAAAAAAATATTCCCAGCACTATC  
 ATTTGCATTTCATATCTAGGTGCGAGTGCTGCAACCATAACCATTAATATAGAAATTCAAACATAAAATCTGGGAGTA  
 AGCGAAGGAATAGCAAAATTTATCAAGCTCCTTTGGAACATCAATTGGGCAAAATGGTTGTGCAGCACTACACCCCG  
 CTATGCTTGCAATAATGATAGCACCAACTCAGGGAATAAACCCACAGATATTTTCAATTATACTCACACTTATTGG  
 ATTAATAATAATAACTTCATTGGAGCTGCTGGCGCTGGTGGAGGCGCAACAACAGCCTCACTAATGGTGCTCTCA  
 GCAATGAACCTTCCAGTGGGATTGGTAGGACTTGTAATATCTGTTGAGCCTATAATTGACATGGGAAGAAGAGCTG  
 TTAATGTAGGCGGCTCAATGCTTGCAGGCGTTATATCTGCTAAACAGCTCAAACAATTCAACCATAATATATACAA  
 CAAAAAGAGCTTGTAACAAATAA

f147.aa

MKIIIIIGGTSAGTSAAAKANRLNKKLDITIYEKTNIVSFGTCGLPYFVGFFDNPNMTISRTOEEFEKTGISVKTN  
 HEVIKVDANKNTIVIKNQKTGTIFNNTYDQLMIATGAKPIIPPINNINLENFHTLKNLEDGQIKKKLMDREEIKNI  
 VIIGGGYIGIEMVEAAKNRKNVRLIQLDKHILIDSFDEEIVTIMEEELTKKGVNLHTNEFVKSLIGEKKAEGVVT  
 NKNTYQADAVILATGIKPDTEFLENQLKTTKNGAIIVNEYGETSIKNIFSAGDCATIYNIVSKKNEYIPLATTANK  
 LGRIVGENLAGNHTAFKGTLGASIKILSLEAARTGLTEKDAKKLQIKYKTIKFKDKNHTNYPGQEDLYIKLIYE  
 ENTKIILGAQAIGKNGAVIRIHALSIAIYSKLTTKELGMDFSYSPFRTWDILNIAGNAAK

t147.aa

AAAKANRLNKKLDITIYEKTNIVSFGTCGLPYFVGFFDNPNMTISRTOEEFEKTGISVKTNHEVIKVDANKNTIV  
 IKNQKTGTIFNNTYDQLMIATGAKPIIPPINNINLENFHTLKNLEDGQIKKKLMDREEIKNIVIIGGGYIGIEMVE  
 AAKNRKNVRLIQLDKHILIDSFDEEIVTIMEEELTKKGVNLHTNEFVKSLIGEKKAEGVVTNKNTYQADAVILAT  
 GIKPDTEFLENQLKTTKNGAIIVNEYGETSIKNIFSAGDCATIYNIVSKKNEYIPLATTANKLGRIVGENLAGNHT  
 AFKGTLGASIKILSLEAARTGLTEKDAKKLQIKYKTIKFKDKNHTNYPGQEDLYIKLIYEENTKIILGAQAIGK  
 NGAVIRIHALSIAIYSKLTTKELGMDFSYSPFRTWDILNIAGNAAK

f147.nt

ATGAAATAATAATTATTGGGGGCACATCAGCAGGAAGTAGTGCCGACAGCTAAAGCAAACCGCTTAAACAAAAAGC  
 TAGACATTACTATCTATGAAAAACAAATATTGTATCTTTTGGAACTGTGGCCTGCCTTACTTTGTGGGGGATT  
 CTTTGACAACCCCAATACAATGATCTCAAGAACACAAGAAGATTTCGAAAAAATGGAATCTCTGTAAACTAAC  
 CACGAAGTTATCAAAAGTAGATGCAAAAAACAATACAATTGTAATAAAAAATCAAAAAACAGGAACCATTTTAAACA  
 ATACTTACGATCAACTTATGATAGCAACTGGTGCAAAACCTATTATTCCACCAATCAATAATATCAATCTAGAAAA  
 TTTTCATACTCTGAAAAATTTAGAAGACGGTCAAAAAATAAAAAAATTAATGGATAGAGAAGAGATTAAAAATATA  
 GTGATAATTGGTGGTGGATACATTGGAATTGAAATGGTAGAAGCAGCAAAAAATAAAAAGAAAAATGTAAGATTAA  
 TTCAACTAGATAAGCACATACTCATAGATTCCTTTGACGAAGAAATAGTCACAATAATGGAAGAAGAACTAACAAA  
 AAAGGGGGTTAATCTTCATACAAATGAGTTTGTAAAAAGTTTAATAGGAGAAAAAAGGCAGAAGGAGTAGTAACA  
 AACAAAAATACTTATCAAGCTGACGCTGTTATACTTGCTACCGGAATAAAACCTGACACTGAATTTTTTAGAAAACC  
 AGCTTAAACTACTAAAAATGGAGCAATAATTGTAAATGAGTATGGCGAACTAGCATAAAAAATATTTTTTCTGC  
 AGGAGATTGTGCAACTATTTATAATATAGTAAGTAAAAAAATGAATACATACCCTTGGCAACAACAGCCAACAAA  
 CTTGGAAGAATAGTTGGTGAAAAATTAGCTGGGAATCATACAGCATTAAAGGCACATTGGGCTCAGCTTCAATTA  
 AAATACTATCTTTAGAAGCTGCAAGAACAGGACTTACAGAAAAAGATGCAAAAAAGCTCCAAATAAAATATAAAAC  
 GATTTTTGTAAAGGACAAAAATCATACAAATTATTATCCAGGCCAAGAAGATCTTTATATTAAATTAAATTTATGAG  
 GAAAAACCAAAATAATCCTTGGGGCACAAGCAATAGGAAAAATGGAGCCGTAATAAGAATTCATGCTTTATCAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTGCAATCTATTCAAACTTACAACAAAAGAGCTAGGGATGATGGATTTCTCATATTCCCCACCCCTTCTCAAGAAC  
TTGGGATATATTAAATATTGCTGGCAATGCTGCCAAATAG

t147.nt

GCCGCAGCTAAAGCAAACCGCTTAAACAAAAAGCTAGACATTACTATCTATGAAAAACAAATATTGTATCTTTTG  
GAACCTGTGGCCTGCCTTACTTTGTGGGGGGATTCCTTGACAACCCCAATACAATGATCTCAAGAACACAAGAAGA  
ATTCGAAAAAATCGGAATCTCTGTTAAAACTAACACGAAAGTTATCAAAGTAGATGCAAAAAACAATACAATTGTA  
ATAAAAAATCAAAAAACAGGAACCATTTTAAACAATACTTACGATCAACTTATGATAGCAACTGGTGCAAAACCTA  
TTATTCCACCAATCAATAATATCAATCTAGAAAAATTTTCATACTCTGAAAAATTTAGAAGACGGTCAAAAAATAAA  
AAAATTAATGGATAGAGAAGAGATTAAAAATATAGTGATAATTGGTGGTGGATACATTGGAATTGAAATGGTAGAA  
GCAGCAAAAAATAAAAGAAAAAATGTAAGATTAAATCAACTAGATAAGCACATACTCATAGATTCTTTTGACGAAG  
AAATAGTCAACAATAATGGAAGAAGAACTAACAAAAAAGGGGGTTAATCTTCATACAAATGAGTTTGTAAAAAGTTT  
AATAGGAGAAAAAAGGCAGAAGGAGTAGTAACAAAAAATACTTATCAAGCTGACGCTGTTTACTTGCTACC  
GGAATAAAACCTGACACTGAATTTTGTAGAAAACAGCTTAAACTACTAAAAATGGAGCAATAATTGTAAATGAGT  
ATGGCGAACTAGCATAAAAAATATTTTTTCTGCAGGAGATTGTGCAACTATTTATAATATAGTAAGTAAAAA  
TGAATACATACCCTTGGAACAACAGCCAACAACTTGAAGAATAGTTGGTGAAAATTTAGCTGGGAATCATACA  
GCATTTAAAGGCACATTGGGCTCAGCTTCAATTAATACTATCTTTAGAAAGCTGCAAGAACAGGACTTACAGAAA  
AAGATGCAAAAAAGCTCCAAATAAAATATAAAACGATTTTTGTAAAGGACAAAAATCATACAAATTATTATCCAGG  
CCAAGAAGATCTTTATATTAAATTAATTTATGAGGAAAAATACCAAAATAATCCTTGGGGCACAAGCAATAGGAAAA  
AATGGAGCCGTAATAAGAATTCATGCTTTATCAATTGCAATCTATTCAAACTTACAACAAAAGAGCTAGGGATGA  
TGGATTTCTCATATTCCCCACCCCTTCTCAAGAACTTGGGATATATTAAATATTGCTGGCAATGCTGCCAAATAG

f152.aa

MLKFEFSDRFLFSYFVLIMFIGSLLMLPISWEGDGKLAYIDALFTAVSAVSITGLTTVKMEGFSTFGFILIMLL  
IQLGGLGFISITTFYLLIPKKKMNLTDARI IKQYSLSNIEYNPIRILKSILFITFSIEMIGLILILICFKLRGVNI  
SFLEALFTTISAFNAGFSMHSESIYAWRDVPEAIVVVSILICGGLGFMVYRDVNNTIKNKKLSLHAKIVFSL  
FFLIIGAILFFFTEMHKLKAGYSMSTLIFNSIFYSISTRTAGFNYLDNSLISGRTOIISLPFMFIGGAPGSTAGG  
IKITTFFLIVLAVVKNQNGNGYIIGSYKVSIDSIRFALLFFARAIFILSFSFFMLLFFEGGSGNWKVIDLGYEVFS  
AFGTVGLSVGVTDQLSFWGKVIIIFTMFAGRIGLFSMAVFVSRKSRFEEFTRPRQDILVG

t152.aa

WEGDGKLAYIDALFTAVSAVSITGLTTVKMEGFSTFGFILIMLLIQLGGLGFISITTFYLLIPKKKMNLTDARI IK  
QYSLSNIEYNPIRILKSILFITFSIEMIGLILILICFKLRGVNISFLEALFTTISAFNAGFSMHSESIYAWRDVP  
EAIVVVSILICGGLGFMVYRDVNNTIKNKKLSLHAKIVFSLSFFLIIGAILFFFTEMHKLKAGYSMSTLIFNS  
IFYSISTRTAGFNYLDNSLISGRTOIISLPFMFIGGAPGSTAGGIKITTFFLIVLAVVKNQNGNGYIIGSYKVSID  
SIRFALLFFARAIFILSFSFFMLLFFEGGSGNWKVIDLGYEVFSAFGTVGLSVGVTDQLSFWGKVIIIFTMFAGRI  
GLFSMAVFVSRKSRFEEFTRPRQDILVG

f152.nt

ATGTTGAAATTTGAATTTAGCGACAGGTTTTTACTTTTTAGTTATTTTTGTTTTAATTATGTTTATAGGCTCTCTTT  
TGTTGATGTTGCCTATTTCCCTGGGAAGGTGATGGCAAATTAGCATACATTGATGCTCTTTTTACTGCTGTTTCTGC  
TGTAAGTATTACGGGCCCTTACAACGGTTAAATGGAAGGCTTTTTCTACTTTTGGATTTATTTTGATAATGTTGCTA  
ATCCAGCTTGGGGGACTTGGATTTATAAGTATTACTACTTTTTATTTGCTTATACCTAAAAAGAAAATGAATTTAA  
CAGATGCAAGAATAATAAGCAGTATTCCTTTCAAATATAGAATATAATCCTATTAGAATTTAAAAAGCATATT  
GTTTATAACTTTTTCAATTGAAATGATAGGTTTAATATTAATACTTATTTGTTTTAACTTAGGGGAGTGAATATT  
TCATTCTTAGAGGCTTTGTTTACGACAATTTCTGCTTTTTGCAATGCAGGTTTTCCATGCATTCTGAGAGTATTT  
ATGCATGGCGAGATGTTCTGAAGCTATAGTTGTGGTCTCTATTTTAATAATTTGTGGTGGGCTTGGGTTTATGGT  
CTATAGAGATGTAAATAACACTATTAAAAACAAAAAATACTATCGCTTCATGCCAAGATAGTTTTTTCTTTAAGC  
TTCTTTTTAATTATAATTGGTGCAATTTTATTTTTTTTACAGAGATGCATAAATTAAAAGCTGGTTATTCAATGA  
GCACTTTAATATTTAATTCATTTTTTATTCGATTAGTACCAGAACAGCTGGTTTAAATTATCTTGATAATTCTTT  
AATAAGCGGAAGAACTCAAATAATTTCTCTACCATTTCATGTTTATTGGTGGTGCACCCGGATCAACTGCAGGAGGG  
ATTAAGATTACAACATTTTTTTTAAATTGTATTGGCTGTTGTTAAAAATCAAAACGGCAATGGATATATTATTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences

CTTACAAGGTTTCAATAGATAGTATAAGATTGCACTTTTATTTTTTGCAAGAGCTATTTTTATTTTAAGTTTTTC  
TTTTTTCATGCTTCTTTTTTTTGGGGAGGATCTGGCAATTGGAAGGTTATTGATTAGGTATGAAGTATTTTCT  
GCTTTTGGAAACGGTTGGTCTTTCAGTTGGAGTAACTCAGGATTTGTCATTTTGGGGGAAAGTCATTATAATTTTA  
CTATGTTTGCAGGACGAATAGGGCTTTTTCAATGGCTGTTTTTGTTCAGAAAGTCGCGTTTTGAAGAATTTAC  
AAGGCCAAGGCAAGATATTTTGGTTGGTTGA

t152.nt

TGGGAAGGTGATGGCAAATTAGCATACATTGATGCTCTTTTTACTGCTGTTTCTGCTGTAAGTATTACGGGCCTTA  
CAACGGTTAAAATGGAAGGCTTTTCTACTTTTGGATTTATTTTGATAATGTTGCTAATCCAGCTTGGGGGACTTGG  
ATTTATAAGTATTACTACTTTTTATTTGCTTATACCTAAAAAGAAAATGAATTTAACAGATGCAAGAATAATAAG  
CAGTATTTCCCTTTCAAATATAGAATATAATCCTATTAGAATTTTAAAAAGCATATTGTTTATAACTTTTTCAATTG  
AAATGATAGGTTTAATATTAATACTTATTTGTTTTAACTTAGGGGAGTGAATATTTTATTCTTAGAGGCTTTGTT  
TACGACAATTTCTGCTTTTTGCAATGCAGGTTTTTCCATGCATCTGAGAGTATTTATGCATGGCGAGATGTTCCCT  
GAAGCTATAGTTGTGGTCTCTATTTTAATAATTTGTGGTGGGCTTGGGTTTATGGTCTATAGAGATGTAAATAACA  
CTATTAATAACAAAAAAACTATCGCTTCATGCCAAGATAGTTTTTCTTTAAGCTTCTTTTTAATTATAATTGG  
TGCAATTTTATTTTTTTTTTACAGAGATGCATAAATTTAAAGCTGGTTATTCAATGAGCACTTTAATATTTAATTCA  
ATTTTTTATTTCGATTAGTACCAGAACAGCTGGTTTTAATTATCTTGATAATTCTTTAATAAGCGGAAGAACTCAAA  
TAATTTCTCTACCATTTCATGTTTATTGGTGGTGCACCCGGATCAACTGCAGGAGGGATTAAGATTACAACATTTTT  
TTAATTGTATTGGCTGTTGTTAAAAATCAAAACGGCAATGGATATATTATTGGTTCTTACAAGGTTTCAATAGAT  
AGTATAAGATTTGCACTTTTATTTTTTGAAGAGCTATTTTTATTTTAAGTTTTTCTTTTTTCATGCTTCTTTTTT  
TTGAGGGAGGATCTGGCAATTGGAAGGTTATTGATTTAGGTTATGAAGTATTTTCTGCTTTTGAACGGTTGGTCT  
TTCAGTTGGAGTAACTCAGGATTTGTCATTTTGGGGGAAAGTCATTATAATTTTTACTATGTTTGCAGGACGAATA  
GGGCTTTTTCAATGGCTGTTTTTGTTCAGAAAGTCGCGTTTTGAAGAATTTACAAGGCCAAGGCAAGATATTT  
TGTTGGTTGA

f154.aa

MKINKTFILLFLFTKFSFVQAQANQILTEISPLSILSKNGKGSVYLKVS KSSDYILTLDKSSNSDFVFKIYDISNK  
KYITDKVKRRDFKIRLDKNSLYAIIYVGTKNENIKFSLTDLDFSILSSDSLKAKTSKIEKEDLFFTLKDL PVLNLT  
AKLK KYVLRIYKSNIYIAYQLENSDDIKVAEFIEDVGWFNLDSSVNRNITNIVNFDFSINSKGNLYIAFVTKSGAD  
FASELIVKKFNSRKWIDISP GHIENFGSLLNISIDLKDRLYLAYLREIRGEYKINLISNMGYGSIWTDVIHAYLSK  
GDSNVNSSNIGLISEPFLGIFYNYKSNNEIKSEFIVNNENAWVNANIPSVYMANFIKGFDFS NFNQIIMSFVSEN  
PIVNICPLKSSRWINISPNVEMEGLSADIGLYKNNLFLAFEDNNNVRLIYFKNKNWYFLNKLENFKSNVKS PQIGI  
YGNQGLVISTLSSNSNELFFTLICQ

t154.aa

NQILTEISPLSILSKNGKGSVYLKVS KSSDYILTLDKSSNSDFVFKIYDISNKKYITDKVKRRDFKIRLDKNSLYA  
IIYVGTKNENIKFSLTDLDFSILSSDSLKAKTSKIEKEDLFFTLKDL PVLNLTAKLK KYVLRIYKSNIYIAYQLEN  
SDDIKVAEFIEDVGWFNLDSSVNRNITNIVNFDFSINSKGNLYIAFVTKSGADFASELIVKKFNSRKWIDISP GHI  
ENFGSLLNISIDLKDRLYLAYLREIRGEYKINLISNMGYGSIWTDVIHAYLSK GDSNVNSSNIGLISEPFLGIFYN  
YKSNNEIKSEFIVNNENAWVNANIPSVYMANFIKGFDFS NFNQIIMSFVSEN RPIVNICPLKSSRWINISPNVEME  
GLSADIGLYKNNLFLAFEDNNNVRLIYFKNKNWYFLNKLENFKSNVKS PQIGIYGNQGLVISTLSSNSNELFFTLI  
CQ

f154.nt

ATGAAAATAAATAAGACATTCATTTTGCTATTTTATTTACAAAATTTCTTTTGTTCAAGCTCAAGCAAATCAAA  
TATTAACAGAAATTAGTCCTTTAAGTATTTTAAGCAAAAATGGGAAAGGAAGTGTCTTAAAGTTAGCAAATC  
TTCCGATTATATTTTAACCTTAGATAAGAGTTCAAATCCGATTTTGTTTTTAAATTTATGACATTTCTAATAAA  
AAATATATAACCGATAAAGTAAAAAGAAGAGATTTTAAAAATAAGATTAGATAAAAATTTCTTTTATGCAATAATAT  
ATGTTGGTACTAAAAATGAAACATAAAGTTTTCGCTTACAGATTTAGATTTTTCAATTTTAAGTAGCGATTCCCT  
GAAAGCTAAAACATCTAAGATTGAAAAAGAAGATTTATTTTTTACTTTTAAAGATTTGCCTGTTTTAAATTTAACT

TABLE 1. Nucleotide and Amino Acid Sequences

GCCAAGCTTAAAAAATATGTATTAAGGATTTATAAAAGCAATATTTATATTGCTTATCAGCTAGAAAATAGCGATG  
 ATATTAAAGTTGCTGAATTTATTGAGGATGTTGGTTGGTTTAATCTTGATTTCATCTGTTAATAGAAAATATTACTAA  
 TATAGTTAATTTTGATTTTTCAATTAATTCATAAAGGAAATTTATATATTGCTTTTGTACGAAATCAGGGGCTGAT  
 TTTGCCAGCGAGCTTATAGTTAAAAAATTTAATAGTAGAAAATGGATTGATATTAGTCCTGGTCACATAGAAAATTT  
 TTGGATCTTTATTAAATATTAGCATTGATTTAAAAGATAGGTTGTATTTAGCATATTTAAGGGAAATTAGGGGTGA  
 ATATAAAATTAATTTAATCTCGAATATGGGTACGGAAGTATTTGGACCGATGTAATACATGCTTATTTAAGTAAA  
 GGTGATTCTAATGTTAATTCATCAAACATTGGTTTAATATCTGAACCTTTTTTGGGCATTTTTTATAATTATAAGT  
 CAAATAATGAGATTAATCTGAATTTATTGTAACAATGAAAATGCTTGGGTAAATGCAAATATTCCTTCTGTTTA  
 TATGGCCAATTTTTATTAAAGGCTTTTTGATTTCTAATTTTAATCAAATAATTATGAGTTTTGTTTTCTGAAAATAGA  
 CCTATTGTAAACATTTGTCCTTTGAAAAGTAGTAGATGGATTAATATAAGTCCTAATGTTGAAATGGAAGGTTTAA  
 GTGCTGACATTGGGCTTTATAAAAAATAATTTGTTTTTAGCTTTTGAGGACAATAATAATGTGAGATTAATTTATTT  
 TAAGAATAAAAAATTGGTATTTTTTAAATAAGCTTGAGAATTTTAAGAGTAATGTTAAAAGCCCTCAGATTGGAATT  
 TATGGCAATCAAGGGCTTGTAATCTCTACTTTAAGCTCTAATCCAATGAATTATTTTTTTACTTTGATTGCGCAAT  
 GA

t154.nt

AATCAAATATTAAACAGAAATTAGTCCTTTAAGTATTTTAAGCAAAAATGGGAAAGGAAGTGTCTTACTTAAAAAGTTA  
 GCAAATCTTCCGATTATATTTTTAACCTTAGATAAGAGTTCAAATTCGATTTTGTTTTTTAAAATTTATGACATTTT  
 TAATAAAAAATATATAACCGATAAAGTAAAAAGAGAGATTTTAAAATAAGATTAGATAAAAAATCTCTTTATGCA  
 ATAATATATGTTGGTACTAAAAATGAAAACATAAAGTTTTCGCTTACAGATTTAGATTTTTCAATTTTAAGTAGCG  
 ATTCCTTGAAAGCTAAAACATCTAAGATTGAAAAAGAAGATTTATTTTTTACTTTAAAAGATTGTCCTGTTTTAAA  
 TTTAACTGCCAAGCTTAAAAAATATGTATTAAGGATTTATAAAAGCAATATTTATATTGCTTATCAGCTAGAAAAT  
 AGCGATGATATTAAAGTTGCTGAATTTATTGAGGATGTTGGTTGGTTTAATCTTGATTCATCTGTTAATAGAAATA  
 TTACTAATATAGTTAATTTTGATTTTTCAATTAATTCATAAAGGAAATTTATATATTGCTTTTGTACGAAATCAGG  
 GGCTGATTTTGGCAGCGAGCTTATAGTTAAAAAATTTAATAGTAGAAAATGGATTGATATTAGTCCTGGTCACATA  
 GAAAATTTTGGATCTTTATTAAATATTAGCATTGATTTAAAAGATAGGTTGTATTTAGCATATTTAAGGGAAATTA  
 GGGGTGAATATAAAATTAATTTAATCTCGAATATGGGTACGGAAGTATTTGGACCGATGTAATACATGCTTATTT  
 AAGTAAAGGTGATTCTAATGTTAATTCATCAAACATTGGTTTAATATCTGAACCTTTTTTGGGCATTTTTTATAAT  
 TATAAGTCAAATAATGAGATTAAATCTGAATTTATTGTAACAATGAAAATGCTTGGGTAAATGCAAATATTCCTT  
 CTGTTTATATGGCCAATTTTATTAAAGGCTTTTTTGATTTCTAATTTTAATCAAATAATTATGAGTTTTGTTTCTGA  
 AAATAGACCTATTGTAAACATTTGTCTTTGAAAAGTAGTAGATGGATTAATATAAGTCCTAATGTTGAAATGGAA  
 GGTTTAAGTGCTGACATTGGGCTTTATAAAAAATAATTTGTTTTTAGCTTTTGAGGACAATAATAATGTGAGATTAA  
 TTTATTTTAAAGAATAAAAAATTGGTATTTTTTAAATAAGCTTGAGAATTTTAAGAGTAATGTTAAAAGCCCTCAGAT  
 TGGAAATTTATGGCAATCAAGGGCTTGTAATCTCTACTTTAAGCTCTAATCCAATGAATTATTTTTTTACTTTGATT  
 TGCCAATGA

f157.aa

MKIFLKVIGRGILGRMLVFRKNYDYLALISLLIVSFVGILLIYSSDYNISGSLTKNEYIKQTFWVVIIGFFLIFIVG  
 KYDLKFVYSMVYPLYFLLILALIFTAFFGMTVNGARSWIGIWKLGQPSEFGKVVIILTLKIFYTEKKGYNEFFTF  
 ITAFLLIFPSVILILLQPDFGTAIVYLTIFIFISFFAGIDLHYVLAFALIGFFSFVFAILPVWYEEKVNMGNVFYL  
 IFSNPFYFRVIMGVLLILLISVLGFFISKYGLSIKIIYFYVFFASSILLVSIVFSKVLKLMKTYQIKRFLVFLD  
 PAIDAKGAGWNLNQVKIAIGSGGLLGKGLKGPYTHANYVPSQSTDFISILAEFGFLGVSTILILFFFLFFKFL  
 IIMNKSQDRYMALVISGILGLLFFHTSFNVGMSLGVLPITGIPFPLSYGGSSTITFFLAMSFYFNIESIVAMD

t157.aa

RKNYDYLALISLLIVSFVGILLIYSSDYNISGSLTKNEYIKQTFWVVIIGFFLIFIVGKYDLKFVYSMVYPLYFLLI  
 LALIFTAFFGMTVNGARSWIGIWKLGQPSEFGKVVIILTLKIFYTEKKGYNEFFTFITAFLLIFPSVILILLQPD  
 FGTAIVYLTIFIFISFFAGIDLHYVLAFALIGFFSFVFAILPVWYEEKVNMGNVFYLIFSFPFYFRVIMGVLLILLI

TABLE 1. Nucleotide and Amino Acid Sequences

LISVLGFFISKYGLSIKIIYFYVFFASSILLVSIVFSKVL SKLMKTYQIKRFLVFLDPAIDAKGAGWNLNQVKIAI  
GSGGLLGKGF LKGPYTHANYVPSQSTDFIFSILAEFGFLGVSTILILFFFLFFKFLIIMNKSQDRYMALVISGIL  
GLLFFHTSFNVGMSLGLVLPITGIPFPFLSYGGSSTITFFLAMSFYFNIESIVAMD

f157.nt

ATGAAGATATTCTTAAAGGTTATAGGCCGTGGTATATTAGGTAGATTAATGGTTTTTAGAAAAAATTATGATTATT  
TGGCTTTGATAAGCTTACTTATAGTTTCTTTTTGTTGGTATATTGTTGATTATTCTAGCGATTATAATATTAGTGG  
ATCTTTAACCAAGAATGAATATATAAAACAAACCTTTTGGGTAATTATTGGATTTTTCTAATTTTTATAGTGGGC  
AAATATGATTTAAATTTGTTTATAGCATGGTATATCCTTTATATTTTTTATTAATATTGGCTTTAATTTTTACTG  
CATTTTTTGGGAATGACAGTAAATGGAGCAAGATCTTGGATTGGCATATGGAACTTGGAGGACAGCCTTCTGAATT  
TGGTAAAGTTGTTATTATTTTAACCCCTTCAAAATTTTACACTGAAAAAAGGGTTATAATGAATTTTTTACCTTT  
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GTTTTTTTCTTTTTGTTTTGCAATTTTACCGGTTTGGTATGAATATAAGGTGAATATGGGTAATGTATTTTTATCTT  
ATTTTCTCAAATCCTTTTTATTTTAGAGTAATAATGGGAGTGCTGCTTTTAATCTTTTGATTTCTGTTTTAGGAT  
TTTTTCATTTCTAAATATGGTTGAGTATTAATAAATTTATTTTTATGTATTTTTTGCAAGTCTATTTTTATTAGT  
TTCAATAGTGTTTTCAAAGGTTCTTTCAAAGTTAATGAAGACTTATCAGATTAAACGGTTTTTGGTATTCTTAGAT  
CCGGCTATTGATGCTAAGGGTGCTGGTTGGAATTTAAATCAGGTTAAATAGCAATTGGTTCTGGCGGTCTTTTGG  
GCAAAGGATTTTTAAAGGGACCTTATACCCACGCATAATTATGTGCCATCTCAAAGCACAGATTTTATTTTTTCTAT  
TCTTGCCGAAGAGTTTGGGTTTTTGGGTGTTAGCACTATTTTAATATTATTTTTTTTCTTTTTTTAAATTTTTG  
ATAATAATGAATAAAAGTCAAGATAGATATATGGCCTTAGTAATATCTGGAATTTTGGGACTTTTATTTTTTTCATA  
CTTCTTTTAATGTTGGAATGTCTTTAGGAGTTCTTCCTATTACCGGGATTCCCTTTCTCTCTCTATGGAGG  
TTCTTCTACTATTACATTTTTTTTAGCAATGTCTTTTTATTTTAATATTGAATCAATAGTTGCTATGGATTGA

t157.nt

AGAAAAATTATGATTATTTGGCTTTGATAAGCTTACTTATAGTTTCTTTTTGTTGGTATATTGTTGATTATTTCTA  
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TCTAATTTTTTATAGTGGGCAAATATGATTTAAATTTGTTTATAGCATGGTATATCCTTTATATTTTTTATTAATA  
TTGGCTTTAATTTTTTACTGCATTTTTTGGAAATGACAGTAAATGGAGCAAGATCTTGGATTGGCATATGGAACTTG  
GAGGACAGCCTTCTGAATTTGGTAAAGTTGTTATTATTTTAACCCCTTTCAAAATTTTACACTGAAAAAAGGGTTA  
TAATGAATTTTTTACCTTTATTACTGCATTTTTTATTAATTTTTTCCATCGGTAATCTTATATTATTGCAACCTGAT  
TTTGGTACAGCAATAGTATATTTAACCATTTTTTATATTTATTTCTTTTTTGCAGGAATAGATTTCGACTATGTTT  
TAGCATTTGCGTTGATAGGGTTTTTTCTTTTGTTTTGCAATTTTACCGGTTTGGTATGAATATAAGGTGAATAT  
GGGTAATGTATTTTATCTTATTTTCTCAAATCCTTTTTATTTTAGAGTAATAATGGGAGTGCTGCTTTAATCTT  
TTGATTTCTGTTTTAGGATTTTTCATTTCTAAATATGGTTGAGTATTAATAAATTTATTTTTATGTATTTTTTG  
CAAGTTCATTTTTATTAGTTTCAATAGTGTTTTCAAAGGTTCTTTCAAAGTTAATGAAGACTTATCAGATTAAACG  
GTTTTTGGTATTCTTAGATCCGGCTATTGATGCTAAGGGTGCTGGTTGGAATTTAAATCAGGTTAAATAGCAATT  
GGTTCTGGCGGTCTTTTGGGCAAAGGATTTTAAAGGGACCTTATACCCACGCTAATTATGTGCCATCTCAAAGCA  
CAGATTTTATTTTTTCTATTCTTGCCGAAGAGTTTGGGTTTTTGGGTGTTAGCACTATTTTAATATTATTTTTTT  
CCTTTTTTTTTAAATTTTTGATAATAATGAATAAAAGTCAAGATAGATATATGGCCTTAGTAATATCTGGAATTTTG  
GGACTTTTATTTTTTCTACTTCTTTAATGTTGGAATGTCTTTAGGAGTTCTTCCTATTACCGGGATTCCCTTTC  
CTTTCTCTCTTATGGAGGTTCTTCTACTATTACATTTTTTTTAGCAATGTCTTTTTATTTTAATATTGAATCAAT  
AGTTGCTATGGATTGA

f17.aa

MIVFLFFSIYLIILFKRSSNSPLYFVPDTKFETLSIRIVLSCSLLLIFFCTMLDARPSTIAVFPTPGSPISIALFL  
FLKSI FVRVLISASLPTKGSNFLAFASAVKFLTYFPISKCSFSSRISSNSL

TABLE 1. Nucleotide and Amino Acid Sequences

t17.aa

PLYFVPDTKFETLSIRIVLSCSLLLIFFCTMLDARPSTIAVFPTPGSPISIALFLFLLKSIFVRVLISASLPTKGS  
NFLAFASAVKFLTYFPISKCSFSSRISSNSL

f17.nt

ATGATTGTGTTTTGTGTTTTTCAATATACTTAATTATATTATTTAAACGATCTTCAAACCTCGCCTCTATATTTTG  
TTCCCGATACCAAGTTTGAAACCTTAAGCATTAGAATTGTTTTGTCTTGTAGTTTGCTACTTATTTTTTTTTGCAC  
TATGCTTGATGCAAGGCCTTCAACTATTGCTGTTTTTCCCACACCAGGTTGCGCTATTAGCATTGCACATTTTTTA  
TTTCTTCTCAAGAGTATATTTGTAAGAGTTTTAATCTCTGCTTCTCTTCCAACCAAGGGGTCTAATTTTTTGGCTT  
TTGCAAGTGCTGTAAATTTTGTACATACTTTCCAATTTCAAAGTGCTCATTTTCAAGTCGTATTTCTTCATCAAA  
TTCTTTGTAG

t17.nt

CCTCTATATTTTGTGTTCCCGATACCAAGTTTGAAACCTTAAGCATTAGAATTGTTTTGTCTTGTAGTTTGCTACTTA  
TTTTTTTTTGCACATATGCTTGATGCAAGGCCTTCAACTATTGCTGTTTTTCCCACACCAGGTTGCGCTATTAGCAT  
TGCACATTTTTATTTCTTCTCAAGAGTATATTTGTAAGAGTTTTAATCTCTGCTTCTCTTCCAACCAAGGGGTCT  
AATTTTTTGGCTTTTGAAGTGCTGTAAATTTTGTACATACTTTCCAATTTCAAAGTGCTCATTTTCAAGTCGTA  
TTTCTTCATCAAATTCTTTGTAG

f170.aa

MKAFKVKNLRRFSNFIRILVIVLFLNSLLSLFVFLAGSYNIFVYNFQKFYLDLAILSSVSFGLESTRLIFFYFLK  
NKKIKYYLILIFSFIIFFIALLVFKIFLSGNK

t170.aa

YNIFVYNFQKFYLDLAILSSVSFGLESTRLIFFYFLKNKKIKYYLILIFSFIIFFIALLVFKIFLSGNK

f170.nt

ATGAAAGCTTTTAAAGTAAAAAATCTAAGACGTTTTTCAAATTTTATTAGAATTTTGTTTATTGTATTGTTTTTAA  
ATTCTTTGTTAAGTTTGTTCGTGTTTTGGCTGGTTCTTACAATATTTTGTTTACAATTTTCAGAAATTTTATCT  
TGATCTTGCTATTATTTTAAGCTCTGTTTCTTTTGGACTTGAATCTACTAGACTGATATTTTTTTATTTTTTGA  
AATAAAAAAATTAAGTATTATTTAATTTTAAATTTTATGTTTTATAATTTTTTTATTGCTCTTGTTTTTAAATTT  
TTCTTTCTGGTAATAA  
ATAG

t170.nt



TABLE 1. Nucleotide and Amino Acid Sequences

TACAATATTTTTGTTTACAATTTTCAGAAATTTTATCTTGATCTTGCTATTATTTTAAGCTCTGTTTCTTTTGGAC  
TTGAATCTACTAGACTGATATTTTTTTATTTTTTGAAAAATAAAAAATTAAGTATTATTTAATTTTAATTTTTAG  
TTTTATAATTTTTTTTATTGCTCTTGTTTAAATTTTCTTTCTGGTAATAAATAG

f186.aa

MKKLIIIFTLFLSQACNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENTRTITHTL  
FGTTPMQRIHKYDQSFNLTREILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRK  
YKN

t186.aa

TMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENTRTITHTLFGTTPMQRIHKYDQSFNL  
REILASGIELNRVVNAWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRKYKN

f186.nt

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AGATGATACCCCTGAAAAAGTTGCAAAAGAATATGCCATTAACTGGGAGAAAAATAGAACAATAACTCACACCCCTT  
TTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACAAGAGAAATACTGGCATCAG  
GAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAAGCCACAAAGAAGCTCTTATTAATACAGATAC  
CGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGATATATTTGTAGTTCTTTTGGAAAAAGAAAA  
TATAAGAATTGA

t186.nt

ACAATGCATAAAATAGATACAAAAGAAGATATGAAAATTTCTATATTCAGAAATTGCTGAATTGAGAAAAAAATTA  
ATCTAAACCATCTAGAAATAGATGATACCCCTGAAAAAGTTGCAAAAGAATATGCCATTAACTGGGAGAAAAATAG  
AACAATAACTCACACCCCTTTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACA  
AGAGAAATACTGGCATCAGGAATTGAACTTAACAGAGTAGTTAATGCATGGCTTAATAGTCCAAGCCACAAAGAAG  
CTCTTATTAATACAGATACCGATAAAATAGGTGGCTATAGATTAAAAACGACTGACAATATAGATATATTTGTAGT  
TCTTTTGGAAAAAGAAAAATATAAGAATTGA

f196.aa

MKLKARMLLLVLILIAFFISILFFAFGMLINSKLVDQQFNLMINLIESIKSSFNLYISSMEEKVRVSSMYFN  
FNEASKIKSKRLSFISDQSEILIQTSNMVTDKEGKIVFTTAVKDNDFGKSGIDREYFTKLKESNSIVNSFVM  
LADPGSIEESLLKDISKIKNKGQIPYILIGMPLRDFETDNIFGYFMFLYSMDYIYRSFRGINFGILSSGRALAYD  
TTGRLLVHVHVLPGDILTDISASYSNIIKKTSEDLLQKNKEISTVYYYDPKSNKKYVGISQKVLLNLSNNKFILLM  
RTSEDDFYMSRATTIILAISFVFTLLMLAIATLYLVKKLSSSLNKILEYSERLASGNFTADINFGKWDTVELYSL  
YEGLEQLRTNFSVAKGVIENLDYLYENAIQIANASQNLSSGAVEQASTLEQMTANIEQISQGVSENTENAAATTEK  
IAVNTNERTKEGHKSUVKAIEAMTVITEKIGIIDEITRQTNLLALNASIEAARVGEKKGFEVVAEVRKLADQSK  
ESAREIIDIANRSLTVASRAGENFEQIVPGMEQARLVKNISNESYKQSVQIEQFKNAIEQVSQVLVQTASSSEEL  
SAMSEKMLESVKDLKESVDYFKIEK

TABLE 1. Nucleotide and Amino Acid Sequences

t196.aa

MLINSKLVDQQFNLMINLIESIKSSFNLYISSMEEKVRVSSMYFNSAEKFNEASKIKSKRLSFISDQSEILIQTGS  
 NMMVTDKEGKIVFTTAVKDNSDFGKSIGDREYFTKLKESNSIVNSFVMLADPGSIEESLLKDISKIKNKKGQIPY  
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 IKKTSEDLLQKNKEISTVYYYDPKSNKKYVGISQKVLNLSNNKFILLMRTSEDDFYMSRATTIILAISFVFTLL  
 MLAIATLYLVKKLSSSLNKILEYSERLASGNFTADINFGKWDTVELYSLYEGLEQLRTNFSSVAKGVIENTLDYLYE  
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 EKIGIIDIEITRQTNLLALNASIEAARVGEKGKGFVVAEEVRKLDQSKESAREIIDIANRSLTVASRAGENFEQI  
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f196.nt

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 TTCTTTTAAATCTTTACATCTCTTCAATGGAAGAGAAAGTTAGGGTTAGTTCATGTATTTCAACTCTGCTGAAAAA  
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 GTAGTAATATGATGGTTACAGACAAAGAAGGTAAAATAGTGTCTACTACGGCGGTTAAGGATAATAGTGATTTTGG  
 CAAATCTATTGGGGATAGAGAAATTTTACAAAACCTTAAGGAGTCTAATAGTATTGTTTACAATTCCTTTGTCATG  
 TTGGCAGATCCCGGCTCTATTGAGGAGTCTTTACTTAAAGATATTTCGAAGATAAAAAATAAAAAAGGTCAGATTC  
 CTTACATATTAATAGGTATGCCATTAAGAGATTTTGAAACAGATAACATTTTGGTTATTTTATGTTTCTTTATTC  
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 ATTGCTGTTAATACTAATGAAAGGACTAAAGAGGGGCATAAATCTGTTGTTAAGGCTATTGAGGCAATGACTGTAA  
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t196.nt

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 GGGTAGATTGTTGGTTCATCATGTAGTATTGCCAGGTGATATTTGACTGATATTAGTGCTTCTTATTCCAATATT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAAGAAAACATCTGAAGATTTGTTGCAAAAGAATAAAGAAATTTCAACTGTTTATTATTATGATCCTAAAAGCA  
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AGGGCTTGAGCAGTTGAGAACCAATTTTCTTCAGTTGCAAAAGGAGTTATTGAAAATCTAGATTATCTTTATGAA  
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TGACAGCAAATATTGAGCAAATTTCAAGGTGTTTCTGAGAATACTGAAAATGCAGCTACTACTGAAAAAATTGC  
TGTTAATACTAATGAAAGGACTAAAGAGGGGCATAAATCTGTTGTTAAGGCTATTGAGGCAATGACTGTAATTACT  
GAAAAAATTGGAATTATTGATGAGATAACAAGGCAAACCAATTTGCTTGCTTTAAATGCCTCGATTGAAGCTGCAC  
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f899.aa

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K

t899.aa

f899.nt

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GAAAGCTTGTTCTTTTTGATACAGATCTTAAAGAATTTTAGTTTTTTAAAGATATTAATGAAAACAAGCTTTATGC  
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AAATAA

t899.nt

TTGCCTCCGGAAGATATTATTTTTGAGAGTTCTTATGAGGTTGCAATTAAAAAAGCTCAAAAATTGAATAAAAATG  
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TATTCACAAAGTATCTAGAAAAAGTGTTTTTTTAGTTATTGATAAGGATAATGAAATTTTTAATAAAATTAATCTA  
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TTTAATGGTAAAGACAGAAAGCTTGTTCTTTTTGATACAGATCTTAAAGAATTTTTTAGTTTTTTAAAGATATTAATG  
AAAACAAGCTTTATGCTATTCCTAAGTCTAGGATTGGTAATATTTATTTTTTCATTATTGGGAAATGAAGAATGGAA  
GCTTTTTTGGAAAAATAAAATAA

TABLE 1. Nucleotide and Amino Acid Sequences

f924.aa

MQDRKFSFRKYFLISVFLIFIVSGITYFYSTQMLEKSQKCVEDNLDAKVKLVDMEDFYFDLNECLNMDDFFIIPRPD  
FLNENLNKNLVVDGLIKNKFLDENFFKDLWIKKENLNFVDIEKENEKLIDKILEISK

t924.aa

TQMLEKSQKCVEDNLDAKVKLVDMEDFYFDLNECLNMDDFFIIPRPD FLNENLNKNLVVDGLIKNKFLDENFFKDLW  
IKKENLNFVDIEKENEKLIDKILEISK

f924.nt

ATGCAAGATAGAAAAGTTTAGTTTTAGAAAATATTTTTTAATTCAGTATTTTGTGATTTTATTGTTTCTGGTATTA  
CTTATTTCTATTCAACACAAATGTTGGAAAAATCTCAAAAGTGTGTTGAAGACAATTTAGACGCTAAGGTTAAATT  
AGTTGATATGGAAGATTTTTATTTTGATTTAAATGAATGTCTAAATATGGATGATTTTTTTATTCCAAGACCTGAT  
TTTTTAAATGAAAATTTAAATAAGAATTTAGTTGTTGATGGATTGATTAAAAATAAATTTCTTGATGAGAATTTTT  
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t924.nt

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CCAAATGA

f925.aa

MIRKYLIYISLLFIVFEVYSKPAFISQDDSYELDFSSGEVDISVNTNSKFNLSEKDESWIYIKSIENEAFIKLIGE  
SYDNGAVFTFQTFKKEGKIKLVFTYQNVKDSSEFNKIIILKITKNFEVAIPQGVGGGSSRDNNIETGNNLELGGGS  
ISGATSKEIIVRALNLSYINDYKGAIDLLNKYNFNDDKYILLKAEIHYKNGDYLSYENYLKLSKYFQSIVFDLI  
RLAIELNIKEEVLENARYLVEKNVDFSESIYLEIFEFLVTRGEHEFALNFSSLYFPKYINSSFSKYSYLLGKLYE  
SESKHKDFLALHYYKLVIDNYPFSYYYERAKIRYLFLKRFF

t925.aa

KPAFISQDDSYELDFSSGEVDISVNTNSKFNLSEKDESWIYIKSIENEAFIKLIGESYDNGAVFTFQTFKKEGKIK  
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DYKGAIDLLNKYNFNDDKYILLKAEIHYKNGDYLSYENYLKLSKYFQSIVFDLIRLAIELNIKEEVLENARYLV  
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f925.nt

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TCTTTCCTTTTAAAGATGAGTCTTGGAATTTATATCAAAAGCATTGAAAATGAAGCTTTTATTAAGTTAATTGGAGAA

TCCTTATGATAACGGTGCTGTTTTTACTTTTCAGACTTTTAAAAAAGAAGGCAAAATTAAATTGGTTTTCTACTTATC  
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AGGCTTGCTATAGAATTAAATATTAAGAAGAGGTTTTAGAGAACGCTAGATATTTAGTTGAAAAGAATGTTGATT  
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TCTGAGAGCAAGCATAAAGATTTTTTAAAGGCTTTGCATTACTATAAAATGGTTATTGATAATTACCCTTTTAGTT  
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AAGCCAGCTTTTATAAGTCAAGACGATTTCGTATGAGCTTGATTTTGTAGTAGTGAGAGGTAGATATTAGTGTAAATA  
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DYDFNIVIQQGLKDKSVLYVFQKSVLNDVSSYRPIFFDKVNGTVLINKYARSSAYEENRSRESYPI SLEKYEKVGE  
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VQGRYCLSSVSEKVGKIDNNIYKTLKNLSKDEVYKFLHGVWYDVHDYKNMHVKDIDEVLFLSFERQSSEINLFRKN  
SQEVAKIEYISKPAYNTLNVSAKSLFSDLIVNFWIKIVDKENIEIKIDTSTNSYDNSGFGTFRFDENVLNVKK  
GSSDIYFIPSGNYVYKDKIYDFSYPHLTYIDENKIYYGIFNIFPLKNNFVLEYEIDMGSYKLVESFFLEHSERIVQ  
KQKFSTIILNPIKILKDDVSLVKGOKLKLRIEKI

f929.nt

TABLE 1. Nucleotide and Amino Acid Sequences

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GATTTAATAATTAGCAAGATTGAAAAATATGAATATTCTAATGTTTCAGGGTAGATATTGTCTTTCTTCTGTGAGCG  
AAAAAGTTGGTAAATTTGATAATAATTTTATAAACTTTTAAAGAATTTAAGCAAAGATGAAGTTTATAAAATTTTT  
GCATGGAGTTTGGTATGATGTTTCATGACTATAATAAAATGCATGTCAAAGATATTGATGAAGTTTTATTCTTGTCT  
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AACCTGCTTACAATACTCTTAATGTTAGTGCAAAGTCTCTTTTTTCAGATTTGATAGTTTATAACTTTTGGATCAA  
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TGGCATTTTTTAATATTTTTCTTTTAAAAATAATTTTGTCTTGAATATGAGATTGACATGGGTAGTTACAAGCTT  
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TAAAATTTTAAAGATGATGTAAGCTTAGTTAAAGGGCAAAAATTAAGCTTGAGCGAATAGAAAAAATATGA

t929.nt

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CACAAATTCCTATGATAATAGTGGATTTTCGGGTACATTTAAGAGGTTTGATGAGAATGTCTTAAATGTTAAAAAA  
GGGAGTAGTGATATTTATTTTATTCCTAGTGGAATTTACGTGTATAAGGATAAAATTTATGATTTTTCTTACCCCC  
ATTTAACTTATATTGATGAGAATAAAATTTATTTATGGCATTTTTAAATATTTTCTTTTAAAAAATAATTTTGTCT  
TGAATATTGAGATTGACATGGGTAGTTACAAGCTTGTGAATCTTTTTTCTTTGAGCATAGCGAAAGAATTGTTCAA  
AAGCAAAAATTTCTACAATCATTTTAAATCCTATTAATTTTAAAGATGATGTAAGCTTAGTTAAAGGGCAAA  
AATTAAAGCTTGAGCGAATAGAAAAAATATGA

f933.aa

MNKLILFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSKQDPIVPFLNLFLGFGIGSFAQGDILGGSLLIL  
GFDVAVGIGLILAGAYLDIKALDGIKKAAFQWTWKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNLVAL  
GGFEPSFDVAMGQSSALGFELSFKKSY

t933.aa

TABLE 1. Nucleotide and Amino Acid Sequences

NDSKNGAFGMSAGEKLLVYETSKQDPFIVPFLNLFLGFGIGSFAQGDILGGSILILGFDVAVGIGLILAGAYLDIKAL  
DGITKKAAFQWTWGKGVMLAGVVMTMAVTRLTEIILPFTFANSYNRKLKNSLNLVALGGFEPSPFDVAMGQSSALGFEL  
SFKKSY

f933.nt

ATGAATAAACTTTTAATTTTTGTTTTGGCAACCTTTTGTGTTTTTCTAGCTTTGCTCAAGCTAATGATTCTAAAA  
ATGGTGCCTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAACTAGCAAGCAAGATCCTATTGTACCATT  
TTTATTGAACCTTTTTTTAGGGTTTGGAAATAGGCTCCTTTGCTCAAGGAGATATTCTTGAGGTTCTCTTATTCTT  
GGATTTGATGCGGTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTA  
AAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTTACTATGGCTGTGACAAGATT  
AACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCTTAATGTAGCTTTA  
GGAGGATTTGAACCTAGTTTTGATGTTGCAATGGGCCAATCCAGTGCTCTTGGGTTTGAAGTGTCTTTCAAAAAA  
GCTATTAA

t933.nt

AATGATTCTAAAAATGGTGCCTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAACTAGCAAGCAAGATC  
CTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAAATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGG  
TTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTT  
GATGGTATTACTAAAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTTACTATGG  
CTGTGACAAGATTAAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCT  
TAATGTAGCTTTAGGAGGATTTGAACCTAGTTTTGATGTTGCAATGGGCCAATCCAGTGCTCTTGGGTTTGAAGTGT  
TCTTTCAAAAAAAGCTATTAA

f940.aa

MRKYIFIILIAVLLIGVNIKKIAAAANIDRHTNSTLGIDLSVGIPIFYNDLSKAYPTNLYPGGIGAICYQYHILNN  
LAIGLELRYMFNFDINHSFNILNPDSSVGKIFYSVPIITFSINYIFDIGELFQIPVFTNIGFSLNTYGDRNNNITNL  
RTFDALPTISFGSGILWNFNFKWAFGATASWMMFEFGNSAKMAHFALVSLSVTVNVNKL

t940.aa

ANIDRHTNSTLGIDLSVGIPIFYNDLSKAYPTNLYPGGIGAICYQYHILNNLAIGLELRYMFNFDINHSFNILNPD  
SSVGKIFYSVPIITFSINYIFDIGELFQIPVFTNIGFSLNTYGDRNNNITNLRTFDALPTISFGSGILWNFNFKWAF  
GATASWMMFEFGNSAKMAHFALVSLSVTVNVNKL

f940.nt

ATGAGAAAGTATATTTTTATAATACTAATTGCAGTCTTGCTAATTGGTGTAAACATAAAAAAATTGCGGCCGCAG  
CCAATATTGATAGGCATACAACTCCACTTTAGGAATAGATTTAAGTGTAGGAATCCCTATTTTTTACAACGACTT  
ATCAAAAGCTTATCCTACCAATTTATATCCAGGAGGTATTGGGGCAATAAAATACCAGTACCATATTTTAAACAAT  
TTAGCAATTGGACTTGAAGTAAGGTATATGTTTAACTTTGATATTAACCATTCCTTTTAAATATATTAAATCCAGATT  
CAAGTGTAGGTAAATTTTTTATAGCGTGCTATTACATTTTCAATAAATTATATATTTGATATAGGAGAATTATT

TABLE 1. Nucleotide and Amino Acid Sequences

TCAAATTCAGTCTTCACAAATATAGGGTTTTCTCTTAATACATATGGAGATAGAAACAACAATATTACAAATTTA  
AGAACTTTTGGATGCACTCCCTACAATCTCTTTTGGATCTGGAATTTTATGGAACTTTAACTATAAATGGGCTTTTG  
GAGCAACAGCATCTTGGTGGATGATGTTTGAATTTGGAAATTCCTGCTAAAATGGCACATTTTGCACCTTGTATCATT  
ATCAGTTACAGTGAATGTAAATAAATTGTAG

t940.nt

GCCAATATTGATAGGCATACAAACTCCACTTTAGGAATAGATTTAAGTGTAGGAATCCCTATTTTTTACAACGACT  
TATCAAAAGCTTATCCTACCAATTTATATCCAGGAGGTATTGGGGCAATAAAATACCAGTACCATATTTTAAACAA  
TTTAGCAATTGGACTTGAACCTAAGGTATATGTTTAACTTTGATATTAACCATTCTTTTAAATATATTAAATCCAGAT  
TCAAGTGTAGGTAAAATTTTTTATAGCGTGCCTATTACATTTTCAATAAATTATATATTTGATATAGGAGAATTAT  
TTCAAATTCAGTCTTCACAAATATAGGGTTTTCTCTTAATACATATGGAGATAGAAACAACAATATTACAAATTT  
AAGAACTTTTGGATGCACTCCCTACAATCTCTTTTGGATCTGGAATTTTATGGAACTTTAACTATAAATGGGCTTTT  
GGAGCAACAGCATCTTGGTGGATGATGTTTGAATTTGGAAATTCCTGCTAAAATGGCACATTTTGCACCTTGTATCAT  
TATCAGTTACAGTGAATGTAAATAAATTGTAG

f943.aa

MKNQFLNSYFQLITTIFLISSITIAEEITSTLKVPNGFKVEIFLNNTIEKPRGITSDDQGNIFIGSGSTFAYFVT  
KNRKIYTIAKTLQKPIGIDYWDNKLYISSVDKIYVVKNVKEEINKSIKSHKDYTWKMQIFALLPKNNSQMHSGRYI  
KVDSKNNKLIVNIGSQHNVKIPPKKEAVILSINLKTKEEIVAFGVRNSVGDFHPIISNEIYFSDNGQDGLDNIIP  
PDEINVITEYKEHFGFPYVFGKNQKNYGFYNKAPKNTKFIPSIYELPAHVAPLGIHFYRGNNFPKEYINKLFIAEH  
GSWNRSSPVGYKITTLDDIDSKTRTARNYKTFLYGFLKHKDSKFGRPVDIITYYDGSILFTDDFGNKIYRVVYEKI

t943.aa

EITSTLKVPNGFKVEIFLNNTIEKPRGITSDDQGNIFIGSGSTFAYFVTKNRKIYTIAKTLQKPIGIDYWDNKLYI  
SSVDKIYVVKNVKEEINKSIKSHKDYTWKMQIFALLPKNNSQMHSGRYIKVDSKNNKLIVNIGSQHNVKIPPKKEA  
VILSINLKTKEEIVAFGVRNSVGDFHPIISNEIYFSDNGQDGLDNIIPDEINVITEYKEHFGFPYVFGKNQKNY  
GFYNKAPKNTKFIPSIYELPAHVAPLGIHFYRGNNFPKEYINKLFIAEHGSWNRSSPVGYKITTLDDIDSKTRTARN  
YKTFLYGFLKHKDSKFGRPVDIITYYDGSILFTDDFGNKIYRVVYEKI

f943.nt

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ACCTAGAGGAATCACAAGCGATCAAGATGGAAAATATATTCATAGGATCTGGAAGCACTTTTGCATACTTTGTAACA  
AAAAACAGAAAAATTTATACCATAGCAAAAACCTTGCAAAAACCTATTGGTATTGATTATTGGGATAATAAACTCT  
ACATATCTTCTGTCGATAAAATATATGTAGTTAAAAATGTAAAAGAAGAAATTAATAAAAGCATAAAATCACATAA  
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AAGCAGTAATCCTTAGTATTAATTTAAAAACAAAAAAGAAGAAATAGTAGCTTTTGGAGTGAGAACTCAGTTGG  
GTTTGATTTTACCCAATTAGCAATGAAATATATTTTAGCGACAATGGCCAAGACGGATTAGGAGACAACATTCCTC  
CCAGATGAAATAAACGTAATAACCGAATATAAAGAACATTTTGGATTTCCCTATGTGTTTGGAAAAAATCAAAAAA  
ATTACGGTTTTTTATAACAAAGCACCCAAAAACACTAAGTTTATCCCATCTATTTACGAACTTCCCGCACATGTAGC  
TCCACTTGGAAATACACTTTTACCGGGGAAATAACTTTCCAAAAGAATACATAAATAAATTATTCATAGCAGAACAC  
GGCTCGTGGAAACAGATCTTCTCCTGTTGGCTACAAAATAACAACACTAGACATTGATTCTAAAACCAGAACAGCAA



TABLE 1. Nucleotide and Amino Acid Sequences

GAAATTACAAGACTTTTTTATATGGATTTTAAAGCACGACAAATCTAAATTTGGACGCCCTGTTGATATAATCAC  
ATATTATGACGGTTCAATTCTTTTACAGATGACTTTGGAAATAAAATATACAGAGTTTACTACGAAAAGATTTAA

t943.nt

GAAATAACAAGCACACTAAAAGTTCCTAATGGATTTAAAGTCGAAATTTTTTTAAACAATACAATTGAAAAACCTA  
GAGGAATCACAAGCGATCAAGATGGAAATATATTCATAGGATCTGGAAGCACTTTTGCATACTTTGTAACAAAAA  
CAGAAAAATTTATACCATAGCAAAAACCTGCAAAAACCTATTGGTATTGATTATTGGGATAATAAACTCTACATA  
TCTTCTGTCGATAAAATATATGTAGTTAAAAATGTAAAAGAAGAAATTAATAAAAGCATAAAATCACATAAAGACT  
ATACATGGAAAATGCAAATTTTTTGCACTTTTGCCAAAAAATAATTCTCAAATGCACTCAGGACGTTACATTAAAGT  
AGATTCTAAAAATAACAAATTAATAGTAAATATAGGATCCCAGCACAAATGT'AAAATTTCCCCAAAAAAGAAGCA  
GTAATCCTTAGTATTAATTTAAAAACAAAAAAGAAGAAATAGTAGCTTTTGGAGTGAGAACTCAGTTGGGTTTG  
ATTTTCACCCAATTAGCAATGAAATATATTTTAGCGACAATGGCCAAGACGGATTAGGAGACAACATTCCCCCAGA  
TGAAATAAACGTAATAACCGAATATAAAGAACATTTTGGATTTCCCTATGTGTTTGGAAAAAATCAAAAAAATTAC  
GGTTTTTTATAACAAAGCACCCAAAAACACTAAGTTTATCCCATCTATTTACGAACCTCCCGCACATGTAGCTCCAC  
TTGGAATACACTTTTACCGGGGAAATAACTTTCCAAAAGAATACATAAATAAATTATTTCATAGCAGAACACGGCTC  
GTGGAACAGATCTTCTCCTGTTGGCTACAAAATAACAACACTAGACATTGATTCTAAAACCAGAACAGCAAGAAAT  
TACAAGACTTTTTTATATGGATTTTTTAAAGCACGACAAATCTAAATTTGGACGCCCTGTTGATATAATCACATATT  
ATGACGGTTCAATTCTTTTACAGATGACTTTGGAAATAAAATATACAGAGTTTACTACGAAAAGATTTAA

f952.aa

MNYARFAVLIVLLFFYIWFFIILRMKRTNLFLEKIQNGAKILDIRSPKEYSKSHYLKSINIPFNNLFAKKDKLGD  
FESPIIVYGKSFNKS YEAKKVLKSMGFKNV FVAGTLKDMPQAKKEVG

t952.aa

RMKRTNLFLEKIQNGAKILDIRSPKEYSKSHYLKSINIPFNNLFAKKDKLGD FESPIIVYGKSFNKS YEAKKVLK  
SMGFKNV FVAGTLKDMPQAKKEVG

f952.nt

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AAAGAACTAATCTGTTTTTGT'TAGAAAAAATCCAAAATGGAGCAAAAATTTTGGATATTCGGTCTCCCAAGAATA  
TAGCAAGTCTCATPATTTGAAGTCAATTAACATTCCTTTTAATAATTTATTTGCTAAAAAGGATAAATTAGGTGAT  
TTTGAGTCCCCAATAATTGTTTATGGTAAAAGTTTTAATAAGTCTTACGAGGCTAAAAAGTTTTTAAAAGCATGG  
GATTTAAGAATGTGTTTGT'TGCTGGAACCTTGAAAGACATGCCACAAGCAAAAAAGAAGTTGGTTGA

t952.nt

AGGATGAAAAGAACTAATCTGTTTTTGT'TAGAAAAAATCCAAAATGGAGCAAAAATTTTGGATATTCGGTCTCCCA  
AAGAATATAGCAAGTCTCATTTATTTGAAGTCAATTAACATTCCTTTTAATAATTTATTTGCTAAAAAGGATAAATT  
AGGTGATTTTGAGTCCCCAATAATTGTTTATGGTAAAAGTTTTAATAAGTCTTACGAGGCTAAAAAGTTTTTAAA  
AGCATGGGATTTAAGAATGTGTTTGT'TGCTGGAACCTTGAAAGACATGCCACAAGCAAAAAAGAAGTTGGTTGA

TABLE 1. Nucleotide and Amino Acid Sequences

f378.aa

MIKKFLLFAMLNIFLTNKAHSNEEIIIEISTEIQKEKYIPFLISRGTQLEDLVKYTLEINPELDKNYVNTVAKTYI  
DESLIEGVNYDIAYAQMMLLETGALKFNGIVSKEQHNFSGIGATNNLTGNSFSNITEGIKAHIQHLKAYASKQNIK  
SNMVDPRFYLVKRGSAPTIYDLTGKWAKDKLYDKKLKKILLELLEYNNANKS

t378.aa

NEEIIIEISTEIQKEKYIPFLISRGTQLEDLVKYTLEINPELDKNYVNTVAKTYIDESLIEGVNYDIAYAQMMLLET  
GALKFNGIVSKEQHNFSGIGATNNLTGNSFSNITEGIKAHIQHLKAYASKQNIKSNMVDPRFYLVKRGSAPTIYD  
LTGWAKDKLYDKKLKKILLELLEYNNANKS

f378.nt

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TCGAAATAAGTACTGAAATACAAAAGGAAAAATATATTCCCTTTTTTAATAAGTAGAGGAAAAACTCAACTAGAAGA  
CCTTGTAATAATATACTCTAGAAATAAATCCAGAGCTTGACAAAAACTATGTAAATACTGTTGCTAAAACCTATATA  
GACGAATCTTTGATTGAAGGGGTTAATTATGACATTGCCTATGCTCAAATGTTACTAGAAACAGGAGCTCTAAAAT  
TCAATGGAATAGTTTCAAAGAACAACACAATTTTTTCAGGAATAGGCGCTACTAATAATCTTACAAAAGGAAATTC  
TTTTTCCAATATTACAGAAGGAATTAAAGCTCATATTTCAACATTTAAAAGCTTATGCTTCAAACAAAATATCAAA  
TCAAATATGGTTGATCCTAGATTTTACCTTGTTAAAAGAGGATCTGCTCCAACAATATATGATTTGACTGGGAAAT  
GGGCAAAAGACAAAACCTTTACGACAAAAAACTTAAAAAAATATTATTAGAACTATTAGAATATAATAATGCAAATAA  
AAGCTAA

t378.nt

AATGAAGAGATAATCGAAATAAGTACTGAAATACAAAAGGAAAAATATATTCCCTTTTTTAATAAGTAGAGGAAAAA  
CTCAACTAGAAGACCTTGTAATAATATACTCTAGAAATAAATCCAGAGCTTGACAAAAACTATGTAAATACTGTTGC  
TAAAACCTATATAGACGAATCTTTGATTGAAGGGGTTAATTATGACATTGCCTATGCTCAAATGTTACTAGAAACA  
GGAGCTCTAAAAATCAATGGAATAGTTTCAAAGAACAACACAATTTTTTCAGGAATAGGCGCTACTAATAATCTTA  
CAAAAAGGAAATCTTTTTTCCAATATTACAGAAGGAATTAAAGCTCATATTTCAACATTTAAAAGCTTATGCTTCAAA  
ACAAAATATCAAATCAAATATGGTTGATCCTAGATTTTACCTTGTTAAAAGAGGATCTGCTCCAACAATATATGAT  
TTGACTGGGAAATGGGCAAAAGACAACTTTACGACAAAAAACTTAAAAAAATATTATTAGAACTATTAGAATATA  
ATAATGCAAAATAAAGCTAA

f4.aa

MKLFRNRVMIKMPSSFTIIFSLIVFVTILTYVIPAGKFDKEFKQMGDGSKREIIVAGTYQYVDRGSRGFLHPIMTI  
LTAMSKGMEHAVEVIVFVLIVGGAYGIIMKTGAIDVGIYFLIKKLGHKDKLLIPLLMFIFSIGGTVTGMSEETLPF  
YFVMIPLIVALGYDSLUGAIIALGAGVGTMASTVNPFATGIASAIASISLQDGFYFRIVLYFVSVLAAITYVCVY  
ASKIKKDPKSLVYSQKDEHYQYFVKKDLSTGDNAQNALLEFTFAHKLVLVLLFGFMILILIFSIVNLGWWMQEMTM  
LYLGVAIIISAFICKLGETEMWDAFVKGSESLTAAALVIGLARGVMIVCDDGLITDMLNAATNFLYNLPRPLFIIL  
NEIIQIFIGFVVPSSSGHASLTMPIMAPLADFLSIPRASVVIAMQTASGLINLITPTSGVIMAVLGISRLSYGTWF  
KFVLPLFMIEFFISILVIIANIYLSF

t4.aa

TABLE 1. Nucleotide and Amino Acid Sequences

KFDKEFKQMGDGSKREIIIVAGTYQYVDRGSRGFLHPIMTILTAMSKGMEHAVEVIVFVLIVGGAYGIIMKTGAIDV  
GIYFLIKKLGHKDKLLIPLLMFIFSIGGTVTGMSEETLPFYFVMIPLIVALGYDSLVGAAI IALGAGVGTMASTVN  
PFATGIASAIASISLQDGFYFRIVLYFVSVLAAITYVCVYASKIKKDPKSLVYSQKDEHYQYFVKKDGLSTGDNA  
QNALEFTFAHKLVLVLLFGFMILILIFSIVNLGWWMQEMTMLYLGVAIISAFICKLGETEMWDAFVKGSSESLTAAL  
VIGLARGVMIVCDDGLITDTMLNAATNFLYNLPRPLFIILNEIIQIFIGFVVPSSSGHASLTMPIMAPLADFLSIP  
RASVVIAMQTASGLINLITPTSGVIMAVLGLISRLSYGTWFKFVLPLFMIEFFISILVIIANIYLSF

f4.nt

ATGAAATTATTTAGGAGAAACGTTATGATCAAAATGCCAAGTAGTTTTACAATAATATTTTCTTTAATTGTATTTG  
TTACCATTTTAAACGTATGTGATTCCTGCCGGTAAGTTTGATAAAGAATTTAAGCAAATGGGTGATGGATCTAAAAG  
GGAAATAATTGTTGCTGGAACCTATCAATATGTAGATCGAGGCTCTAGGGGATTTTTACATCCTATTATGACTATT  
TTAACCGCAATGTCAAAGGGGATGGAACATGCAGTTGAAGTTATTGTTTTTGTTTTAATTGTTGGGGGTGCTTATG  
GGATTATTATGAAAACCTGGAGCAATAGATGTGGGAATTTATTTTTTAATCAAGAAGTTGGGGCACAAGATAAGTT  
GCTTATTCCTTTGTAAATGTTTATTTTTTCAATTGGTGGAACGTAAACCGGAATGAGTGAAGAGACCCCTTCCTTTT  
TATTTTGTTATGATTCCTTGATAGTAGCTTTGGGTATGATAGTCTTGTGGAGCGGCTATTATTGCTTTAGGAG  
CTGGAGTGGGAACATAGGCTTCTACTGTAAATCCATTTGCGACAGGAATTGCATCTGCAATAGCTTCTATTAGCTT  
GCAGGATGGATTTTATTTTAGAATTGTTCTTTATTTTGTATCAGTATTGGCTGCTATAACCTATGTTTGTGTTTAT  
GCGTCTAAAATTAAAAAGGATCCCTCAAAATCGCTTGTTGTTATCTCAAAAAGATGAACATTATCAATATTTTGTTA  
AAAAAGATGGACTTCTACCGGAGATAATGCTCAGAATGCTCTTGAGTTTACTTTTGCTCATAAATTAGTTTACT  
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TTGTATCTTGAGTTGCTATTATATCGGCTTTTATTTGTAAATTAGGTGAACTGAAATGTGGGATGCGTTTGTTGA  
AAGTTCTGAAAGTCTGCTAACCCTGCTCTTGTATTGGACTTGCTAGAGGTGTTATGATAGTATGTGATGATGG  
GTTGATTACAGATACTATGTTAAATGCTGCTACTAATTTTATACAAATCTTCCAAGACCCCTTTTTATCATATTG  
AATGAAATTATTCAAATATTTATAGGATTTGTTGTTCCATCTTCATCAGGACATGCTAGTCTCACTATGCCAATAA  
TGGCTCCTCTTGCCGATTTTTTGTCAATTCCAAGAGCTTCAGTTGTTATTGCCATGCAGACTGCATCTGGGCTTAT  
TAATTTGATAACACCTACCAGCGGAGTTATAATGGCTGTATTGGGGATATCCAGATTGAGTTATGGTACGTGGTTT  
AAGTTTGTTTTACCATTATTTATGATTGAGTTTTTTATCTCTATTTTAGTTATTATAGCTAACATTTATTTAAGTT  
TTTAG

t4.nt

AAGTTTGATAAAGAATTTAAGCAAATGGGTGATGGATCTAAAAGGGAAATAATTGTTGCTGGAACCTATCAATATG  
TAGATCGAGGCTCTAGGGGATTTTTACATCCTATTATGACTATTTTAAACCGCAATGTCAAAGGGGATGGAACATGC  
AGTTGAAGTTATTGTTTTTGTTTTAATTGTTGGGGGTGCTTATGGGATTATTATGAAAACCTGGAGCAATAGATGTG  
GGAATTTATTTTTTAATCAAGAAGTTGGGGCACAAGATAAGTTGCTTATTCCTTTGTTAATGTTTATTTTTTCAA  
TTGGTGGAACGTAAACCGGAATGAGTGAAGAGACCCCTTCCTTTTTATTTTGTATGATTCCCTTGATAGTAGCTTT  
GGTTATGATAGTCTTGTGGAGCGGCTATTATTGCTTTAGGAGCTGGAGTGGGAACCTATGGCTTCTACTGTAAAT  
CCATTGCGACAGGAATTGCATCTGCAATAGCTTCTATTAGCTTGCAGGATGGATTTTATTTTAGAATTGTTCTTT  
ATTTTGTATCAGTATTGGCTGCTATAACCTATGTTTGTGTTTATGCGTCTAAAATTAAAAAGGATCCCTCAAAATC  
GCTTGTGTATTCTCAAAAAGATGAACATTATCAATATTTTGTTA AAAAAGATGGACTTCTACCGGAGATAATGCT  
CAGAATGCTCTTGAGTTTACTTTTGCTCATAAATTAGTTTACTTTTATTTGGATTTATGATATTGATTTTGATAT  
TTAGCATTGTTAATCTTGTTGGTGGTGGATGCAAGAAATGACAATGTTGTATCTTGAGATTGCTATTATATCGGCTTT  
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GTTATTGGACTTGCTAGAGGTGTTATGATAGTATGTGATGATGGGTTGATTACAGATACTATGTTAAATGCTGCTA  
CTAATTTTTTATACAATCTTCCAAGACCCCTTTTTATCATATTGAATGAAATTATTCAAATATTTATAGGATTTGT  
TGTTCATCTTCATCAGGACATGCTAGTCTCACTATGCCAATAATGGCTCCTCTTGCCGATTTTTTGTCAATTCCA  
AGAGCTTCAGTTGTTATTGCCATGCAGACTGCATCTGGGCTTATTAATTTGATAACACCTACCAGCGGAGTTATAA  
TGGCTGTATTGGGGATATCCAGATTGAGTTATGGTACGTGGTTTAAGTTTGTTTTACCATTATTTATGATTGAGTT  
TTTTATCTCTATTTTAGTTATTATAGCTAACATTTATTTAAGTTTTTAG

TABLE 1. Nucleotide and Amino Acid Sequences

f43.aa

MKYFYFLFFLLIFNVYAQNVNSPALPSPPLLPEITENKPVERENSSKGENFSNVGLDGKYVNDTILYGLDSQVTSI  
IKALKKSSDSQYNFSLKKRLEKTFNAELKREILELFISLKYSGGIDTANYILENYESKRYSNALFGLAISYLKEFD  
DKEKLKKTLDILENKEGNVVSIAAYYLGELNSLEYSKNMMEVFEEKYSGNDGARREILIALGKMSAVDYQDRIYEI  
SLDNYEGPSIKAAAIEALSYLASDKVTENADLYLQSNNNNLNVKLAIIASLSKDP SLKSKEILQGFLRSDDNIRF  
KAINAIKGRDSSAKDILYKLSKDP SLKVREASAKALIDMDLGNIEIKNIMFDFKIDNNFKISMFSYLLDKDSLK  
ALSIALEIVNKENINRPSNVLRGVASMLAGKKGNFDNFYSKIIDSKNIDLRHLALKGAVYNKSSSLSDKLKKIKSE  
TNSEYIKMLLKDY

t43.aa

LPSPPPLLPEITENKPVERENSSKGENFSNVGLDGKYVNDTILYGLDSQVTSIIKALKKSSDSQYNFSLKKRLEKTF  
NAELKREILELFISLKYSGGIDTANYILENYESKRYSNALFGLAISYLKEFDDKEKLKKTLDILENKEGNVVSIA  
AYYLGELNSLEYSKNMMEVFEEKYSGNDGARREILIALGKMSAVDYQDRIYEISLDNYEGPSIKAAAIEALSYLASD  
KVTENADLYLQSNNNNLNVKLAIIASLSKDP SLKSKEILQGFLRSDDNIRFKAINAIKGRDSSAKDILYKLS  
DPSLKVREASAKALIDMDLGNIEIKNIMFDFKIDNNFKISMFSYLLDKDSLKALSIALEIVNKENINRPSNVLRGV  
ASMLAGKKGNFDNFYSKIIDSKNIDLRHLALKGAVYNKSSSLSDKLKKIKSETNSEYIKMLLKDY

f43.nt

ATGAAATACTTTTATTTTTTATTTTTTTACTTATTTTTAATGTGTATGCTCAAAATGTTAATTCTCCAGCTCTTC  
CTAGTCCGCCTTTGTTGCCCGAAATTACAGAAAATAAGCCTGTTGAGAGAGAAAATTCTTCTAAGGGAGAGAATTT  
TTCTAATGTTGGTTTAGATGGTAAGTATGTTAACGATACAATTCTTTATGGGCTTGATAGTCAAGTGACAAGCATT  
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TCTTGAAAATTATGAGAGTAAAGATATTCAAACGCTTTATTTGGCTTGGCAATTTCTGATCTTAAGGAGTTTGAT  
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ATTATTTAGGAGAGCTTAATTTCTCTTGAGTATTTCTAAAAACATGATGGAAGTTTTTGAAAAATATTCTGGAAATGA  
TGGGGCTAGAAAGAGAAATACTTATTGCTCTTGGA AAAATGTCCGCTGTTGATTATCAGGATAGAATTTATGAAAT  
TCGCTAGATAATTACGAGGGCCCATCAATTAAGGCTGCTGCAATCGAAGCGTTGTCAATCTTGCTTCAGATAAAG  
TAACTGAAAATGCTGATTTGTATCTTCAGAGTAATAACAATAATTTAAATGTTAAATTAGCTATTATTGCTTCTTT  
GTCCAAAGATCCTTCTTTAAAGTCTAAAGAGATTTTACAAGGATTTTAAAGAGATTCTGATGATAATATTAGGTTT  
AAAGCTATTAAATGCAATCAAAGGACATAGGGACTCTTCTGCAAAGGATATTTTGATTTATAAGCTTAAAGCGATC  
CATCTCTTAAAGTTAGGGAGGCTTCTGCTAAGGCCTTAATTGATATGGATCTTGGAATATTGAGATAAAAAACAT  
TATGTTTGATTTTAAAGATTGACAATAATTTTAAAAATTTCAATGTTTAGTTACCTTTTAGATAAGGATTTCTCTAAAA  
GCATTTGTCAATTGCTTTAGAAATTGTTAATAAAGAAAAATTAATAGACCCTCAAATGTTTAAAGGGCGTTGCTT  
CAATGTTGGCTGGTAAAAAGGGTAATTTTGATAATTTTATTCTTAAATCATTGACAGCAAAAATATTGATTTAAG  
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ACGAACTCCGAATATATTAAATGCTTTTAAAGATTATTGA

t43.nt

CTTCCTAGTCCGCCTTTGTTGCCCGAAATTACAGAAAATAAGCCTGTTGAGAGAGAAAATTCTTCTAAGGGAGAGA  
ATTTTTCTAATGTTGGTTTAGATGGTAAGTATGTTAACGATACAATTCTTTATGGGCTTGATAGTCAAGTGACAAG  
CATTATAAAAGCTCTTAAAAAATCAAGCGATAGTCAATATAATTTTTCTCTTAAAAAAGACTTGAGAAAACTTT  
AATGCTGAGCTTAAAAGGGAAATACTTGAATTGTTTATTTCTCTTAAAGTATTCGGGGGGCATTGATACAGCAAAT  
ATATTCTTGAAAATTATGAGAGTAAAGATATTCAAACGCTTTATTTGGCTTGGCAATTTCTGATCTTAAGGAGTT

TABLE 1. Nucleotide and Amino Acid Sequences

TGATGATAAAGAAAAATTAAAAAACTCTTATTGACATTCTTGAAAAATAAGAGGGCAATGTGGTATCTATTGCA  
GCTTATTATTAGGAGAGCTTAATTCCTTGAGTATTCTAAAAACATGATGGAAGTTTTTGAAAAATATTCTGGAA  
ATGATGGGGCTAGAAGAGAAATACCTATTGCTCTTGAAAAATGTCCGCTGTTGATTATCAGGATAGAATTTATGA  
AATTTTCGCTAGATAATTACGAGGGGCCATCAATTAAGGCTGCTGCAATCGAAGCGTTGTCATATCTTGCTTCAGAT  
AAAGTAACTGAAAAATGCTGATTGTATCTTCAGAGTAATAACAATAATTTAAATGTTAAATTAGCTATTATTGCTT  
CTTTGTCCAAAGATCCTTCTTTAAAGTCTAAAGAGATTTTACAAGGATTTTTAAGAGATTCTGATGATAATATTAG  
GTTTAAAGCTATTAATGCAATCAAAGGACATAGGGACTCTTCTGCAAAGGATATTTTGATTATAAGCTTAAAGC  
GATCCATCTCTTAAAGTTAGGGAGGCTTCTGCTAAGGCCTTAATTGATATGGATCTTGGGAATATTGAGATAAAAA  
ACATTATGTTTGAATTTAAGATTGACAATAATTTTAAAAATTTCAATGTTTAGTTACCTTTTAGATAAGGATTCTCT  
AAAAGCATTGTCAATTGCTTTAGAAATTGTTAATAAAGAAAAATATTAATAGACCCTCAAATGTTTTAAGGGGCGTT  
GCTTCAATGTTGGCTGGTAAAAAGGGTAATTTTGATAATTTTTATTCTAAAATCATTGACAGCAAAAATATTGATT  
TAAGGCATTTAGCATTAAGGAGCTGTTTATAATAAATCTTCATCGCTTTCTGATAAGCTTAAAAAATTAAAAG  
TGAAACGAACTCCGAATATATTAATGCTTTTTAAAGATTATTGA

f50.aa

MKFVLNNLFKGC LICFFLFFSCLTTDRSIQDSHISDIVEKKKEAVIIDNNVVLGSNEGKFKRDYILIGLKDNESEFF  
LSDAFLKENNFYFKKARESYAKKNIGLTNYLKNKIVTNNQHSRELLAKANLFFGYVNYENGFYDLSEYNFDLFLK  
DYKYSHASRLAELKYLVEKSDAISAFKEINEFSISGYDREIYGFLSNKLGVSHLNLESLGFLDNSVFDTFVFND  
NIFVTNIGLLRLYNIKKNDRCRVYLDKKSIFLNGIRGFADYNGTIYIGGKNVVYYIDDVDGDLKQINVPGNADFS  
NVQVLLAVKNGIFVGTNLNSGLWFYDLKNWKNIPLGSNKISSLCFDSLKNLLLVGTVDKAIYSVNVDNLKKIEHLDF  
FSKNDNEKNINFIKEYKDSYFVGTYGGGLFELNLNKNYSYKKHVIANNIDVNYFMDMEIKDKKLLFATFDHGLLIYD  
SENDNWDYFGPNNGLLNLNLIKVSRFENYVILGTINNGLVFVDENIKKQL

t50.aa

CLTTDRSIQDSHISDIVEKKKEAVIIDNNVVLGSNEGKFKRDYILIGLKDNESEFFLSDAFLKENNFYFKKARESYA  
KKNIGLTNYLKNKIVTNNQHSRELLAKANLFFGYVNYENGFYDLSEYNFDLFLKDYKYSHASRLAELKYLVEK  
SDAISAFKEINEFSISGYDREIYGFLSNKLGVSHLNLESLGFLDNSVFDTFVFNDNIFVTNIGLLRLYNIKKND  
RVYLDKKSIFLNGIRGFADYNGTIYIGGKNVVYYIDDVDGDLKQINVPGNADFSNVQVLLAVKNGIFVGTNLNSGL  
WFYDLKNWKNIPLGSNKISSLCFDSLKNLLLVGTVDKAIYSVNVDNLKKIEHLDFFSKNDNEKNINFIKEYKDSYF  
VGTYGGGLFELNLNKNYSYKKHVIANNIDVNYFMDMEIKDKKLLFATFDHGLLIYDSENDNWDYFGPNNGLLNLNL  
IKVSRFENYVILGTINNGLVFVDENIKKQL

f50.nt

ATGAAATTTGTTTTGAATAAATTTATTTAAAGGTTGTCTTATATGTTTTTTCTTGTTTTTTTCTGCCTTACTACAG  
ATAGATCTATTCAAGATTCTCATATTAGTGATATTGTAGAGAAGAAAAAGAGCAGTCATTATTGATGATAATAA  
TGTTGTTCTTGAGGAGTAATGAGGGTAAATTTAAAGAGACTATTTGATAGGATTAAGATAATGAATCTTTTTTT  
CTTAGTGATGCTTTTTTAAAGAAAAATAATTTTTATTTTAAAAAGCCAGGAAAGTTATGCTAAAAAAATATTG  
GCTTGACAAATTATTATTTGAATAAAATAGTAATAATGAGAATCAGCACAGCAGAGAATTGCTAGCTAAAGCGAA  
TTTGTTTTTTGGATATGTAAATTATGAGAATGGTTTTTATGATCTTTCCGAATATAATTTTGATCTATTTTTAAA  
GACTATAAATATTCTCATGCTAGTTTAAAGATTAGCTGAATTAATAATATCTTGTTAAAGAAAAATCTGATGCAATTT  
CTGCATTTAAAGAGATTAATGAATTTTCTATCTCAGGTTATGATAGAGAGATTTATGGCTTTTTAAGTAATAAACT  
TGGAGTAAGTCATTTAACTTAGAGTCTTTAGGATTTCTTGACAACAGCGTTTTTGATACATTTGTCTTTAATGAC  
AATATATTTGTAATAATATATGGGAGGGCTTTTAAAGATATAATATTAAGAAAAATGATTGTAGAGTCTATCTTA  
AGGATAAAAAAGCATTTTTTTAAATGGCATTAGGGGTTTTGCGGATTATAATGGAACAATTTATATTGGTGGTAA  
AAATGTTGTTTATTATATAGATGATGTTGATGGGGATTTAAAGCAAATAAATGTTCCCGGTAATGCTGATTTTAGC  
AATGTACAAGTTTGTCTGCTGTTAAAAATGGAATATTTGTTGGCACTCTAAATCTGGATTATGGTTTTATGATT  
TAAAAAATTGAAAAATATACCGCTTGATCTAATAAAATTTCTTCACTCTGCTTTGATAGTTTAAAAAATTTATT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAGTTGGAACAGTTGACAAGGCTATTTATAGTGTTAATGTCGATAATTTGAAAAAGATTGAACATTTGGATTTT  
TTTAGCAAAAATGATAATGAAAAAATATTAATTTTATAAAAGAAATATAAAGATAGTTATTTTGGTTGGAACATATG  
GTGGGGGTCTTTTGAATTAAATTTAAATAAAAAATAGTTACAAAAAGCACGTTATTGCCAATAATATTGATGTTAA  
TTATTTTATGGATATGGAGATTAAAGATAAAAAAGCTATTGTTTGCAACCTTTGATCATGGGTTATTGATTTATGAT  
TCTGAAAAATGACAACCTGGGATTATTTTGGACCCAATAATGGGCTTCTTAATTTGAATTTAATAAAAGTTTCTAGAT  
TTGAAAAATTATGTCATACTGGGCACTATTAATAACGGTTTGGTTTTTGTAGATGAAAATATTAAAAAACAGTTATC  
A

t50.nt

TGCTTACTACAGATAGATCTATTCAAGATTCTCATATTAGTGATATTGTAGAGAAGAAAAAGAAGCAGTCATTA  
TTGATGATAATAATGTTGTTCTTGGGAGTAATGAGGGTAAATTTAAAAGAGACTATTTGATAGGATTAAAAGATAA  
TGAATCTTTTTTCTTAGTGATGCTTTTTTAAAAGAAAATAATTTTATTTTAAAAAAGCCAGGGAAAGTTATGCT  
AAAAAAAATATTGGCTTGACAAATTATTATTTGAATAAAAATAGTAACTAATGAGAATCAGCACAGCAGAGAATTGC  
TAGCTAAAGCGAATTTGTTTTTGGATATGTAAATTATGAGAATGGTTTTTATGATCTTCCGAATATAATTTTGA  
TCTATTTTTTAAAAGACTATAAATATTCTCATGCTAGTTTAAAGATTAGCTGAATTAATAATATCTTGTTAAAGAAAA  
TCTGATGCAATTTCTGCATTTAAAGAGATTAATGAATTTCTATCTCAGGTTATGATAGAGAGATTTATGGCTTTT  
TAAGTAATAAACTTGGAGTAAGTCATTTAAACTTAGAGTCTTTAGGATTTCTTGACAACAGCGTTTTTGATACATT  
TGTCTTTAATGACAATATATTTGTAACATAATATTTGGGAGGGCTTTTAAAGATATAATATTAATAAAAAATGATTGT  
AGAGTCTATCTTAAGGATAAAAAAAGCATTTTTTTAAATGGCATTAGGGGTTTTGCGGATTATAATGGAACAATTT  
ATATTGGTGGTAAAAATGTTGTTTATTATATAGATGATGTTGATGGGGATTAAAGCAAATAAATGTTCCCGGTAA  
TGCTGATTTTAGCAATGTACAAGTTTGCTTGCTGTTAAAAATGGAATATTTGTTGGCACTCTAAATCTGGATTA  
TGGTTTTATGATTTAAAAAATTGGAATAATATACCGCTTGGATCTAATAAAATTTCTTCACCTGCTTTGATAGTT  
TAAAAAATTATTATTAGTTGGAACAGTTGACAAGGCTATTTATAGTGTTAATGTCGATAATTTGAAAAAGATTGA  
ACATTTGGATTTTTTTAGCAAAAATGATAATGAAAAAATATTAATTTTATAAAAGAATATAAAGATAGTTATTTT  
GTTGGAACATATGGTGGGGGTCTTTTTGAATTAATTTAAATAAAAAATAGTTACAAAAAGCACGTTATTGCCAATA  
ATATTGATGTTAATTATTTTATGGATATGGAGATTAAAGATAAAAAAGCTATTGTTTGCAACCTTTGATCATGGGTT  
ATTGATTTATGATTCTGAAAATGACAACCTGGGATTATTTTGGACCCAATAATGGGCTTCTTAATTTGAATTTAATA  
AAAGTTTCTAGATTTGAAAATTATGTCATACTGGGCACTATTAATAACGGTTTGGTTTTTGTAGATGAAAATATTA  
AAAAACAGTTATGA

f65.aa

MHIFKNVPFQINLILFLLVSVAKINASSKFYYAEQWYVIFNSQMKKKPENYKKNIFFLQKALKYPFGNPKYSLTKI  
ETKEQWEKYKLLFKMHVNLLLVRQNLHLGLDFDTRNLYFFKTPEKDGII SNLEKSKKLYKLAINYYSEALKYHKKL  
ENYTTVKLENDGITNWEDEYHKISLKELNYYDIIKKELLRIDETKAFFEQGPNNY

t65.aa

KINASSKFYYAEQWYVIFNSQMKKKPENYKKNIFFLQKALKYPFGNPKYSLTKIETKEQWEKYKLLFKMHVNLLL  
RQNLHLGLDFDTRNLYFFKTPEKDGII SNLEKSKKLYKLAINYYSEALKYHKLENYTTVKLENDGITNWEDEYHK  
ISLKELNYYDIIKKELLRIDETKAFFEQGPNNY

f65.nt

ATGCATATTTTCAAAAATGTCCCCTTCCAAATAAAATTTAATTTTATTTCTTTTAGTATCAGTTGCAAAGATAAATG  
CATCGTCCAAATTTTATTACGCAGAACAATGGTATGTAATTTTAAATCTCAAATGAAAAAAAACCTGAAAACTA  
TAAAAAAAATATATTTTTCTTCAAAAAGCCTTAAATACCCATTGGAATCCAAAATATTCTCTAACTAAAATA  
GAAACCAAAGAACAGTGGGAAAAATATAAACTTCTTTTCAAAATGCATGTAACTTGCTTCTAGTTAGGCAAAATT  
TACATTTAGGAGATTTATTCGACACAAGAAATTTATATTTTTTCAAACTCCAGAAAAAGATGGAATTATTTCCAA  
TCTAGAAAAATCAAAAAAATTATATAAACTAGCTATTAATTACTACAGCGAAGCACTAAAATACCACAAAAAATTT  
GAAAATTACACAACCTGTTAACTAGAAAACGATGGAATAACAACTGGGAAGATGAATATCATAAAATTTCTCTTA

TABLE 1. Nucleotide and Amino Acid Sequences

AAGAGCTTAATTACTATGACATTATTAAAAAAGAACTACTAAGAATTGACGAACTAAAGCATTTTTTGAACAAGG  
GCCAACTATTATTAA

t65.nt

KINASSKFYYAEQWYVIFNSQMKKKPKENYKKNIFFLQKALKYPFGNPKYSLTKIETKEQWEKYKLLFKMHVNLLLV  
RQNLHLGDLFDRNLYFFKTPEKDGIIISNLEKSKKLYKLAINYYSEALKYHKLENYTTVKLENDGITNWEDEYHK  
ISLKELNYYDIIKKELLRIDETKAFFEQGPNNY

f8.aa

MKNINRLILLILTHTLLFSCALIADNKSKNLSTSEIILTQKTLLESSLIKPNPSNVEYRIPISSIQEILNNNDSF  
LIKKTAAKIKISPQKLEEKNYLNAYKNYLNNETEWIKFIDQSSVNGNLTIKIDTAFEKKTNFNHTNSDNENLT  
IELQMHLEKEILNLIEQTFHDKNLGYIQLSHINSFFPQENINSITKEIIDGKEYIAPHIIANQLLKIKDKKYFEQF  
MHFLKVENSKIKTIIIEKQKISDLHNELYYSKQSPRRRRKRSTADSDNNNKYDIIIPKIIDPNTGIEITPKNLSILS  
NGDIILIKPKIDWTEFFYFWQHVGFDEEKYEATKKIAFNIGDSFDIKSIITSNQIKFDTASTQSGGYEKLSTYVQ  
SRILKIFSPITDIRTIQKAINFGRSRYIDNNGYMPVLISSNLWTDSEFNLEEIHNKTYCSLMVDRIYKIAGLNVSR  
NYEISGIITPGEINAAAYNFYMSYTIAGILPSVLPKRLIKPTLKEKFIGYNKEIVDAIELKKSKEKIFGRACNITN  
LWCSGS

t8.aa

CALIADNKSKNLSTSEIILTQKTLLESSLIKPNPSNVEYRIPISSIQEILNNNDSFLIKKTAAKIKISPQKLEEK  
NYLNAYKNYLNNETEWIKFIDQSSVNGNLTIKIDTAFEKKTNFNHTNSDNENLTIELQMHLEKEILNLIEQTFH  
DKNLGYIQLSHINSFFPQENINSITKEIIDGKEYIAPHIIANQLLKIKDKKYFEQFMHFLKVENSKIKTIIIEKQKI  
SDLHNELYYSKQSPRRRRKRSTADSDNNNKYDIIIPKIIDPNTGIEITPKNLSILSNGDIILIKPKIDWTEFFYFW  
QHVGFDEEKYEATKKIAFNIGDSFDIKSIITSNQIKFDTASTQSGGYEKLSTYVQSRILKIFSPITDIRTIQKAI  
NFGRSRYIDNNGYMPVLISSNLWTDSEFNLEEIHNKTYCSLMVDRIYKIAGLNVSRNYEISGIITPGEINAAAYNF  
YMSYTIAGILPSVLPKRLIKPTLKEKFIGYNKEIVDAIELKKSKEKIFGRACNITNLWCSGS

f8.nt

ATGAAGAATATTAATAGATTAATATTATTAATATTAACACACACTTTATTATTCTCTTGTGCCTTAATTGCAG  
ATAATAAGTCAAAAAATTTAAGCACATCAGAAATCATATTAACACAAAAAAGCTCTTTAATAAAA  
AAATCCTTCTAATGTAGAATATCGAATACCAATATCCAGTATCCAAGAAATTTTAAACAATAACAATGATTCTTTT  
TTAATAAAAAAACAGCAGCAAAAATCAAAAATAAGCCCTCAAAAACCTTGAAGAAATAAAAAACTATCTAAATGCTT  
ATAAAAAATTATCTAAATAATGAAACAGAATGGATAAAGTTTATAGATCAAAGTAGCGTCAATGGAAATTTAACAAT  
TAAAAATTGATACTGCTTTTGAAGAAAAAACAATTTTAAATCATACAAATTCAGATAATGAAATTTAACAGAACTA  
ATAGAACTACAAATGCATCTGGAAAAAGAAATTTTAAACTTAATTGAGCAAACATTTTCATGATAAAAAATTTAGGAT  
ATATACAATTAAGTCACATCAACTCATTCTTTTCTCAAGAAAATATAAACTCAATAACAAAAGAAATAATAGATGG  
AAAAGAATATATTGCACCGCACATAATAGCAAATCAATTATTAATAAATAAAGATAAAAAATATTTTGAACAATTT  
ATGCACTTTTTAAAGTTGAAAACAGCAAAAATAAAAAACAATAATTGAAAACAAAAAATTTTCAGATCTTCACAATG  
AACTGTATTATTCAAAACAATCCCGCCCCAGAAGAAGAAAAAGGTCAACTGCCGATTCCGATAATAACAATAAATA  
CGATATAATACCAAAAATAATAGACCCAAATACAGGCATTGAAATAACTCCTAAAAATTTAAGATCTATTTTATCA  
AATGGCGACATAATACTAATAAAACCAAAAATAGATTGGACAGAATTTTTTTTATTTTGGCAACATGTGGGAATAT  
TTGATGAAGAAAAATATGAAGCCACTAAAAAAATTCGATTCAATGGAATTGATAGCTTTGATATAAAATCAATAAT  
TACAAGCAATCAAATCAAATTCGATACAGCATCTACTCAAGGTTTCAGGATACGAAAAGCTTTCAACATACGTACAA  
TCAAGAATATTAATAATATTCTCACCAATAACAGACATAAGAACAATTCAAAAAGCTATTAATTTTGGGAAGAAGTA  
GATACATTGACAATAACTTTGGATATATGGTTCCATTAAATATCCTCTAATTTATGGACAGATTCAATCAATCTTGA  
AGAAATTCACAACAAAACCTATTGCTCTTTAATGGTTGATAGAATATATAAAATAGCAGGACTTAATGTATCAAGA

TABLE 1. Nucleotide and Amino Acid Sequences

AATTACGAAATTTTCGGAATAATTACTCCTGGAGAAATAAATGCAGCAGCTTACAATTTTTTACATGTCTTATACGA  
TTGCAGGAATACCTTCCAAGCGTGCTTCCAAAAAGGCTCATTTAAACCAACATTAAAAGAAAAATTCATTGGTTACAA  
TAAAGAAATAGTAGATGCAATAGAATTAAAAAAATCGAAAGAAAAAATTTTTGGGAGAGCTTGCAACATTACAAAT  
CTCTGGTGCTCAGGAAGTTAA

t8.nt

TGTGCCTTAATTGCAGATAATAAGTCAAAAAATTTAAGCACATCAGAAATCATATTAACACAAAAAACACTACTAG  
AAAGCTCTTTAATAAAAAATCCTTCTAATGTAGAATATCGAATACCAATATCCAGTATCCAAGAAATTTTAAACAA  
TAACAATGATTCTTTTTTAATAAAAAAACAGCAGCAAAAAATCAAAATAAGCCCTCAAAAACTTGAAAGAAATAAAA  
AACTATCTAAATGCTTATAAAAAATTATCTAAATAATGAAACAGAATGGATAAAGTTTATAGATCAAAGTAGCGTCA  
ATGGAAATTTAACAATTAATAATTGATACTGCTTTTGAAAAAACAATTTTAATCATACAAATTCAGATAATGA  
AAATTTAACAGAACTAATAGAACTACAAATGCATCTGGAAAAAGAAATTTTAACTTAATTGAGCAACATTTTCAT  
GATAAAAAATTTAGGATATATACAATTAAGTCACATCAACTCATCTTTCTCAAGAAAATATAAACTCAATAACAA  
AAGAAATAATAGATGGAAAAGAATATATTGCACCGCACATAATAGCAAATCAATTATTAATAAATAAAAGATAAAAA  
ATATTTTGAACAATTTATGCACTTTTTAAAGTTGAAACAGCAAAATAAAACAATAATTGAAAAACAAAAAATT  
TCAGATCTTCACAATGAAGTGTATTATTCAAAACAATCCCCGCCAGAGAAGAAAAAGGTCAACTGCCGATTCCG  
ATAATAACAATAAATACGATATAATACCAAAAAATAATAGACCCAAATACAGGCATTGAAATAACTCCTAAAAATTT  
AAGATCTATTTTATCAAATGGCGACATAATACTAATAAAACCAAAATAGATTGGACAGAATTTTTTTATTTTTTG  
CAACATGTGGGAATATTTGATGAAGAAAAATATGAAGCCACTAAAAAATTGCATTCAATGGAATTGATAGCTTTG  
ATATAAAATCAATAATTACAAGCAATCAAATCAAATTCGATACAGCATCTACTCAAGGTTGAGGATACGAAAAGCT  
TTCAACATACGTACAATCAAGAATATTAATAATATCTCACCAATAACAGACATAAGAACAATTCAAAAAGCTATT  
AATTTTGGAAGAAGTAGATACATTGACAATAACTTTGGATATATGGTTCCATTAATATCCTCTAATTTATGGACAG  
ATTCAATCAATCTTGAAGAAATTCACAACAAAACCTATTGCTCTTTAATGGTTGATAGAATATATAAAATAGCAGG  
ACTTAATGTATCAAGAAATTCAGAAATTTTCGGAATAAATTAATCTCTGGAGAAATAAATGCAGCAGCTTACAATTTT  
TACATGCTTATACGATTGCAGGAATACTTCCAAGCGTGCTTCCAAAAAGGCTCATTTAAACCAACATTAAAAGAAA  
AATTCATTGGTTACAATAAAGAAATAGTAGATGCAATAGAATTAAAAAAATCGAAAGAAAAAATTTTTGGGAGAGC  
TTGCAACATTACAAATCTCTGGTGCTCAGGAAGTTAA

f82.aa

MTRVFSKFFLFFCFSMLLFANSEDSNEKDIVSKDENPVFENEVLGYWVGYNVSNIKNSIIYIYKYNGEVYGRILT  
IIKDGGKYDAKNPSGDTVVGFEENLAIEGLDFMWGLKYSSSSKKWDRGKIIDPKNGKIYNSEMRVDSKTGNLITKKG  
VWIFGRSKIWTRAKDDEIPKLDLHNLVPAPPVKK

t82.aa

EDSNEKDIVSKDENPVFENEVLGYWVGYNVSNIKNSIIYIYKYNGEVYGRILTIKDGGKYDAKNPSGDTVVGFE  
NLAIEGLDFMWGLKYSSSSKKWDRGKIIDPKNGKIYNSEMRVDSKTGNLITKGVWIFGRSKIWTRAKDDEIPKLD  
LHNLVPAPPVKK

f82nt

ATGACTAGAGTTTTTCAAAGTTTTTCTTTTTTTTTGTTTTTCAATGCTTTTATTTGCAAATTCAGAAGATTCAA  
ATGAAAAGGACATTGTTAGCAAGGATGAAAACCTGTTTTTGAAATGAAGTTTATAGGATATTGGGTTGGTTATAA  
TGATGTAAGTAACATAAAGAATTCTATTATCTATATTTATAAAATAAATGGGGAAGTTTATGGCCGAATTTTAACT  
ATAATAAAAGATGGCAAAAAGTATGATGCTAAAAATCCTTCAGGAGATACTGTAGTTGGGTTTGAAATCTTGCAA  
TAGAGGGTCTTGATTTTATGTGGGTCTTAAGTATTCTTCTTCTTCTAAAAAGTGGGATAGGGGCAAAATAATAGA



TABLE 1. Nucleotide and Amino Acid Sequences

TCCTAAAAACGGTAAAAATTTATAATTCTGAGATGCGTGTGATAGTAAAAACCGGAAATCTTATTACCAAGGGGAAA  
GTTTGGATTTTGGTAGAAGTAAAAATTTGGACAAGAGCTAAAGATGATGAAATACCAAATTAGATTTGCATAATC  
TTGTTCCAGCGCCCCCTGTGAAAAAATAA

f82.nt

GAAGATTCAAATGAAAAGGACATTGTTAGCAAGGATGAAAACCTGTTTTTGAAAATGAAGTTTTAGGATATTGGG  
TTGGTTATAATGATGTAAGTAACATAAAGAATTCTATTATCTATATTTATAAATATAATGGGGAAGTTTATGGCCG  
AATTTTAACTATAATAAAAGATGGCAAAAAGTATGATGCTAAAAATCCTTCAGGAGATACTGTAGTTGGGTTTGAA  
AATCTTGCAATAGAGGGTCTTGATTTTATGTGGGGTCTTAAGTATTCTTCTTCTTCTAAAAAGTGGGATAGGGGCA  
AAATAATAGATCCTAAAAACGGTAAAAATTTATAATTCTGAGATGCGTGTGATAGTAAAAACCGGAAATCTTATTAC  
CAAGGGGAAAGTTTGGATTTTGGTAGAAGTAAAAATTTGGACAAGAGCTAAAGATGATGAAATACCAAATTAGAT  
TTGCATAATCTTGTTCCAGCGCCCCCTGTGAAAAAATAA

f86.aa

MNKLMLMLITFATSLLAQTNKASTGLKTDQSFNNSLSESVKLKEIADIYPTNTNFLTGIGIVAGLAGKGDSEIKQKD  
LIIKILEENNIINEIGSNNIESKNIALVNVSLQVKNTIKGSKHKACVASILDSKDLTNGILLKTNLKNKEGEIIA  
IASGITQPNNKLKSGYITIDSVIINENQNINHSYNIILKKNYTLINRIHKILTSKINNKKIKSDSTIEIEAKNIS  
LLEEIENIKIETNPKILIDKNGIILASENAKIGTFTFSIEKDNQNIFLSKNNKTTIQVNSMKLNEFILKNSNNLS  
NKELIQIIQAAQKINKLNGELILEEIDGNQN

t86.aa

LKTDQSFNNSLSESVKLKEIADIYPTNTNFLTGIGIVAGLAGKGDSEIKQKDLIIKILEENNIINEIGSNNIESKNI  
ALVNVSLQVKNTIKGSKHKACVASILDSKDLTNGILLKTNLKNKEGEIIAIASGITQPNNKLKSGYITIDSVIIN  
ENQNINHSYNIILKKNYTLINRIHKILTSKINNKKIKSDSTIEIEAKNISLLEEIENIKIETNPKILIDKNGIIL  
LASENAKIGTFTFSIEKDNQNIFLSKNNKTTIQVNSMKLNEFILKNSNNLSNKELIQIIQAAQKINKLNGELILEE  
IDGNQN

f86.nt

ATGAACAACTAATGTTGATGTTAATTACATTTGCAACGAGTCTATTAGCCCAAACAAACAAAGCTTCAACAGGAC  
TAAAAACAGATCAATCATTTAACAATAGCCTATCTGAAAGCGTAAATTTAAAGAAATTGCGGATATTTATCCCAC  
AAATACAAATTTTTTAACAGGTATTGGAATAGTAGCGGGACTTGCTGGAAGGAGACTCTATAAAACAAAAAGAC  
CTTATAATTAAATTTTAGAAGAAAACAATATAATAATGAAATAGGCTCTAATAACATAGAAAGTAAAAATATTG  
CACTAGTAAATGTCAGTCTCCAAGTAAAAGGTAATACAATCAAAGGTTCAAACATAAAGCTTGCGTTGCATCAAT  
ACTGGACTCAAAGATTTAACAATGGAATACTTTTAAAAACAAATCTTAAAAATAAAGAGGGGGAAATAATAGCA  
ATTGCATCAGGAATTACACAGCCCAATAATAAATTTAAAGGATCTGGATATACTATAGATAGTGTAAATAATAATG  
AGAATCAAAATATTAACCACAGTTATAATATAATTCTTAAAAAGGAAATTATACATTAATAAATAGAATTCATAA  
AATATTAACCTCTAAAAAAATCAACAACAAAATTAATCAGACAGCACAATAGAAATAGAAGCAAAAAACATAAGC  
CTATTAGAAGAGATTGAAAAATATTAATAAGAAACCAACCCCAAGATATTAATAGACAAAAAAATGGTATTATTT  
TAGCAAGTGAAAATGCAAAAAATAGGAACTTTTACATTTTCCATTGAAAAAGACAATCAAACATTTTTTTTAAGTAA  
AAATAACAAAACAACAAATCAAGTAACTCAATGAAATTAATGAATTTATATTAAAAAATTTCCAACAATCTTAGC  
AATAAAGAATTAATTCAAATAATTCAAGCTGCGCAAAAAATTAATAAATTAATGGGGAACCTTATCTTGGAGGAAA  
TTGATGGAAACCAAAATTA

t86.nt

TABLE 1. Nucleotide and Amino Acid Sequences

CTAAAAACAGATCAATCATTTTAACAATAGCCTATCTGAAAGCGTAAAATTAAAAGAAATTGCGGATATTTATCCCA  
CAAATACAAATTTTTTAAACAGGTATTGGAATAGTAGCGGGACTTGCTGGAAAAGGAGACTCTATAAAACAAAAAGA  
CCTTATAATTAAAATTTTAGAAGAAAAACAATATAATAATGAAATAGGCTCTAATAACATAGAAAGTAAAAATATT  
GCACTAGTAAATGTCAGTCTCCAAGTAAAAGGTAATACAATCAAAGGTTCAAAACATAAAGCTTGCGTTGCATCAA  
TACTGGACTCAAAAGATTTAACAATGGAATACTTTTAAAAACAAATCTTAAAAATAAAGAGGGGGAAATAATAGC  
AATTGCATCAGGAATTACACAGCCCAATAATAAATTAAAAGGATCTGGATATACTATAGATAGTGAATAATAAAT  
GAGAATCAAAATATTAAACCACAGTTATAATATAATTCTTAAAAAAGGAAATTATACATTAATAAATAGAATTCATA  
AAATATTAACTCTAAAAAAATCAACAACAAAATTAAATCAGACAGCACAAATAGAAATAGAAGCAAAAAACATAAG  
CCTATTAGAAGAGATTGAAAATATTAAAAATAGAAACCAACCCCAAGATATTAATAGACAAAAAAAATGGTATTATT  
TTAGCAAGTGAAAATGCAAAAATAGGAACCTTTTACATTTTCCATTGAAAAAGACAATCAAAACATTTTTTTAAAGTA  
AAAATAACAAAACAACAATTCAAGTAACTCAATGAAATTAAATGAATTTATATTAAAAAATTCCAACAATCTTAG  
CAATAAAGAATTAATTCAATAAATTCAAGCTGCGCAAAAAATTAATAAATTAAATGGGGAACTTATCTTGGAGGAA  
ATTGATGGAAACCAAAATTAA

f90.aa

MCPITFTIPFFLAIFFAFSSSFVTDSSVSLLSRNTSLFSTLTPISLPIISGTLPAIVTLISKYLSISLSFSKMFIF  
KSLFEVIKLPWLFIIFASGYFLNAFSIFLCISSFLSFMFI

t90.aa

SSFVTDSSVSLLSRNTSLFSTLTPISLPIISGTLPAIVTLISKYLSISLSFSKMFIFKSLFEVIKLPWLFIIFAS  
GYFLNAFSIFLCISSFLSFMFI

f90.nt

ATGTGTCCTATTACTTTTACCATTCCATTTTTTCTAGCAATATTTTTTGCTTTTTCAAGCTCCTTTGTTACGGACT  
CTTCTGTGTCCTTTGCTATCAAGAAATACGTCTCTTTTTTCTACTTTAACTCCAATTTCTTTGCCTATTATTTCTGG  
TACGCTTCCTGCAATAGTTACGCTGTCGAAAAAATATCTGTCAATCTCTTTAAGCTTTTCTAAAATGATTTTTCATC  
AAATCTTTTATTTGAAGTGATTAACTTCCCATATGGTTATTCAATTATTTTTGCATCAGGATACTTTTTAAATGCCTT  
TTTCGATTTTTTTGTGTATTTCTTCTTTTTTATCTTTTATGTTTATATGA

t90.nt

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CTTTGCCTATTATTTCTGGTACGCTTCCTGCAATAGTTACGCTGTCGAAAAAATATCTGTCAATCTCTTTAAGCTT  
TTCTAAAATGATTTTCATCAAATCTTTATTTGAAGTGATTAACTTCCCATATGGTTATTCAATTATTTTTGCATCA  
GGATACTTTTTAAATGCTTTTTTCGATTTTTTGTGTATTTCTTCTTTTTTATCTTTTATGTTTATATGA

f469.aa

MANVALSSGFISQKIFGIIIMVFLPTIIATPIINFLFKINKSGLKKELPIDQNTNHCVSFEYDNLAKILIWDFKN  
ELRKEGFFTQIKNDSSQYINARKNNISFSIKREGSKITFECPNNHIIIIQDLFRETIINLEKITKEVETVSLRAK  
KLDYSINYDKILSNINLNKRIKKENIILELKSSNKADVIRELLSVINIEIDKERIFQDLMEREKLITTTALKEGFAI  
PHLKTNLISKIHIAIGISHEGIDFNALDKNLSHVFILILCPAKDYVSYPRILASVVGKVDLYKKEILNAKTDKEIY  
NIIVSZ

t469.aa

TABLE 1. Nucleotide and Amino Acid Sequences

VFLPTIIATPIINFLFKINKSGLKKELPIDQNTHTICVSFEYDNLAKILIWDFKNELRKEGFFTQQIKNDSSQYINA  
RKNNISFSIKREGSKITFECPNNHLIIIIQDLFRETILNLEKITKEVETVSLRAKKLDYSINYDKILSNINLNKRIK  
KENIILELKSSNKADVIRELLSVINIEIDKERIFQDLMEREKLITTALKEGFAIPHLKTNLISKIHIAIGISHEGI  
DFNALDKNLSHVFLILILCPAKDYVSYPRILASVVGKVDLYKKEILNAKTDKEIYNIIVS2

f469.nt

ATGGCAAATGTAGCATTATCTTCAGGATTTATTAGCCAAAAATATTTGGAATCATAATAATAATGGTGTGTTTTGC  
CAACAATCATTGCAACACCCATAATAAACTTTTTATTAAAAATAAAAGTGGACTTAAAAAAGAACTCCCAAT  
AGATCAAAATACACACATATGCGTATCATTGGAATATGATAATTTAGCCAAAATCTTATATGGGACTTTAAAAAT  
GAGTTAAGAAAAGAAGGATTTTTTACACAACAAATTAATAATGATTCTTCACAATATATTAATGCAAGAAAAACA  
ATATATCCTTCTCAATAAAAACGAGAAGGTAGCAAAATCACATTTGAATGCCCAAATAATCATTTAATTATAATACA  
AGATCTTTTTAGAGAAACAATCTTAAACCTAGAAAAATAACCAAAGAAGTTGAAACAGTCTCTTTAAGAGCAAAA  
AAACTAGATTACTCAATAAATTACGATAAAATCCTTAGTAATATCAACCTAAATAAAAGAATAAAAAAGGAAAAACA  
TTATTCTAGAATTAAAAATCAAGCAATAAGGCTGATGTAATAAGAGAGCTTCTAAGCGTAATAAACATTGAAATTGA  
TAAAGAAAGAATATCCAAGATTTAATGGAAAGAGAAAAGTTAATTACTACTGCACATAAAGAAGGCTTTGCCATT  
CCCCATTTAAAAACAAATTTAATATCAAAAATACATATTGCAATAGGAATAAGCCATGAGGGAATTGACTTTAATG  
CTCTTGACAAGAAGCTTAAGTCATGTTTTTATATTAATACTGTGCCCAGCAAAAGATTACGTTAGCTACCCTAGAAT  
TTTAGCATCTGTTGTGGGCAAAGTTGATCTGTACAAAAAAGAAATTTTAAATGCAAAAACAGATAAAGAAATTTAT  
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t469.nt

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AAAAACAATATATCCTTCTCAATAAAAACGAGAAGGTAGCAAAATCACATTTGAATGCCCAAATAATCATTTAATTA  
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GAAACATTATTCTAGAATTAAAAATCAAGCAATAAGGCTGATGTAATAAGAGAGCTTCTAAGCGTAATAAACATTG  
AAATTGATAAAGAAAGAATATCCAAGATTTAATGGAAAGAGAAAAGTTAATTACTACTGCACATAAAGAAGGCTT  
TGCCATTCCCCATTTAAAAACAAATTTAATATCAAAAATACATATTGCAATAGGAATAAGCCATGAGGGAATTGAC  
TTTAATGCTCTTGACAAGAAGCTTAAGTCATGTTTTTATATTAATACTGTGCCCAGCAAAAGATTACGTTAGCTACC  
CTAGAATTTTAGCATCTGTTGTGGGCAAAGTTGATCTGTACAAAAAAGAAATTTTAAATGCAAAAACAGATAAAGA  
AATTTATAATATAATAGTGAGCTAA

f477.aa

MEKPQGSIVGAISGAMHVHLM AEHYGVPVVLHTDHC AKNLLPWVEGLLEYGEKYYSQHKKPLFSSHMLDLSEEP  
KENIEISKKFLERMAK IEMFLEIELGITGGEEDGVDNSDRALHEL FSTPEDIYYGYSELLKVS PNFQIAAAF  
GNVHGVYKPGNVKLT PPKVLKDGQDYVISKTGVNMAKPVSYVFHGGSGSTIDEINEALSYGVVKMNI  
DIDTQWAAWEGVLNYYKNESR LQGQLGDGKDIDI PNKKFYDPRVWLREAEVSMKDRVKIACKNLNNINRNZ

t477.aa

MHVHLM AEHYGVPVVLHTDHC AKNLLPWVEGLLEYGEKYYSQHKKPLFSSHMLDLSEEP  
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PNFQIAAAF GNVHGVYKPGNVKLT PPKVLKDGQDYVISKTGVNMAKPVSYVFHGGSGSTIDEINEALSYGVVKMNI  
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f477.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

AAAGAAAATATTGAAATTTCTAAAAAATCTTAGAAAAGAAATGGCAAAAATGAAATGTTTTTGGAAATAGAGCTTG  
GAATTACGGGTGGGGAAGAGGATGGAGTTGACAATTCAGATAGAGCTTTCATGAACATTTTTCTACTCCTGAGGA  
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CAGGAGTAAATATGGCTAAGCCAGTTTCTTATGTTTTTCATGGAGGGTCTGGATCTACAATTGATGAGATTAATGA  
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TATTACAAAAAAATGAAAGTCGTTTGCAAGGTCAATTAGGAGATGGCAAGGATATTGATATTCCAAATAAGAAAT  
TTTATGATCCAAGGGTTTGGTTAAGAGAAGCTGAAGTTTCTATGAAAGACCGTGTGAAGATTGCATGCAAAAATCT  
TAATAATATTAATAGAAATTAA

t477.nt

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TTCCTTGGGTTGAAGGCCTTTTAGAATATGGAGAGAAATACTATAGTCAGCACAAAAACCATTATTTTCTTCACA  
TATGTTAGATTTATCAGAAGAACCATTAAAGAAAAATATTGAAATTTCTAAAAAATCTTAGAAAAGAAATGGCAAAA  
ATTGAAATGTTTTTGGAAATAGAGCTTGAATTACGGGTGGGGAAGAGGATGGAGTTGACAATTCAGATAGAGCTT  
TGCATGAACATTTTTCTACTCCTGAGGATATTTATTATGGATATTCAGAACTTTTAAAAGTTAGCCCCAAATTTTCA  
GATTGCAGCAGCTTTTGGAAATGTTTCATGGGGTATATAAACCGGGGAATGTTAAGCTTACTCCAAAAGTTTAAAA  
GATGGTCAAGATTATGTCATATCAAAAACAGGAGTAAATATGGCTAAGCCAGTTTCTTATGTTTTTCATGGAGGGT  
CTGGATCTACAATTGATGAGATTAATGAGGCGCTTCTTATGGCGTTGTAAAGATGAATATTGACACAGATACACA  
GTGGGCTGCCTGGGAGGGTGTTTTAAATTATTACAAAAAAATGAAAGTCGTTTGCAAGGTCAATTAGGAGATGGC  
AAGGATATTGATATTCCAAATAAGAAATTTTATGATCCAAGGGTTTGGTTAAGAGAAGCTGAAGTTTCTATGAAAG  
ACCGTGTGAAGATTGCATGCAAAAATCTTAATAATATTAATAGAAATTAA

f488.aa

MPSSFPFLLVNGSSGIAVGMATNMAPHNLREICDAIVYMLDNENASIFDLLKIVKGPDPFPTFGEIVYNDNLIKAYK  
TGKGSVVIRARYHIEERAEDRNAIIVTEIPYTVNKSALLMKVALLAKEEKLGLLDIRDESDREGIRIVLEVVRGFD  
DPHVIMNLLYEYTEFKKHFSINNLAALVNGIPKQLNLEELLFEFIEHRKNIIERRIEFDLRKAKEKAHVLEGLNIAL  
NNIDEVIKIIKSSKLAKDARERLVS NFGLSEIQANSVLDMLRQLKLTAL EIFKLEELNILLSLIKDYEDILLNPVR  
IINI IREETINLGLKFGDERRTKIIYDEEVLKTSMSDLMQKENIVVMLTKKGFLKRLSQNEYKLQGTGGKGLSSFD  
LNDGDEIVIALCVNTHDYL FMI SNEGKLYLINAYEIKDSSRASKGQNI SELINLGDQEEILTIKNSKDLTDDAYLL  
LTTASGKIARFESTDFKAVKSRGVIVIKLNDKDFVTSAEIVFKDEKVICLSKKGS AFIFNSRDVRLTNRGTQGVCG  
MKLKEGDLFVKVLSVKENPYLLIVSENGYGKRLNMSKISELKR GATGYTSYKKS DKKAGSVVDAIAVSEDEILLV  
SKRSKALRTVAGKVSEQGDARGIQVFLDNDSLVSVSKFIKZ

t488.aa

MATNMAPHNLREICDAIVYMLDNENASIFDLLKIVKGPDPFPTFGEIVYNDNLIKAYKTGKGSVVIRARYHIEERAE  
DRNAIIVTEIPYTVNKSALLMKVALLAKEEKLGLLDIRDESDREGIRIVLEVVRGFDPHVIMNLLYEYTEFKKH  
SINNLAALVNGIPKQLNLEELLFEFIEHRKNIIERRIEFDLRKAKEKAHVLEGLNIALNNIDEVIKIIKSSKLAKDA  
RERLVS NFGLSEIQANSVLDMLRQLKLTAL EIFKLEELNILLSLIKDYEDILLNPVRIINI IREETINLGLKFGDE  
RRTKIIYDEEVLKTSMSDLMQKENIVVMLTKKGFLKRLSQNEYKLQGTGGKGLSSFDLNDGDEIVIALCVNTHDYL  
FMI SNEGKLYLINAYEIKDSSRASKGQNI SELINLGDQEEILTIKNSKDLTDDAYLLLTASGKIARFESTDFKAV  
KSRGVIVIKLNDKDFVTSAEIVFKDEKVICLSKKGS AFIFNSRDVRLTNRGTQGVCGMKLKEGDLFVKVLSVKENP  
YLLIVSENGYGKRLNMSKISELKR GATGYTSYKKS DKKAGSVVDAIAVSEDEILLVSKRSKALRTVAGKVSEQGD  
DARGIQVFLDNDSLVSVSKFIKZ

f488.nt

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CTCATAATTTAAGAGAAATTTGTGATGCCATTGTTTACATGCTAGATAATGAGAATGCTTCTATATTTGATTTGCT  
TAAAATAGTTAAAGGGCCTGATTTCCCAACTTTTGGAGAGATTGTTTATAATGATAATTTAATTAAAGCATACAAA  
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TTACAGAAATACCTTATACGGTAAATAAATCTGCACTTCTTATGAAAGTTGCGCTTTTAGCAAAAAGAGAAAAGCT  
AGAAGGACTTTTAGATATAAGAGATGAATCTGATCGAGAAGGTATTAGGATAGTTCTTGAAGTTAAAAGAGGATTT

TABLE 1. Nucleotide and Amino Acid Sequences

GATCCTCATGTTATTATGAATTTGCTTTATGAATATACTGAATTTAAAAAGCATTTTAGTATAAATAATTTAGCCC  
TTGTTAATGGTATTCCCAAACAGTTAAATTTAGAAGAATTGTTATTTGAATTTATTGAGCATAGAAAAATATTAT  
CGAAAGACGTATTGAATTTGACTTGAGAAAGGCCAAAAGAGAAAGCACATGTTCTTGAGGGATTAAATATTGCTTTA  
AATAATATAGATGAGGTTATTAAGATTATTAAATCATCTAAATTAGCAAAAAGATGCAAGGGAGAGGCTTGTTCGA  
ATTTTGGTCTTTTCAGAGATTCAAGGCCAATTCAGTTCTTGATATGAGGTTACAAAACTTACAGCCCTTGAGATTTT  
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ATTATTAATATTATAAGAGAAGAACTATTAAATTTAGGTTTGAAATTTGGCGATGAACGTCGAACTAAAATAATTT  
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AGGTTTCCTTAAAAAGACTTTTCAAAAATGAGTATAAATTGCAAGGTACGGGAGGAAAAGGACTAAGTTCGTTTGAT  
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TTATTAAACTGAATGATAAAGATTTTGTACAAAGTGCAGAGATTGTTTTTAAGGATGAAAAAGTAATTTGTCTTTC  
TAAAAAGGGTAGTGCAATTTATATTTAATTCAGGGATGTTAGGCTTACTAATAGAGGTACCCAAGGTGTTTGTGGA  
ATGAAATTAAGAAGGTTGATTTGTTTGTAAAGTTTTATCGGTTAAAGAAAATCCTTATCTTTTGATTGTTTCTG  
AAAATGGGTATGGAAGGTTAAACATGTCTAAAATATCTGAGCTTAAAGAGGAGCCACTGGTTATACTAGTTA  
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AGTAAACGTTCAAAAGCTTTAAGAACAGTAGCTGGAAGAGTATCTGAACAAGGCAAAGATGCTAGAGGAATTCAG  
TATTATTTCTTGATAATGACAGCTTGGTTTCTGTTTCAAAATTTATTAAATAA

t488.nt

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TTTAATTAAGCATACAAAAGCTGGCAAGGGAAGTGTGTTATTAGGGCAAGATATCATATTGAAGAAAGAGCAGAA  
GATAGAAATGCTATAATTTGTACAGAAATACCTTATACGGTAAATAAATCTGCACCTCTTATGAAAGTTGCGCTTT  
TAGCAAAAGAAGAAAAGCTAGAAGGACTTTTAGATATAAGAGATGAATCTGATCGAGAAGGTATTAGGATAGTTCT  
TGAAGTTAAAGAGGATTTGATCCTCATGTTATTATGAATTTGCTTTATGAATATACTGAATTTAAAAAGCATT  
AGTATAAATAATTTAGCCCTTGTTAATGGTATTTCCCAAACAGTTAAATTTAGAAGAATTGTTATTTGAATTTATTG  
AGCATAGAAAAAATATTATCGAAAGACGTATTGAATTTGACTTGAGAAAGGCAAAAGAGAAAGCACATGTTCTTGA  
GGGATTAAATATTGCTTTAAATAATATAGATGAGGTTATTAAGATTATTAAATCATCTAAATTAGCAAAAGATGCA  
AGGGAGAGGCTTGTTTCGAATTTTGGTCTTTTCAGAGATTCAAGGCCAATTCAGTCTTGATATGAGGTTACAAAAAC  
TTACAGCCCTTGAGATTTTAAAGCTTGAAGAGGAGCTTAATATACTGTTAAGCTTAATAAAAGATTATGAAGATAT  
TCTCTTGAATCCAGTAAGGATTATTAAATATTATAAGAGAAGAACTATTAATTTAGGTTTGAAATTTGGCGATGAA  
CGTCAACTAAAATAATTTATGATGAGGAGGTTTTAAAACTAGTATGTCGGATTTAATGCAAAAAGAAAATATTG  
TTGTTATGCTTACAAAAGAAAGGTTTCCTTAAAAAGACTTTTCAAAAATGAGTATAAATTGCAAGGTACGGGAGGAAA  
AGGACTAAGTTTCGTTTGATCTAAATGATGGAGATGAGATTGTTATTGCTTTGTGTGTCAATACTCATGATTATTTA  
TTTATGATTTCAAATGAAGGAAAGCTTTATTTAATCAATGCTTATGAAATAAAAAGATTCTTCAAGAGCTTCAAAAG  
GTCAGAATATTAGTGAGCTTATTAATTTAGGAGATCAAGAAGAAATATTAACCTATTAAGAATAGTAAAGATTTAAC  
TGATGATGCTTATTTATTGCTTACAACCTGCAAGTGGAAGATAGCTAGATTTCGAATCTACAGATTTTAAAGCAGTA  
AAGTCACGAGGTGTTATTGTTATTAACTGAATGATAAAGATTTTGTACAAAGTGCAGAGATTGTTTTTAAGGATG  
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TATCTTTTGATTGTTTCTGAAAATGGGTATGGAAGAGGTTAAACATGTCTAAAAATATCTGAGCTTAAAGAGGAG  
CCACTGGTTATACTAGTTATAAAAAATCTGATAAAAAAGCGGGTAGTGTTGTTGATGCTATAGCAGTTTCAGAGGA  
TGATGAAATCTTGCTTGTAAGTAAACGTTCAAAAGCTTTAAGAACAGTAGCTGGAAGAGTATCTGAACAAGGCAA  
GATGCTAGAGGAATTCAGTATTATTTCTTGATAATGACAGCTTGGTTTCTGTTTCAAAATTTATTAAATAA

f494.aa

MFALIRKIFMIYFLCITLAGFAMIFIDSKFTEQPNVKENQSKINQHTIEPNLIMFTSSIGGFLGVYVGIWIFNYDK  
SNFYLNWGNLIILIIYNIALIITVYSKSHS

t494.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MIFIDSKFTEQPNVKENQSKINQHTIEPNLIMFTSSIGGFLGVYVGIWIFNYDKSNFYLNWGNLIILIYNIALIIT  
VYSKSHS

f494.nt

ATGTTTGCATTAATTAGAAAAATATTTATGATCTATTTTTTATGCATTACTCTTGCAGGTTTTGCCATGATTTTTTA  
TTGACAGCAAATTTACCGAACAGCCTAATGTTAAAGAAAAATCAAAGCAAATTAATCAACATACAATTGAACCCAA  
TTTAATCATGTTTACATCTTCTATAGGAGGATTTTTAGGTGTTTATGTTGGAATTTGGATCTTTAACTATGACAAA  
AGCAATTTTTACCTAAATTGGGGAAATTTAATAATATTAATATACAACATAGCCCTAATTATCACTGTATACTCAA  
AATCACATAGTTAG

t494.nt

ATGATTTTTATTGACAGCAAATTTACCGAACAGCCTAATGTTAAAGAAAAATCAAAGCAAATTAATCAACATACAA  
TTGAACCCAAATTTAATCATGTTTACATCTTCTATAGGAGGATTTTTAGGTGTTTATGTTGGAATTTGGATCTTTAA  
CTATGACAAAAGCAATTTTTACCTAAATTGGGGAAATTTAATAATATTAATATACAACATAGCCCTAATTATCACT  
GTATACTCAAAATCACATAGTTAG

f516.aa

MKKTPNTCIFLTLIIISNLNALANEEGNTNEKNDQPKQISNFFSPERGFYISTGIGIGVGFFLNSNIKHLIFRPYY  
TFSNNTFDLIVAMILTRESLNI PKKMQYFKSYIGGGINWHIANLIKTKYFSATIGIGGRFYLSTNFIEDIRFYE  
KLPHYVIEPYMFIEISSKKAIPMLGLDFKIDFLDLDTFNISFNFTIRYNFKDKNEMET

t516.aa

NEEGNTNEKNDQPKQISNFFSPERGFYISTGIGIGVGFFLNSNIKHLIFRPYYTFSNNTFDLIVAMILTRESLNI  
PKKMQYFKSYIGGGINWHIANLIKTKYFSATIGIGGRFYLSTNFIEDIRFYEKLPHYVIEPYMFIEISSKKAIPML  
GLDFKIDFLDLDTFNISFNFTIRYNFKDKNEMET

f516.nt

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TTTTTCCGCCACCATTTGGCATAGGTGGTCGTTTTTACCTATCTACAACTTTATAGAAGACATTCGATTTTACGAA  
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ACTTTAAATTTGATTTTTTATTTTATAGATACATTTAACATTTCTTTTAATTTTACTATTAGATATAATTTTAAGGA  
CAAAAACGAGATGGAAACATGA

t516.nt

AATGAAGAAGGCAATACTAATGAAAAAATGATCAACCCAAACAAATCTCTAATTTTTTTAGCCAGAAAGAGGGT  
TCATATATTCAACAGGAATTGGGATTGGAGTTGGATTTTTTCTAAATTCAAATATTAAACACCTTATCTTTAGACC  
TTATTATACATTCTCTAATAATACTTTTGATTTTTTAATCGTTGCTATGATATTAACAAGGGAAAGCCTTAATATC  
CCCCAAAAAATGCAATACTTTAAATCTTATATTGGAGGAGGAATAAACTGGCACATTGCAAACTTAATTAAAAAA  
CAAATATTTTTCCGCCACCATTTGGCATAGGTGGTCGTTTTTACCTATCTACAACTTTATAGAAGACATTCGATT  
TTACGAAAAATTGCCTTATGTAATAGAGCCTTATATGTTTATTGAAATTTCTTCTAAAAAGGCAATTCCTTTAATG  
GGGTTAGACTTTAAATTTGATTTTTTATTTTATAGATACATTTAACATTTCTTTTAATTTTACTATTAGATATAATT  
TTAAGGACAAAAACGAGATGGAAACATGA

f517.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MIPVVASGGILIALSIAFVGIGPDGPNFAEHFPYKQIADIGSIAFGMMLPVLAGFIAMAIADKPGLTPGLVGGVMS  
GNVKAGFLGAIFAGFLAGYVARFLARRSVPEWLRPVMPIFVIPLISTIIVGFFMLYFGVYIGKFMGVLESGLKSLQ  
SNSETFGVLGKIFLGLVLGSMITVDMGGPFNKVAFLEFGVGLIPQVPEIMGMVAAAI PVPPMAMGLATFLAPKLFEN  
EEKESGKIAFLISFIGISEGAIPFAASDPGRVIPSIVVGGAVSSIIAFLGVANHAPHGGPIVLPVIDNKFGEIIA  
IAVGVAVATALVIFLKSLLKKESE

t517.aa

DKPGLTPGLVGGVMSGNVKAGFLGAIFAGFLAGYVARFLARRSVPEWLRPVMPIFVIPLISTIIVGFFMLYFGVYI  
GKFMGVLESGLKSLQSNSETFGVLGKIFLGLVLGSMITVDMGGPFNKVAFLEFGVGLIPQVPEIMGMVAAAI PVPPM  
AMGLATFLAPKLFENEEKESGKIAFLISFIGISEGAIPFAASDPGRVIPSIVVGGAVSSIIAFLGVANHAPHGGP  
IVLPVIDNKFGEIIAIAVGVAVATALVIFLKSLLKKESE

f517.nt

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CTAATTTTGTCTGAGCATCCATTTTATAAGCAGATTGCAGATATTGGTTCTATAGCTTTTGGGATGATGTTGCCCGT  
GCTTGCTGGTTTATTGCAATGGCAATTGCTGATAAGCCTGGTCTTACCCCCGGTCTTGTGTTGGTGGAGTAATGTCT  
GGGAATGTAAAAGCAGGTTTCTTGGGCGCAATATTTGCGGGCTTTCTTGCAAGTTATGTTGCAAGGTTTTTAGCAA  
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GGTAGCAGCAGCAATTCCTGTTCCTCCTATGGCTATGGGGCTTGAACCTTTTAGCACCTAAATTGTTTGAATAAT  
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CGTTGCTAATCATGCTCCACACGGAGGACCAATAGTACTTCCTGTTATTGATAATAAATTTGGGTTTATTATTGCA  
ATTGCTGTTGGAGTTGCGGTTGCAACAGCTTTGGTAATTTTTTTGAAATCTTTAAATTAAGGAATCTGAATGA

t517.nt

GATAAGCCTGGTCTTACCCCCGGTCTTGTGTTGGTGGAGTAATGTCTGGAATGTAAAAGCAGGTTTCTTGGGCGCAA  
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AATGCCTATATTTGTAATTCCGCTAATAAGCACCATTATTGTCTCGGCTTTTTTATGCTGTATTTTGGTGTATTATTT  
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TTTTTGGTGTAGGGCTAATTCCTCAAGTGCCAGAAATAATGGGAATGGTAGCAGCAGCAATTCCTGTTCTCCTATG  
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AGTGGTAGGGGAGCTGTATCAAGCATTATTGCCGCTTTTTTAGGCGTTGCTAATCATGCTCCACACGGAGGACCA  
ATAGTACTTCCTGTTATTGATAATAAATTTGGGTTTATTATTGCAATTGCTGTTGGAGTTGCGGTTGCAACAGCTT  
TGGAATTTTTTTGAAATCTTTAAATTAAGGAATCTGAATGA

f519.aa

MIKIFKKIYILTLVLGMAHLSFASDNYMVRCSEEDSTTCIAKLKEIKEKKNYDLFSMGIGIGDPIANIMITIPYI  
NIDFGYGGFIGLKSNNFENYLNNGIDVIFKKQIGQYMKIGGGIGIGADWSKTSIIPPNEEEETDYERIGAVIRIPF  
IMEYNFAKNLSIGFKIYPAVGPTILLTKPSILFEGIKFNFFGFGFIKFAFN

t519.aa

DNYMVRCSEEDSTTCIAKLKEIKEKKNYDLFSMGIGIGDPIANIMITIPYINIDFGYGGFIGLKSNNFENYLNNG  
IDVIFKKQIGQYMKIGGGIGIGADWSKTSIIPPNEEEETDYERIGAVIRIPFIMEYNFAKNLSIGFKIYPAVGPTI  
LLTKPSILFEGIKFNFFGFGFIKFAFN

TABLE 1. Nucleotide and Amino Acid Sequences

f519.nt

ATGATAAAAAATTTTTAAAAAATATACATTTTAAACATTAGTATTAGGTATGGCACACCTTTCTTTTGCATCTGACA  
ATTATATGGTCAGATGCAGCAAGGAAGAAGATTCAACCACCTGTATCGCAAAGCTTAAAGAAATAAAAGAAAAGAA  
AAATTATGACTTATTTTCAATGGGCATTGGAATAGGAGATCCTATTGCAAATATTATGATTACAATTCCTTATATA  
AATATTGATTTTGGATATGGAGGTTTTATTGGCCTTAAGTCAAACAATTTTGAAAATTATCTAAATGGTGGAAATAG  
ACGTTATTTTAAAAAGCAAATTGGACAATATATGAAAATTGGCGGCGGCATTGGAATAGGTGCGGATTGGTCAAA  
AACATCCCTTATACCCCTAATGAAGAAGAAGAACTGATTATGAGAGAATAGGCGCTGTTATAAGAATTCCTTTT  
ATAATGGAATATAATTTTGCAAAAAATTTATCCATAGGATTCAAAATTTATCCTGCAGTAGGGCCAACAATATTAC  
TAACAAAACCAAGCATTTTATTTGAAGGAATTAAATTCATTTTTTTTGGATTGGATTTCATAAAATTTGCATTTAA  
TTAA

t519.nt

GACAATTATATGGTCAGATGCAGCAAGGAAGAAGATTCAACCACCTGTATCGCAAAGCTTAAAGAAATAAAAGAAA  
AGAAAAATTATGACTTATTTTCAATGGGCATTGGAATAGGAGATCCTATTGCAAATATTATGATTACAATTCCTTA  
TATAAATATTGATTTTGGATATGGAGGTTTTATTGGCCTTAAGTCAAACAATTTTGAAAATTATCTAAATGGTGGAA  
ATAGACGTTATTTTAAAAAGCAAATTGGACAATATATGAAAATTGGCGGCGGCATTGGAATAGGTGCGGATTGGT  
CAAAAACATCCCTTATACCCCTAATGAAGAAGAAGAACTGATTATGAGAGAATAGGCGCTGTTATAAGAATTCC  
TTTTATAATGGAATATAATTTTGCAAAAAATTTATCCATAGGATTCAAAATTTATCCTGCAGTAGGGCCAACAATA  
TTACTAACAAAACCAAGCATTTTATTTGAAGGAATTAAATTCATTTTTTTTGGATTGGATTTCATAAAATTTGCAT  
TTAATTAA

f520.aa

MRLLLATIILILTGLLAAQSKSKSMTEDDDFDKLLAKEESVRRLFGIGFGVGYPLANITISVPYVDIDLGYGGF  
VGLKPNNFLPYVVMGVDLLFKDEIHKNTMISGGIGIGADWSKGSPEKSNEKLEEEENEAAQQVASLQNRIGVVIRL  
PLVIEYSFLKNIVIGFKAVATIGTTMLLGSPMSFEGARFNFLGTGFIKIYI

t520.aa

QSKSKSMTEDDDFDKLLAKEESVRRLFGIGFGVGYPLANITISVPYVDIDLGYGGFVGLKPNNFLPYVVMGVDLL  
FKDEIHKNTMISGGIGIGADWSKGSPEKSNEKLEEEENEAAQQVASLQNRIGVVIRLPLVIEYSFLKNIVIGFKAV  
ATIGTTMLLGSPMSFEGARFNFLGTGFIKIYI

f520.nt

ATGAGAATGCTATTAGCAACAATAACTTATATTAACAACGGGTTTATTAGCTGCACAATCCAAAAGCAAAAGTA  
TGACTGAAGATGACTTTGATTTTGATAAACTTCTTGCAAAAGAAGAGTCTGTGCGCCGTTTATTTGGCATAGGTTT  
TGGAGTTGGATATCCACTTGCAAACATTACAATATCTGTTCCATATGTAGACATAGACCTTGGGTACGGAGGATTC  
GTAGGGCTTAAACCCAACAATTTCTTGCCCTATGTTGTGATGGGTGTAGATCTTCTATTTAAAGATGAAATACACA  
AAAACACTATGATTTCTGGAGGCATTGGAATAGGTGCAGATTGGTCAAAAGGAAGTCCTGAAAAATCAAAATGAAAA  
ACTTGAAGAAGAGGAAGAAAAATGAAGCACAACAAGTAGCTTCTCTTCAAAATAGAATAGGGGTTGTGATAAGATTG  
CCTTTGGTAATAGAGTACAGCTTTCTTAAAAAATATTGTGATTGGATTAAAGCTGTTGCTACTATTGGAACAATA  
TGCTACTTGGCAGCCCAATGTCATTTGAAGGAGCTAGATTTAATTTCTTAGGCACAGGCTTTATAAAAATATATAT  
ATAG

t520.nt

CAATCCAAAAGCAAAAGTATGACTGAAGATGACTTTGATTTTGATAAACTTCTTGCAAAAGAAGAGTCTGTGCGCC  
GTTTATTTGGCATAGGTTTTGGAGTTGGATATCCACTTGCAAACATTACAATATCTGTTCCATATGTAGACATAGA  
CCTTGGGTACGGAGGATTCGTAGGGCTTAAACCCAACAATTTCTTGCCCTATGTTGTGATGGGTGTAGATCTTCTA  
TTTAAAGATGAAATACACAAAACACTATGATTTCTGGAGGCATTGGAATAGGTGCAGATTGGTCAAAAGGAAGTC  
CTGAAAAATCAAAATGAAAACTTGAAGAAGAGGAAGAAAAATGAAGCACAACAAGTAGCTTCTCTTCAAAATAGAAT  
AGGGGTGTGTGATAAGATTGCCTTTGGTAATAGAGTACAGCTTTCTTAAAAATATTGTGATTGGATTAAAGCTGTT



TABLE 1. Nucleotide and Amino Acid Sequences

GCTACTATTGGAACAACTATGCTACTTGGCAGCCCAATGTCATTTGAAGGAGCTAGATTTAATTTCTTAGGCACAG  
GCTTTATAAAAAATATATATATAG

f523 .aa

MNIKINFFFTLP I G I F L G L F F P L G I Y S S L S H A F I R L S Y L S L I P F L I F S I P L G I E N I I E N K N F K K L F G K T I Y Y G I L T  
N L S G V A V S I I A A T I Y L P Q R I P I L E K T I Q N T C F F E K E A L L E T F F P K N I F K I F T S S N P N L L S I Y M I S I I I G T S F Y Y A K  
Q K G R I A R E L M L S A S N L F Y H A N G F I V N I L N I G I I F I T A N Y A A N L K N F K D Y P N Y T N S I T F F L A W T I I I L F V I L P T I S Y  
R L T K S F K M I Y K G I F V S F Q N I I F S G L A K D S Y S P Y V I L I E D I K N E R I N I K K S I I I N I P L I N F V S K F G T I F V S V I S F F I  
I L K S Y S S L P I S I Y E I S Y M S T L S F V F V F A F P H I P N S L I Y I I T M L C S T Y T K G I E L N V S N I T P M L P I L I S L A L L I D F A F  
N I A I I H I I N F K E L K D Q E K I N

t523 .aa

I E N I I E N K N F K K L F G K T I Y Y G I L T N L S G V A V S I I A A T I Y L P Q R I P I L E K T I Q N T C F F E K E A L L E T F F P K N I F K I F T  
S S N P N L L S I Y M I S I I I G T S F Y Y A K Q K G R I A R E L M L S A S N L F Y H A N G F I V N I L N I G I I F I T A N Y A A N L K N F K D Y P N Y  
T N S I T F F L A W T I I I L F V I L P T I S Y R L T K S F K M I Y K G I F V S F Q N I I F S G L A K D S Y S P Y V I L I E D I K N E R I N I K K S I I  
I N I P L I N F V S K F G T I F V S V I S F F I I L K S Y S S L P I S I Y E I S Y M S T L S F V F V F A F P H I P N S L I Y I I T M L C S T Y T K G I E  
L N V S N I T P M L P I L I S L A L L I D F A F N I A I I H I I N F K E L K D Q E K I N

f523 .nt

ATGAATATAAAATCAATTTTTTTTTCACCTTTCCTATTGGAATCTTTTATAGGATTGTTTTTCCCTCTTGGAATTT  
ATAGCTCCTTATCACATGCTTTTATAAGATTATCATACTTATCTCTTATCCCTTTTTTAATATTTTCAATTCATT  
AGGAATTGAAAATATTATTGAAAAATAAAAGCTTTTGGTAAAAACAATTTATTATGGAATTTTAACT  
AACCTATCTGGAGTTGCTGTATCAATAATAGCTGCAACAATATATCTTCCGCAAAGAATTCCAATACTAGAAAAAA  
CAATACAAAATACATGTTTTTTTGAAAAAGAAGCTTTACTAGAAACATTCTTTCCAAAAAATATTTTCAAAATATT  
TACATCTAGCAATCCAAATCTACTAAGCATTTACATGATTTCAATAATAATAGGCACAAGTTTTTATTATGCAAAA  
CAAAAAGGCAGAATAGCTAGAGAACTGATGCTAAGCGCATCCAATCTTTTTTACCATGCAAATGGGTTTTATTGTAA  
ACATATTAAATATAGGGATCATTTTTTATAACAGCAAATTACGCTGCAAACTTAAAAAACTTCAAAGATTACCCAAA  
TTATACAAACAGCATAACATTCTTTTTGGCATGGACAATTATAATTTTATTCGTAATATTGCCAACAATTAGTTAT  
AGATTAACAAAAAGTTTTTAAATGATATATAAAGGCATTTTTTGTATCATTTCAAACATAATATTTTCAGGACTTG  
CAAAAGATTCTTATTTCCCTTATGTGATATTAATAGAAGATATTAACAAACGAAAGAATAAATATAAAAAAATCCAT  
AATTATAAACATACCTTTAATAAATTTTGTATCTAAATTTGGCACTATTTTGTTCAGTAATATCATTTTTTTATA  
ATTTTAAATCATATTCTAGCTTACCCATTTCTATTTATGAAATAAGCTATATGAGCACTTTATCATTTGTTTTTG  
TCTTTGCATTTCTCATATACCAAATAGTTTAAATTTATATAATTACAATGCTTTGCTCTACATATACAAAAGGAAT  
AGAGCTAAATGTTTCAAACATAACACCAATGCTGCCGATATTAATCTCTTTGGCTTTACTAATCGACTTTGCTTTT  
AACATTGCAATCATTCATATAATAAATCTCAAAGAATTAAAGATCAAGAAAAAATTAATTA

f523 .nt

ATTGAAAATATTATTGAAAATAAAAGCTTTTAAAGCTTTTGGTAAAAACAATTTATTATGGAATTTTAACTAACC  
TATCTGGAGTTGCTGTATCAATAATAGCTGCAACAATATATCTTCCGCAAAGAATTCCAATACTAGAAAAAACAAT  
ACAAAATACATGTTTTTTTGAAAAAGAAGCTTTACTAGAAACATTCTTTCCAAAAAATATTTTCAAAATATTTACA  
TCTAGCAATCCAAATCTACTAAGCATTTACATGATTTCAATAATAATAGGCACAAGTTTTTATTATGCAAAAACAAA  
AAGGCAGAATAGCTAGAGAACTGATGCTAAGCGCATCCAATCTTTTTTACCATGCAAATGGGTTTTATTGTAAACAT  
ATTAAATATAGGGATCATTTTTTATAACAGCAAATTACGCTGCAAACTTAAAAAACTTCAAAGATTACCCAAATTAT  
ACAAACAGCATAACATTCTTTTTGGCATGGACAATTATAATTTTATTCGTAATATTGCCAACAATTAGTTATAGAT  
TAACAAAAAGTTTTTAAATGATATATAAAGGCATTTTTTGTATCATTTCAAACATAATATTTTCAGGACTTGCAAA  
AGATTCTTATTTCCCTTATGTGATATTAATAGAAGATATTAACAAACGAAAGAATAAATATAAAAAAATCCATAATT  
ATAAACATACCTTTAATAAATTTTGTATCTAAATTTGGCACTATTTTGTTCAGTAATATCATTTTTTTATAATTT  
TAAATCATATTCTAGCTTACCCATTTCTATTTATGAAATAAGCTATATGAGCACTTTATCATTTGTTTTTGTCTT  
TGCATTTCTCATATACCAAATAGTTTAAATTTATATAATTACAATGCTTTGCTCTACATATACAAAAGGAATAGAG  
CTAAATGTTTCAAACATAACACCAATGCTGCCGATATTAATCTCTTTGGCTTTACTAATCGACTTTGCTTTTAAACA  
TTGCAATCATTCATATAATAAATCTCAAAGAATTAAAGATCAAGAAAAAATTAATTA

TABLE 1. Nucleotide and Amino Acid Sequences

f526.aa

MKKEFIMLLLLLQTIMNLSINTNTSTTSIVKELQKNLYIFNSKEYQKDKDTLNEFINSININDKEILQSLEKIKNE  
LFIIISVFFNNKKGILIALNLGAEINFKYKISPISISIINNEFEITKILIDYGISLNQIDDTGYSPIFWAIYTNNEK  
IFEFLKESGADLSFTLKNRKTPMQAAIETENIKLIKSLKKKIYIDDNFKKKLKKLKNKEIVRILVK

t526.aa

NSINTNTSTTSIVKELQKNLYIFNSKEYQKDKDTLNEFINSININDKEILQSLEKIKNELFIIISVFFNNKKGILIAL  
NLGAEINFKYKISPISISIINNEFEITKILIDYGISLNQIDDTGYSPIFWAIYTNNEKIFEFLKESGADLSFTLKN  
RKTPMQAAIETENIKLIKSLKKKIYIDDNFKKKLKKLKNKEIVRILVK

f526.nt

ATGAAAAAGAATTCATTATGCTTTTACTGTTATTGCAAACAATAATGAATTTAAACTCAATAAATACTAATACAA  
GTACTTCAATAGTAAAGAATTGCAAAAAATTTATATATTTTCAATAGCAAAGAATATCAAAAAGATAAAGACAC  
TTTAAATGAATTTATAAATTCAATAAATATAAATGACAAAGAAATCTTACAAAGTTTAGAAAAATCAAAAATGAG  
CTTTTATAATATCTGTTTTTTTCAACAATAAAAAAGGGATTTTAATTGCACTAAATCTTGGAGCAGAAATAAAT  
TTAAATATAAATATCTCCAATTTCAATTTCAATAATAACAATGAATTTGAAATCACAAAAATATTGATAGATTA  
CGGAATAAGCCTTAATCAAATAGATGATACAGGTTATTCTCCAATATTTTGGGCAATATATACTAATAACGAAAA  
ATATTTGAATTTTAAAAGAAAGCGGAGCTGATTTAAGTTTCACACTTAAAAATAGAAAAACACCAATGCAAGCCG  
CAATAGAAACAGAAATATAAACTAATTAATCTCTGGAAAAGAAAAAATTTACATTGACGACAATTTCAAAAA  
AAAACTTAAAAAGCTTAAAAACAAAGAAATAGTTCGAATTTTAGTAAAATAG

t526.nt

AACTCAATAAATACTAATACAAAGTACTTCAATAGTAAAGAATTGCAAAAAATTTATATATTTTCAATAGCAAAG  
AATATCAAAAAGATAAAGACACTTTAAATGAATTTATAAATTCATAAATATAAATGACAAAGAAATCTTACAAAG  
TTTAGAAAAATCAAAAATGAGCTTTTATAATATCTGTTTTTTTCAACAATAAAAAAGGGATTTTAATTGCACTA  
AATCTTGGAGCAGAAATAAATCTTTAAATATAAATATCTCCAATTTCAATTTCAATAATAACAATGAATTTGAAA  
TCACAAAAATATTGATAGATTACGGAATAAGCCTTAATCAAATAGATGATACAGGTTATTCTCCAATATTTTGGGC  
AATATATACTAATAACGAAAAATATTTGAATTTTAAAAGAAAGCGGAGCTGATTTAAGTTTCACACTTAAAAAT  
AGAAAAACACCAATGCAAGCCGCAATAGAAACAGAAAAATATAAACTAATTAATCTCTGGAAAAGAAAAAATTT  
ACATTGACGACAATTTCAAAAAAACTTAAAAAGCTTAAAAACAAAGAAATAGTTCGAATTTTAGTAAAATAG

f544.aa

MTKNRIIWLLVLMVSSTFTATIIISNYQNLMLSLVVLANFIPLMDTSGNAGSQASALIIRELALGTVKVKDFFKVF  
LKEICVSILVGAILASVNFRLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPVAKLLKLDPALMAGPL  
ITTIADAITLIAYFNIKWVLSYAV

t544.aa

STFTATIIISNYQNLMLSLVVLANFIPLMDTSGNAGSQASALIIRELALGTVKVKDFFKVFLLKEICVSILVGAILA  
SVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPVAKLLKLDPALMAGPLITTIADAITLIAYFN  
IAKWVLSYAV

f544.nt

ATGACAAAAATAGAATAATTTGGCTTTTAGTTCTTATGGTGTCTTCTACTTTTACAGCTACAATTATTTCAAATT  
ATCAAAATTTAATGTTGTCTTTAGTGGTTTATAGCTAATTTTATCCCTTTTAAATGGATACTTCAGGCAATGCCGG  
CTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAGATTTTTTAAAGTGTTT  
TTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATCTTGTCTAGTGTTAATTTTTTAAAGATTTGCTTTTTT  
TAGCTCCACACCATTTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTAGC  
AAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

ATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAATATAGCAAAATGGGTTTTAGTTAGCTATGCTG  
TTTAA

t544.nt

TCTACTTTTACAGCTACAATTATTTCAAATTATCAAATTTAATGTTGTCTTTAGTGGTTTTAGCTAATTTTATTC  
CCCTTTTAAATGGATACTTCAGGCAATGCCGGCTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTAC  
TGTC AAGGTAAAAGATTTTTTTAAAGTGTTTTTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCCTTGCT  
AGTGTTAATTTTTTAAGAATTGTCTTTTTTGTAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTT  
CATCTTGCTTGATGGTAAGTTTGACAGTAGCAAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAA  
GTTGGATCCAGCACTTATGGCAGGCCCTTTAATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAAT  
ATAGCAAAATGGGTTTTAGTTAGCTATGCTGTTTAA

f545.aa

MTKNRIIWLLVLMVSSTFTATIISNYQNLMLSLVLANFIPLMDTSGNAGSQASALIIRELALGTVKVKDFFKVF  
LKEICVSILVGAILASVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTVAKILGGLLPIVAKLLKLDPALMAGPL  
ITTIADAITLIAYFNIKWVLVSYAV

t545.aa

GSQASALIIRELALGTVKVKDFFKVF LKEICVSILVGAILASVNFLRIVFFVAPHHSDKLKIAFVVSSCLMVSLTV  
AKILGGLLPIVAKLLKLDPALMAGPLITTIADAITLIAYFNIKWVLVSYAV

f545.nt

ATGACAAAAAATAGAATAATTTGGCTTTTAGTTCTTATGGTGTCTTCTACTTTTACAGCTACAATTATTTCAAATT  
ATCAAATTTAATGTTGTCTTTAGTGGTTTTAGCTAATTTTATCCCCTTTTAAATGGATACTTCAGGCAATGCCGG  
CTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAAAGATTTTTTTAAAGTGTTT  
TTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCCTGCTAGTGTTAATTTTTTAAGAATTGTCTTTTTTG  
TAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTAGC  
AAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTTTA  
ATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAATATAGCAAAATGGGTTTTAGTTAGCTATGCTG  
TTTAA

t545.nt

GGCTCTCAGGCATCTGCGCTAATAATTCGTGAGCTTGCTCTTGGTACTGTCAAGGTAAAAGATTTTTTTAAAGTG  
TTTTAAAGGAAATATGTGTTAGCATTCTAGTGGGAGCAATTCCTGCTAGTGTTAATTTTTTAAGAATTGTCTTTTT  
TGTTAGCTCCACACCATTCTGATAAGCTGAAAATAGCTTTTGTAGTTTCATCTTGCTTGATGGTAAGTTTGACAGTA  
GCAAAGATATTGGGAGGTCTTTTACCCATTGTTGCTAAACTTTTAAAGTTGGATCCAGCACTTATGGCAGGCCCTT  
TAATCACTACAATTGCAGATGCTATTACTTTAATAGCTTATTTTAATATAGCAAAATGGGTTTTAGTTAGCTATGC  
TGTTTTAA

f577.aa

MRIKNLILIAILLISPSCSTNKNIVVLTDNKTIPFYINQFNIEKANFIIKFRNNIDLQTIKENAQIIISKNIGN  
TNIANHFKSVKINYNPDYPILKHIFKQFNYKIIPLGFDIPILYKNTHHIKKYINTKYLKEEYENFIKDGKFFISP  
YVSENLFYVISQINNVRFSFEKNKLNYNENQILKMLEYFSSFLNTKQMDLQKDFNKGYLKLNKILLNKKSLLIA  
GLSDITFYNSLSEQEKSQIKFSYLINDNNEIVISNPNFIGILETSVLTKKFINWILYKKTQKTLIGFNNQSQSNIC  
FGFANGFTPYKELNLKIKHSIDGISPFIIDETQINSHSYVLSKKTIEKENLLINEWFFSKANNLKKKN

t577.aa

NKNIVVLTDNKTIPFYINQFNIEKANFIIKFRNNIDLQTIKENAQIIISKNIGNTNIANHFKSVKINYNPDYPI  
LKHIFKQFNYKIIPLGFDIPILYKNTHHIKKYINTKYLKEEYENFIKDGKFFISPYVSENLFYVISQINNVRFSF

TABLE 1. Nucleotide and Amino Acid Sequences

EKNKLNYNENQILKMLEYFSSFLNLTQMDLQKDFFNKYGYLKLNLKILLNKKSLLIAGLSDITFYNSLSEQEKSQIK  
FSYLINDNNEIVISNPNFIGILETSVLTKKFINWILYKKTQKTLIGFNNQSQSNICFGFANGFTPYKELNLKIKHS  
IDGISPFIIDETQINSHSYVLSKKTIEKENLLINEWFFSKANNLKKKN

f577.nt

ATGAGAATAAAAAATTTAATACTAATAGCAATTTTATTAATTAGCCCTAGCTGTTCAACAAATAAGAACATCGTTG  
TACTAACTGACAATAAAACAATACCATTTTATATAAATCAATTTAATATAGAAAATAAAGCAAATTTTATAATTAA  
GTTTAGAAAATAATATTGATCTGCAAAACAATAGAAAAAGAAAATGCACAAATAATTATTCTAAAAACATTGGTAAC  
ACAAATATTGCTAACCATTTTAAATCTGTAAAAATCAATTATAATCCAGATTATCCTATCTTAAAGCATATTTTCA  
AGCAATTTAACTACAAAATTATTCCATTGGGCTTTGACATTCCTATTTTAAATCTATAAAAAATACACATCATATTAA  
AAAAATACATAAACACTAAATATCTAAAAGAAGAATACGAAAATTTTCATTAAAGATGGAAAATTTTTTATATCGCCT  
TATGTTTCTGAAAATTTATTTTATGTGATTTCTCAAATAAATAATGTGAGATTTTCTTTTGAAAAAATAAATTAA  
ATTATAATGAGAATCAAATTTTAAAAATGCTAGAATATTTCTCATCATTTTAAATACAAAACAAATGGACTTGCA  
AAAAGATTTCTTTAATAAATACGGCTACCTAAAGTTAAATAAATATTGCTTAATAAAAAATCTCTTTAATAGCA  
GGATTGAGCGATATAACCTTCTACAATAGCTTAAGCGAACAAGAGAAGTCACAAATAAAATTTTCTTATTTAATAA  
ACGATAACAATGAAATTGTTATCTCAAACCCAAATTTTATTGGCATTTTAGAAACATCTGTTTAACTAAAAAATT  
TATCAACTGGATATTGTATAAAAAAATCAAAAAACCCTAATTGGATTTAACAATCAATCCCAATCAAATATATGT  
TTTGGATTTGCCAATGGTTTTACCCCTTACAAAGAATTAAATTTAAAAATAAAACATTCAATTGATGGAATATCTC  
CTTTTATTATTGACGAACTCAAATCAATAGCCATTCCCTATGTATTAAAGCAAAAAACAATTGAAAAAGAAAACCTT  
ACTAATAAATGAATGGTTTTTCTCTAAAGCTAATAATCTAAAAAAAATAAAAAATTAA

t577.nt

AATAAGAACATCGTTGTACTAACTGACAATAAAACAATACCATTTTATATAAATCAATTTAATATAGAAAATAAAG  
CAAATTTTATAATTAAGTTTAGAAATAATATTGATCTGCAAAACAATAGAAAAGAAAATGCACAAATAATTATTTC  
TAAAAACATTGGTAACACAAATATTGCTAACCATTTTAAATCTGTAAAAATCAATTATAATCCAGATTATCCTATC  
TTAAAGCATATTTTCAAGCAATTTAACTACAAAATTATTCCATTGGGCTTTGACATTCCTATTTTAAATCTATAAAA  
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AACAAATGGACTTGCAAAAAGATTTCTTTAATAAATACGGCTACCTAAAGTTAAATAAAATATTGCTTAATAAAAA  
ATCTCTTTTAAATAGCAGGATTGAGCGATATAACCTTCTACAATAGCTTAAGCGAACAAGAGAAGTCACAAATAAAA  
TTTTCTTATTTAATAAACGATAACAATGAAATTGTTATCTCAAACCCAAATTTTATTGGCATTTTAGAAACATCTG  
TTTTAACTAAAAAATTTATCAACTGGATATTGTATAAAAAAATCAAAAAACCCTAATTGGATTTAACAATCAATC  
CCAATCAAATATATGTTTTGGATTTGCCAATGGTTTTACCCCTTACAAAGAATTAAATTTAAAAATAAAACATTCA  
ATTGATGGAATATCTCTTTTATTATTGACGAACTCAAATCAATAGCCATTCCCTATGTATTAAAGCAAAAAACA  
TTGAAAAAGAAAACCTTACTAATAAATGAATGGTTTTTCTCTAAAGCTAATAATCTAAAAAAAATAAAAAATTAA

f584.aa

MIKTILLLVLPVVFVSQISANQYFEGIYAKYQNIEDMQATINFTLKLKQGTGVLLYKFPDKFIINLDSNNQVFVS  
DGEFLTUVYVPSLGTSTFNQQLKGSSGGGLMKVLNSEYSVSYTNSPNLEDLDSSEPGKYIKLTFSRKLYKGAATINS  
FIIAFAPDGIIRITAFPTSGGREIVIDLTAVKFNVGILDSKFYDPPKSSNKVDNFLYDIKKN

t584.aa

QISANQYFEGIYAKYQNIEDMQATINFTLKLKQGTGVLLYKFPDKFIINLDSNNQVFVSDGEFLTUVYVPSLGTSTFN  
QQLKGSSGGGLMKVLNSEYSVSYTNSPNLEDLDSSEPGKYIKLTFSRKLYKGAATINSFIIAFAPDGIIRITAF  
PTSGGREIVIDLTAVKFNVGILDSKFYDPPKSSNKVDNFLYDIKKN

f584.nt

ATGATAAAAACAATACTTTTATTAGTTTTGTATCCTGTTGTTGTGTTTTCTCAAATATCTGCAAAATCAATATTTTG  
AAGGAATTTATGCTAAATATCAAAATATAGAGGACATGCAAGCAACAATTAATTTTACTTTAAAGGGGTAAAGCA

TABLE 1. Nucleotide and Amino Acid Sequences

AACAGGTGTTTTGCTTTATAAGTTTCCAGACAAGTTTATTATCAATTTAGATTCAAATAATCAAGTTTTTGTAAGT  
GATGGTGAATTTTTGACAGTTTATGTTCCATCTCTTGGGACTTCTTTTAATCAGCAATTATTAAAGGGTAGTAGTG  
GGGGAGGTCTTATGAAAGTTTAAATAGTGAGTATAGCGTATCTTATACCAATTCTCCAAATTTAGAAGATCTCGA  
TTCATCTGAGCCTGGAAAAATATATTAAATTAACCTTTTCTAGAAAGCTTTACAAGGGGGCTGCTACTATTAATTCT  
TTTATTATTGCTTTTGCTCCGGATGGAATAATTAGAAGAATTACTGCTTTTCTACTAGTGGTGGGCGCGAAATAG  
TTATTGATTTGACTGCTGTGAAGTTTAATGTTGGAATTCTTGATAGCAAATTTAAATATGATCCTCCAAATCTTC  
AAATAAGGTAGATAATTTTTTATATGATATTAATAAAAAATTAA

t584.nt

CAAATATCTGCAATCAATATTTTTGAAGGAATTTATGCTAAATATCAAAATATAGAGGACATGCAAGCAACAATTA  
ATTTTACTTTAAAGGGGTAAAACAGGTGTTTTGCTTTATAAGTTTCCAGACAAGTTTATTATCAATTTAGA  
TTCAAATAATCAAGTTTTTGTAAGTGATGGTGAATTTTTGACAGTTTATGTTCCATCTCTTGGGACTTCTTTTAA  
CAGCAATTATTAAAGGGTAGTAGTGGGGGAGGTCTTATGAAAGTTTAAATAGTGAGTATAGCGTATCTTATACCA  
ATTCTCCAAATTTAGAAGATCTCGATTCATCTGAGCCTGGAAAAATATATTAAATTAACCTTTTCTAGAAAGCTTTA  
CAAGGGGGCTGCTACTATTAATTCTTTTATTATTGCTTTTGCTCCGGATGGAATAATTAGAAGAATTACTGCTTTT  
CCTACTAGTGGTGGGCGCGAAATAGTTATTGATTTGACTGCTGTGAAGTTTAATGTTGGAATCTTTGATAGCAAAT  
TTAAATATGATCCTCCAAATCTTCAAATAAGGTAGATAATTTTTTATATGATATTAATAAAAAATTAA

f596.aa

MKERCLYLLVFVALCVNNLFSDDYLIYDFDLSLNEFLEVSTRKDNLEPMVDSNRILLFYPPKKEIRKIFAAFDQ  
YSKKYLFKKNEHGVFFVKVNI PHGTSSIKYRLIVDGVWNTDEYNKNVVYNEDLIPFSKIEIAKEKSSYISLRNPIQ  
SYDNNEIEIFYIGRPGQIVTIAGSFNNFNPFLNRLIEKEDNKGIYTIKLNLPKDRIYYYFIDSGNKVIDKNNVNR  
INLYFVEGIDNKIDFEVSYFDHK

t596.aa

DDYLIYDFDLSLNEFLEVSTRKDNLEPMVDSNRILLFYPPKKEIRKIFAAFDQYSKKYLFKKNEHGVFFVKVNI  
PHGTSSIKYRLIVDGVWNTDEYNKNVVYNEDLIPFSKIEIAKEKSSYISLRNPIQSYDNNEIEIFYIGRPGQIVTI  
AGSFNNFNPFLNRLIEKEDNKGIYTIKLNLPKDRIYYYFIDSGNKVIDKNNVNRINLYFVEGIDNKIDFEVSYFD  
HK

f596.nt

ATGAAAGAAAGGTGTTTGTATTTATTGGTTTTTGTAGCTTTATGTGTTAACAATCTTTTTTCAGATGATTATTTAA  
TTTATGACTTTGATTTAAGTTTAAATGAATTTCTAGAAGTTTCAACAAGAAAAGACAATCTTGAGCCTATGGTTGA  
TTCCAATCGTATATTATTGTTTTATCCTCCTAAAAAGAAATTAGAAAAATTTTTGCTGCCTTTGACTTTGATCAG  
TATTCTAAGAAATATTTATTCAAAAAAATGAGCATGGAGTTTTTTTTGTAAAGTTAATATTCCTCATGGCACAA  
GCAGTATAAAATATAGGCTTATTGTAGACGGTGTGGGACTAATGACGAGTATAATAAAAAATGTAGTTTATAATGA  
GGATTTAATCCCATTTTCTAAAATTGAGATCGCTAAAGAGAAGTCCAGCTATATTTCTTTGAGAAATCCAATACAA  
TCATATGATAACAATGAAATTGAAATTTTTTACATAGGTCGTCTGACAAATAGTTACAATAGCTGGTAGTTTTTA  
ACAATTTTAATCCTTTTTTAAATAGGCTTATTGAGAAAGAGGACAATAAGGGAATTTATACTATTAAGCTTAAAAA  
TTTACCCAAGGATAGAATTTATTATTATTTTATTGATTCTGGTAACAAAGTAATAGATAAAAAATAATGTTAATAGA  
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t596.nt

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TGACTTTGATCAGTATTCTAAGAAATATTTATTCAAAAAAATGAGCATGGAGTTTTTTTTGTAAAGTTAATATT  
CCTCATGGCACAAAGCAGTATAAAATATAGGCTTATTGTAGACGGTGTGGGACTAATGACGAGTATAATAAAAAATG  
TAGTTTATAATGAGGATTTAATCCCATTTTCTAAAATTGAGATCGCTAAAGAGAAGTCCAGCTATATTTCTTTGAG  
AAATCCAATACAATCATATGATAACAATGAAATTGAAATTTTTTACATAGGTCGTCTGACAAATAGTTACAATA  
GCTGGTAGTTTAAACAATTTAATCCTTTTTTAAATAGGCTTATTGAGAAAAGAGGACAATAAGGGAATTTATACTA  
TTAAGCTTAAAAATTTACCCAAGGATAGAATTTATTATTATTTATTGATTCTGGTAACAAAGTAATAGATAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

TAATGTTAATAGAAATTAATTTATATTTTGTGAGGGAATTGATAATAAAATAGATTTCTGAAGTTTCCTATTTTGAT  
CATAAGTAA

f598.aa

MRQRMAMALSCHPSLLIADEPTTALDVTIQEQILLIKNLSKKFNTSTIFITHDLAVVAEICDTVSVMYQGKIV  
EEGTVVEEIFNPNKHPYTIGLLKSILTLEHDPNKKLYSTKENPMKITKTSTEEF

t598.aa

EPTTALDVTIQEQILLIKNLSKKFNTSTIFITHDLAVVAEICDTVSVMYQGKIVEEGTVVEEIFNPNKHPYTIGLL  
KSILTLEHDPNKKLYSTKENPMKITKTSTEEF

f598.nt

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CCCTTGATGTTACAATCCAAGAGCAAATATTATTATTAATCAAAAACCTATCTAAAAAATTCAATACTTCTACCAT  
ATTTATAACTCATGATCTTGCGGTTGTTGCTGAAATTTGTGATACAGTATCTGTAATGTATCAAGGAAAAATTGTA  
GAAGAAGGAACAGTAGAGGAAATATTTAACAATCCTAAGCATCCTTACACCATTGGGCTTTTAAAAATCAATTCTTA  
CGCTAGAACACGATCCAAATAAAAAGCTTTATTCAACAAAAGAAAACCTATGAAGATCACAAAACCAGCACCGA  
GGAGTTTTAA

t598.nt

GAACCAACAACAGCCCTTGATGTTACAATCCAAGAGCAAATATTATTATTAATCAAAAACCTATCTAAAAAATTCA  
ATACTTCTACCATATTTATAACTCATGATCTTGCGGTTGTTGCTGAAATTTGTGATACAGTATCTGTAATGTATCA  
AGGAAAAATTGTAGAAGAAGGAACAGTAGAGGAAATATTTAACAATCCTAAGCATCCTTACACCATTGGGCTTTTA  
AAATCAATTCTTACGCTAGAACACGATCCAAATAAAAAGCTTTATTCAACAAAAGAAAACCTATGAAGATCACAA  
AAACCAGCACCGAGGAGTTTTAA

f600.aa

MAIMERSIIGLFIALAFVSWLTVARVVRGQVQSLSSSEFIQAAKTLGATNQRIILKHLIPNSIGMIVIFTTIRVPS  
FIMAEAFLSFLGLGISAPMTSWGELVQNGIATFVEYPWKVFIPIVMTIFLLFMNFLGDGLRDAFDPKDSI

t600.aa

RVVRGQVQSLSSSEFIQAAKTLGATNQRIILKHLIPNSIGMIVIFTTIRVPSFIMAEAFLSFLGLGISAPMTSWGE  
LVQNGIATFVEYPWKVFIPIVMTIFLLFMNFLGDGLRDAFDPKDSI

f600.nt

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AAGAATAATCTTAAAACACTTGATCCCTAATAGCATTGGAATGATAGTTATATTCACAACAATAAGGGTTCCAAGC  
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TGCAAAATGGAATTGCTACATTTGTTGAATATCCATGGAAAGTTTTTATTCAGCTATAGTTATGACAATATTTCT  
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t600.nt

CGAGTTGTACGAGGCCAAGTACAATCACTATCAAGTTCGGAATTTATACAAGCAGCCAAAACCTTGGTGCAACAA  
ATCAAGAATAATCTTAAAACACTTGATCCCTAATAGCATTGGAATGATAGTTATATTCACAACAATAAGGGTTCC  
AAGCTTTATTATGGCTGAAGCATTTTTATCCTTTTTAGGACTTGGAAATTCAGCTCCAATGACAAGCTGGGGAGAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTAGTGCAAAATGGAATTGCTACATTTGTTGAATATCCATGGAAAGTTTTTATTCCAGCTATAGTTATGACAATAT  
TTCTATTATTTATGAACTTTTTAGGTGATGGGCTAAGGGATGCTTTTGATCCAAAAGATAGCATCTAA

f603 .aa

MLKFTLKKILGIIPTLLVLIIFLCFFVMRMAPGSPFDSEKPIDPQVKARLMEKYHLDKPFYIQAFYYITNALRGDLG  
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FFAIKWGLLYTSGWITERGGFSNLILPIITLSMPNVAIFARIIRGSMLEIIQSDFIRTARAKGLSFKKIVIKHMLR  
GAMLPVVSIGPAFAAIIISGSVVEIKIFRIAGMGMFITESALNRDYPVLMGGLLVYSIILLISILISDIIYKILDP  
RV

t603 .aa

SPFDSEKPIDPQVKARLMEKYHLDKPFYIQAFYYITNALRGDLGPSLKKKDLTVSQYIKLGFPKSLTLGVISLIIS  
LSIGIPIGILAAIYKNTYVDYIITSIAILGISIPLFVIGPILOQYFFAIKWGLLYTSGWITERGGFSNLILPIITLS  
MPNVAIFARIIRGSMLEIIQSDFIRTARAKGLSFKKIVIKHMLRGAMLPVVSIGPAFAAIIISGSVVEIKIFRIAG  
MGMFITESALNRDYPVLMGGLLVYSIILLISILISDIIYKILDPV

f603 .nt

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AAAATATCACCTTGACAAGCCTTTTTATATTCAAGCTTTTTATTACATTACAAACGCTCTCAGGGGAGATCTGGGA  
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ACAAAGCGACTTTTATAAGAACTGCGCGTGCAAAAGGGCTAAGCTTCAAAAAGATAGTTATAAAGCATATGTTAAGA  
GGAGCAATGTTGCCGTGTAGTAAGCTATATAGGTCCAGCATTTGCTGCTATAATATCTGGAAGCGTGGTTATTGAAA  
AAATATTTAGAATTGCTGGAATGGGAATGTTTATAACAGAATCCGCACATAACAGAGATTACCCAGTATTAATGGG  
CGGATTGTTAGTATATTCAATAATACTGCTTATTTCTATATTAATATCAGATATTATATATAAAATATTAGATCCA  
AGAGTATAA

t603 .nt

AGTCCATTTGATTCTGAAAAACCTATTGATCCTCAAGTAAAAGCAAGATTGATGGAAAAATATCACCTTGACAAGC  
CTTTTTATATTCAAGCTTTTTATTACATTACAAACGCTCTCAGGGGAGATCTGGGACCTTCTTTGAAAAAGAAAGA  
CCTTACAGTTAGTCAATACATAAAATTAGGATTTCCAAAATCACTTACACTAGGAGTAATATCCCTTATTATATCA  
CTATCAATAGGAATACCAATAGGTATATTAGCTGCCATTTATAAAAATACTTATGTGGATTATATAATAACATCAA  
TAGCAATATTGGGGATTTCAATACCATTATTTCGTAATAGGGCCAATTTTACAATATTTTTTTGCAATTAAATGGGG  
TTTGCTTTATACCTCTGGATGGATTACAGAAAGAGGAGGATTTTCAAATTTAATTCTACCCATAATAACTCTTAGC  
ATGCCCAACGTAGCTATTTTCGCAAGAATAATCAGAGGATCAATGCTAGAAATAATACAAAGCGACTTTTATAAGAA  
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AAGCTATATAGGTCCAGCATTTGCTGCTATAATATCTGGAAGCGTGGTTATTGAAAAAATATTTAGAATTGCTGGA  
ATGGGAATGTTTATAACAGAATCCGCACATAACAGAGATTACCCAGTATTAATGGGCGGATTGTTAGTATATTCAA  
TAATACTGCTTATTTCTATATTAATATCAGATATTATATATAAAATATTAGATCCAAGAGTATAA

f607 .aa

MKYIKIALMLIIFSLIACISNAKKEKIVFRVSNLSEPSLDPQLSTDLYGSNIITNLFLGLAVKDSQTKYKPGLA  
KSWNISEDGIIYTFNLREDIVWSDGVAITAEI IKSYLRILNKKTAAMYANLIKSTIKNAQEYFDETVPESELGIK  
AIDSKTLEITLTSKPYFPDMLTHSAYIPVPMHIVEKYGENWNTNPENIVVSGAYKLKERSINDKIVIEKNEKYNA  
KNVEIDEVIFYPTEGSVAYNMYINGELDFLQGA EKNLEEKIRDDYYSGLKNGMAYIAFNNTTIKPLDNLKVRQAI  
SLAIDRET LTKVVLKGSSDPTRNLTPKFDDYSYGKNLILFDPENAKLLAEAGYPDGKGFPTLKYKISEGRPTTAE

TABLE 1. Nucleotide and Amino Acid Sequences

FLQEQFKKILNINLEIENEETTFGLSRRTGNYQMSSVGWIGDYFDPLTFLDSLFTTENHFLGAYKYSNKEYDALI  
KKS NFELDPIKRQDILRQAEIIAEKDFPMAPLYIPKSHYLFNRNDKWTGWVPNIAESYLYEDIKTKK

t607.aa

CISNAKKEKIVFRVSNLSEPSLDPQLSTDLYGSNIITNLFGLAVKDSQTGKYKPLAKSWNISEDGIIYTFNLR  
EDIVWSDGVAITAEI KKS YLRILNKKTAAMYANLIKSTIKNAQEYFDETVPESELGIKAIDSKTLEITLTSPKPY  
FPDMLTHSAYIPVPMHIVEKYGENWTPENIVVSGAYKLRKERSINDKIVIEKNEKYNAKNVEIDEVIFYPTEGSV  
AYNMYINGELDFLQGA EKNNLEEIKIRDDYSSGLKNGMAYIAFNNTTIKPLDNLKVRQAISLAIDRET LTKVVLKGS  
SDPTRNLTPKFDDYSYGKNIILFDPENAKKLLAEAGYPDGKGFPTLKYKISEGRPTTAEF LQEQFKKILNINLEIE  
NEEWTTFLGSRRTGNYQMSSVGWIGDYFDPLTFLDSLFTTENHFLGAYKYSNKEYDALIKKS NFELDPIKRQDILR  
QAEIIAEKDFPMAPLYIPKSHYLFNRNDKWTGWVPNIAESYLYEDIKTKK

f607.nt

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CAACATTATTACAAACCTATTCTTAGGCCTAGCGGTAAAAGATTCTCAAACCTGGAATAATAAACAGGACTTGCA  
AAAAGTTGGAATATTTCTGAAGATGGAATTATTTACACATTTAACCTAAGAGAAGATATAGTTTGGAGCGATGGAG  
TTGCCATTACTGCCGAGGAGATAAAAAATCATACCTAAGAATTTTAAATAAAAAAACAGCTGCAATGTATGCTAA  
TTTAATAAAATCTACAATAAAAAATGCACAAGAATATTTTCGATGAGACAGTGCCTGAATCTGAGCTTGGCATAAAG  
GCTATTGACAGCAAAACCTTAGAGATAACATTAACATCTCCAAAGCCTTATTTTCTGATATGCTAACACACTCAG  
CATACATACCAGTTCCAATGCATATTGTTGAAAAATATGGAGAAAATTGGACAAATCCTGAAAATATAGTTGTTAG  
TGGCGCATACAAACTTAAAGAAAGATCAATTAACGATAAAATCGTAATAGAAAAAATGAAAAATACTATAATGCA  
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AACTCGATTTTTCTACAAGGAGCAGAAAAGAATAATTTAGAAAGAAATTAATAAGAGATGATTATTATTTCTGGGTT  
AAAAACGGAATGGCATACATAGCATTCAATAACAATAAAACCACTAGACAATTTAAAAGTTAGACAAGCCATC  
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CAAAATTTGATGATTATTCTTATGAAAAAATTTAATACTATTGATCCTGAGAATGCAAAAAAATTTTAGCTGA  
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TTTTTGCAAGAACAATTTAAAAAATACTAAACATTAACCTAGAAATCGAGAATGAAGAATGGACAACATTCCTAG  
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AGACAGCTTATTTACAACAGAAAATCATTTTTTAGGAGCGTACAAATATTCAAACAAGAGTATGATGCTTTAATA  
AAAAATCTAATTTTGAACCTTGATCCAATAAAAAGACAAGACATTTTAAGACAAGCTGAAGAGATAATAGCAGAAA  
AAGACTTTCCTATGGCACCTTTATATATACCCAAATCTCATTATCTTTTCAGAAATGATAAATGGACAGGGTGGGT  
ACCAATATCGCAGAAAGCTATTTATATGAAGATATTAAACTAAAAAATAA

t607.nt

TGTATTAGTAATGCTAAAAAAGAAAAAATAGTTTTTCAGAGTATCAAACCTTAAGCGAGCCATCATCACTTGATCCTC  
AACTCTCAACAGACCTTTACGGTAGCAACATTATTACAAACCTATTCTTAGGCCTAGCGGTAAAAGATTCTCAAAC  
TGGAAAAATATAAACAGGACTTGCAAAAAGTTGGAATATTTCTGAAGATGGAATTATTTACACATTTAACCTAAGA  
GAAGATATAGTTTGGAGCGATGGAGTTGCCATTACTGCCGAGGAGATAAAAAATCATACCTAAGAATTTTAAATA  
AAAAACAGCTGCAATGTATGCTAATTTAATAAAATCTACAATAAAAAATGCACAAGAATATTTTCGATGAGACAGT  
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GCTTACAATATGTACATAAACGGTGAACCTCGATTTTCTACAAGGAGCAGAAAAGAATAATTTAGAAAGAAATAAAA  
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GGAGGGAAGACCAACAACAGCAGAAATTTTTCAGAAACAATTTAAAAAATACTAAACATTAACCTAGAAATCGAG  
AATGAAGAATGGACAACATTCCTAGGAAGCAGAAAGAACTGGAAATTACCAATGTCAAGCGTGGGGTGGATAGGAG  
ATTATTTTGATCCCTTAACATTCTTAGACAGCTTATTTACAACAGAAAATCATTTTTTAGGAGCGTACAAATATTC



TABLE 1. Nucleotide and Amino Acid Sequences

AAACAAAGAGTATGATGCTTTAATAAAAAAATCTAATTTTGAAGCTTGATCCAATAAAAAAGACAAGACATTTTAAGA  
CAAGCTGAAGAGATAATAGCAGAAAAAGACTTTCCCTATGGCACCTTTATATATACCCAAATCTCATTATCTTTTCA  
GAAATGATAAATGGACAGGGTGGGTACCAAATATCGCAGAAAGCTATTTATATGAAGATATTTAAACTAAAAATA  
A

f611.aa

MKKIFLFLFISFYLFGEFEDSSLKIGIDDVYVEAHEEGFHLFIRKKPAIKSVILTESFEIPDKKKDVATYSFRTLSY  
NKVNGDEIRILNGRVIKNKELLSLTSSTPVPNKKFGEAFHILIPKKLKYGFPNFSTRSGDIDLEVLKSKKEPWFWS  
IRSFEEKYNDYLGRYQDNAYELLFKDDQNQKIEFNELKDTFTKFSDEVVIANNGIDIVDKINKILKNSEDSVYDL  
DLVLVDVTDMSKSNIEILKEHLFSIIEPQLQKFYSYRIGLVFYKDYLEDFLTAKAFDNFTIPLYLNNILKYVNVGGG  
GDYPEAVFEGIDAAVTQFDWRAERRFIIVIGDAPPHEYPRGSIVYKDVINSACEKIDITYGIIFQ

t611.aa

FEDSSLKIGIDDVYVEAHEEGFHLFIRKKPAIKSVILTESFEIPDKKKDVATYSFRTLSYNKVNGDEIRILNGRVI  
KNKELLSLTSSTPVPNKKFGEAFHILIPKKLKYGFPNFSTRSGDIDLEVLKSKKEPWFWSIRSFEEKYNDYLGRYQ  
DNAYELLFKDDQNQKIEFNELKDTFTKFSDEVVIANNGIDIVDKINKILKNSEDSVYDLDLVLVDVTDMSKSNIE  
ILKEHLFSIIEPQLQKFYSYRIGLVFYKDYLEDFLTAKAFDNFTIPLYLNNILKYVNVGGGGDYPEAVFEGIDA  
AVTQFDWRAERRFIIVIGDAPPHEYPRGSIVYKDVINSACEKIDITYGIIFQ

f611.nt

ATGAAGAAAATTTTTTTATTTCTTTTATTAGTTTTTTATTTGTTTGGATTTGAAGATAGTCTTTTGAAAATAGGTA  
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TCCAAATTTTTCAACAAGAAGTGGTGATATTGACTTAGAAGTATTAAGAAAGTAAAAAGAGCCCTTTTGGTTTTCT  
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TAATAGAACCTCAACTTCAAAAGTTTAAATCCTACAGAATAGGTCTTGTTTTTTATAAAGACTATCTTGAAGATTT  
TTTAACCAAAGCTTTTGATTTTAATACTATTCCTTATTTAAATAATATTCTTAAGTATGTTAATGTTGGTGGCGGT  
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TTATTATTGTTATAGGAGATGCACCTCCTCATGAGTATCCAAGAGGGTCTATTGTTTATAAAGATGTTATCAATTC  
TGCAAAGGAAAAAGATATTACAATTTATGGAATAATATTTTCAGTAA

t611.nt

TTTGAAGATAGTTCCTTTGAAAATAGGTATTGATGATGTTTATGTTGAGGCTCATGAAGAGGGATTTCATCTTTTTTA  
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TACTTATTCATTTTCGTACATTAAGTTATAATAAGGTTAATGGAGATGAAATTCGGATTTTAAATGGAAGAGTTATT  
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TGATTCCAAAAAAATTTAAATATGGATTTCCAAATTTTTCAACAAGAAGTGGTGATATTGACTTAGAAGTATTAAA  
AAGTAAAAAGAGCCCTTTTGGTTTTCTATAAGATCTTTTGAGAAAAATATAATGATTATTTGGGCAGATATCAA  
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TCTTAAGTATGTTAATGTTGGTGGCGGTGGGGATTATCCAGAAGCTGTTTTTGAGGGGATTGATGCTGCTGTGACC  
CAATTTGATTGGCGGGCAGAAAGAAGGTTTATTATTGTTATAGGAGATGCACCTCCTCATGAGTATCCAAGAGGGT  
CTATTGTTTATAAAGATGTTATCAATTCGCAAAGGAAAAAGATATTACAATTTATGGAATAATATTTTCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

f617.aa

MIFFRNSFMALIFSFSILSISYFFGDFQFSYIKMISWRFILFLIMATGIATCAKSNSLNLGNEGQIYFGAFLVYI  
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NSLFALDSSSLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNINEFKYKFFAVFGSAFLNGLAGSMF  
VVFFRPYLVLGLTSGLGWSSLIVAVISGFNYVYVLFSSLLFSILIEFNFLNINYDFKYEFIGLCQSI AIFISLFL  
IKARKK

t617.aa

AKSNSLNLGNEGQIYFGAFLVYIFSSFFGLTYFNFVFLILLSSFFVGLLGLIPFFITFFFGLNKALTGLLLISYGNQ  
RLVDGFILNMLKTGSFSNQTKRINSLFALDSSSLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNIN  
EFKYKFFAVFGSAFLNGLAGSMFVVFFRPYLVLGLTSGLGWSSLIVAVISGFNYVYVLFSSLLFSILIEFNFLNI  
NYDFKYEFIGLCQSI AIFISLFLIKARKK

f617.nt

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GTAGTGTTTTTAGACCATATTTGGTTTTAGGGCTAACTTCAGGACTTGGTTGGAGTAGTCTAATTGTTGCTGTAA  
TTTCAGGATTTAATTATGTTTATGTATTATTTTTTAGCTTATTGTTTTCAATATTAATTGAATTTAATAATTTTCT  
TAATATAAATTATGACTTTAAGTATGAATTTATTGGGCTTTGTCAATCAATTGCTATTTTTATCTCTTTATTTTTG  
ATTAAGCTAGGAAAAAGTAG

t617.nt

GCCAAGAGTAATTCATTAAATCTTGGGAATGAAGGTCAGATTTATTTTGGGGCATTTTTAGTTTATATATTTTTCAA  
GTTTTTTTGGATTAACTATTTTAAATTTTGATTTTTGATACTTTTAAAGTTCTTTTTTGTAGGACTTTTGGGGCT  
TATCCCCCTTTTTTATTACTTTTTTCTTCGGATTAAATAAAGCCTTAACAGGCTTTTAAATATCTTATGGAAATCAA  
AGATTGGTGGATGGATTTATTTTAAATATGTTAAAAACAGGTAGTTTTTCTAATCAGACAAAAAGGATTAATAGTT  
TGTTTGCTTTAGATTCACTACTTATTTACTTGTTTTGCTTGGTGTATCAGTTTGGCTTTTTTATGTTTTTATTCA  
CAAAAAAACTATTTATGGTCTTCAGCTTGAAATATTAAGCAATAAAAAAAGATAGACATTTTTTTCAATATAAAT  
GAATTTAAATATAAGTTTTTCGCTGTATTTGGCAGTGCTTTTTTAAATGGTCTTGCAGGTTCTATGTTTGTAGTGT  
TTTTTAGACCATATTTGGTTTTAGGGCTAACTTCAGGACTTGGTTGGAGTAGTCTAATTGTTGCTGTAAATTCAGG  
ATTTAATTATGTTTATGTATTATTTTTTAGCTTATTGTTTTCAATATTAATTGAATTTAATAATTTTCTTAATATA  
AATTATGACTTTAAGTATGAATTTATTGGGCTTTGTCAATCAATTGCTATTTTTATCTCTTTATTTTTGATTAAAG  
CTAGGAAAAAGTAG

f631.aa

MVVEINSLRTCYLLVLLLLVAYGLVVFYTSFFLSLELTGNPNFLFFTRLNLYLFLFSMVFLVFERISLNLKKSIF  
PVLIIITFLIMATFLSPSISGAKRWIFFQGVSIQPSIEFKISFTIYLSAYLSKFDPRKNNGISYWKPMILIFAIFW  
VLIILQNDYSTAIYFAILFFIVLFVSNMAFSYVFAIVVTFLPVSAIFLMLEPYRVSRIFAFLNPYDDPSGKGQII  
ASLNALKSGGILGKGLGMGEVKGKLPEANSDFIFSVLGEELGFLGVLFALSLFFLFFYFGYFIAIHSNSRKFIFI  
AFISSLAIFLQSMNIIAIGLLPPTGINLPFFSSGGSSIIVTMALSGLISNVSKNLSNN

t631.aa

TABLE 1. Nucleotide and Amino Acid Sequences

RISLNFLKKSIFPVLIITLFLIMATFLSPSISGAKRWIFFQGVSIQPSEIFKISFTIYLSAYLSKFDPRKNNGISY  
WIKPMLIFAIFWVLIILQNDYSTAIYFAILFFIVLFVSNMAFSYVFAIVVTFLPVSAIFLMLEPYRVSRIFAFLNP  
YDDPSGKGYQIIASLNALKSGGILGKGLGMGEVKLGKLPEANSDFIFSVLGEELGFLGVLFALISLFFLFYFGYFI  
AIHSNSRFKFFIAFISSLAIFLQSMNLIAGLLPPTGINLPFFSSGGSSIIVTMALSGLISNVSKNLSNN

f631.nt

ATGGTTGTAGAGATAAATTCACCTTAGGACATGTTATTTGCTTGTTTTGCTGCTATTGGTAGCCTATGGCCTTGTAG  
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TTATCTTTTTTTAAGTTTTATGGTTTTTCTTGTTTTTGAAAGGATTCTTTTAAATTTTTTAAAAAAATCAATATTT  
CCTGTATTGATTATAACTCTTTTTTTAATTATGGCAACTTTTTTATCTCCAAGTATTTCTGGAGCAAAGAGATGGA  
TATTCTTTCAAGGTGTTAGCATTCAACCTTCTGAGATTTTTTAAATATCTTTTACTATTTATCTTTTACGCTTATTT  
GAGCAAGTTTGACCCAAGAAAAACAATGGTATTTTCACTGAGATAAAGCCAATGTTGATTTTTTGCAATTTTTTGG  
GTGTTAATAATTTTGCAAAACGATTATTTCAACAGCTATTTATTTTGCCATTCTTTTTTTTTATGTTTTGTTTGT  
CTAATATGGCATTAGCTATGTTTTGCTATTGTGGTTACTTTTTTACCAGTTCTGCTATATTCTTGATGCTTGA  
ACCTTATAGGGTTTCTAGAATTTTTGCCTTTCTCAATCCTTACGATGATCCTTCTGGCAAAGGTTACCAGATAATA  
GCATCTCTTAATGCTTTTAAAAAGTGGAGGAATTTTAGGTAAAGGGCTGGGAATGGGAGAGGTAAAACCTGGAAAAT  
TACCAGAGGCCAATTCGGATTTTATTTTTTTCAGTTCTTGGAGAAGAATTAGGATTTTATAGGGGTTTTGTTTGTCTAT  
AAGCTTGTTTTTTTTGTTTTTTTACTTTTGGTTATTTTATAGCTATTCATTCTAATAGTAGGTTTAAATTTTTTATT  
GCATTTATTTCAAGTCTTGCAATTTTTTCTTCAAAGCATGATGAATATTTTAAATTGCAATCGGTCTTTTGCCTCCTA  
CAGGGATAAATTTACCATTTTTTTTCATCTGGGGGATCTTCTATTATTGTTACCATGGCATTGTCTGGCCTTATTTT  
AAATGTTTCAAAAAATTTAAGTAATAATTGA

t631.nt

AGGATTTCTTTAAATTTTTTAAAAAAATCAATATTTCTGTATTGATTATAACTCTTTTTTTTAAATTATGGCAACTT  
TTTTATCTCCAAGTATTTCTGGAGCAAAGAGATGGATATTCTTTCAAGGTGTAGCATTTCAACCTTCTGAGATTTT  
TAAATATCTTTTACTATTTATCTTTTACGCTTATTTGAGCAAGTTTGACCCAAGAAAAACAATGGTATTTTATAC  
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ATTTTGCCATTCTTTTTTTTATTGTTTTGTTTGTCTAATATGGCATTAGCTATGTTTTGCTATTGTGGTTAC  
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TACGATGATCCTTCTGGCAAAGGTTACCAGATAATAGCATCTCTTAATGCTTTAAAAAGTGGAGGAATTTTAGGTA  
AAGGGCTGGGAATGGGAGAGGTAAAACCTGGAAAATTACCAGAGGCCAATTCGGATTTTATTTTTTTCAGTTCTTGG  
AGAAGAATTAGGATTTTTAGGGGTTTTGTTTGTCTATAAGCTTGTTTTTTTTGTTTTTTTACTTTGGTTATTTTATA  
GCTATTCTATTCTAATAGTAGGTTTAAATTTTTTATTGCATTTATTTCAAGTCTTGCAATTTTTCTTCAAAGCATGA  
TGAATATTTTAAATTGCAATCGGTCTTTTGCCTCCTACAGGGATAAATTTACCATTTTTTTTCATCTGGGGGATCTTC  
TATTATTGTTACCATGGCATTGTCTGGCCTTATTTCAAATGTTTCAAAAAATTTAAGTAATAATTGA

f647.aa

MKVNNFLSFFFRAFFLLFLIVILFFVLFIDFIGMYNTRYFPEFVRTKLLGETSLVFDHNSNIILDEARLVKER  
EAIDIKNQIEKLKEDLKLKEDSLNKLEFELKQKQKDLDLKQKIIDDINKYNDEEANILQTAVYLMNMPPEDAVK  
RLEDLNP ELAISYMRKIEELSKKEGRLSIVPYWLSLMDSKKAAAILIRKMSVSSLE

t647.aa

IDFIGMYNTRYFPEFVRTKLLGETSLVFDHNSNIILDEARLVKEREIDIKNQIEKLKEDLKLKEDSLNKLEFE  
LKQKQKDLDLKQKIIDDINKYNDEEANILQTAVYLMNMPPEDAVKRLEDLNP ELAISYMRKIEELSKKEGRLSIV  
PYWLSLMDSKKAAAILIRKMSVSSLE

f647.nt

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TTGTATTATTCTTTATTGATTTTATTGGAATGTATAATACTAAAAAGATATTTCCCCGAATTTGTAAGAACCAAGTT  
GTTAGGAGAAACTTCTCTGGTCTTTGATCATAATTCTAATATAATTCTTGATGAAGCTAGACTTGTGAAGGAAAGA  
GAAGCTATTGATATTAAGAATCAGCAGATTGAAAAGCTTAAAGAAGATCTAAAGTTAAAGAAGACAGTTTAAATA

TABLE 1. Nucleotide and Amino Acid Sequences

AGCTTGAATTTGAGCTTAAGCAAAAGCAGAAAGATTTAGATTTAAACAAAAAATAATAGATGACATTATAAATAA  
ATATAATGATGAGGAAGCAAATATTTTGCACAGCTGTATATTTAATGAATATGCCACCAGAAGATGCTGTTAAG  
CGGCTTGAAGATTTAAATCCCGAGCTTGCAATATCTTATATGCGGAAAAATTGAAGAGCTTTCCAAAAAAGAAGGTC  
GTTTATCAATTGTTCCCTTATTGGTTATCTCTTATGGATTCTAAAAAAGCTGCTATATTGATTAGAAAAATGCTCTGT  
TAGTTTCATTGGAGTAG

t647.nt

ATTGATTTTATTGGAATGTATAATACTAAAGATATTTCCCCGAATTTGTAAGAACCAAGTTGTTAGGAGAACTT  
CTCTGGTCTTTGATCATAATTCCTAATATAATTCTTGATGAAGCTAGACTTGTGAAGGAAAGAGAAGCTATTGATAT  
TAAGAATCAGCAGATTTGAAAAGCTTAAAGAAGATCTAAAGTTAAAGAAGACAGTTTAAATAAGCTTGAATTTGAG  
CTTAAGCAAAAGCAGAAAGATTTAGATTTAAACAAAAAATAATAGATGACATTATAAATAAATATAATGATGAGG  
AAGCAAATATTTTGCACAGCTGTATATTTAATGAATATGCCACCAGAAGATGCTGTTAAGCGGCTTGAAGATTT  
AAATCCCGAGCTTGCAATATCTTATATGCGGAAAAATTGAAGAGCTTTCCAAAAAAGAAGGTCGTTTATCAATTGTT  
CCTTATTGGTTATCTCTTATGGATTCTAAAAAAGCTGCTATATTGATTAGAAAAATGCTCTGTTAGTTTCATTGGAGT  
AG

f653.aa

MLTYGDMVTLLLVFFVTMFLNDIIFQENVIRIMSASFTGAGFFKGGKTLDFSKLSYLSNSFMSLPSTVRNKQASQ  
TAKNKSMEFIEKIQSKNIVVRQEERGIVISLAADAFDSDASADVKLEENRDSIQKIASFIGFLSPRGYNFKIEGH  
TDNIDTDVNGPWKSNWELSAARSVNMLEHILNYLDQSDVKRIENNFEVSGFGGSRPIATDDTPEGRAYNRRIDILI  
TTDASLSFPKEIKQ

t653.aa

NDIIFQENVIRIMSASFTGAGFFKGGKTLDFSKLSYLSNSFMSLPSTVRNKQASQTAKNKSMEFIEKIQSKNIVV  
RQEERGIVISLAADAFDSDASADVKLEENRDSIQKIASFIGFLSPRGYNFKIEGHTDNIDTDVNGPWKSNWELSA  
RSVNMLEHILNYLDQSDVKRIENNFEVSGFGGSRPIATDDTPEGRAYNRRIDILITTDASLSFPKEIKQ

f653.nt

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ACTGCTAAAAATAAATCCATGATTGAATTTATTGAGAAGATTCAGTCTAAAAATATTGTAGTTAGGCAAGAAGAAA  
GAGGTATTGTAATATCTCTTGCAGCAGATGCATTTTTTTGATTCTGCTAGTGCAGATGTTAAGCTTGAAGAGAATAG  
AGATTCTATTCAAAAAATAGCATCTTTTATTGGCTTTTTAAGTCCTAGAGGCTATAATTTTAAATAGAAGGGCAT  
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TGCTGGAACATATTTTGAACATTTTAGATCAATCTGATGTTAAAAGAATTGAAAATAATTTTGAAGTATCTGGTTT  
TGGTGGAAAGTAGGCCTATTGCAACAGACGATACCCCTGAGGGTAGGGCTTATAATAGAAGAATTGATATATTAATT  
ACTACAGATGCATCTTTAAGTTTCCCTAAGGAAATTAAGCAGTAA

t653.nt

AATGATATTATTTTTCAAGAAAATGTGATAAGAATAATGTCTGCTTCTTTACGGGTGCTGGATTTTTCAAGGGCG  
GTAAAACCTTTAGATTTTAGTAAATTATCTTATTTGAGTAATAGCTTTATGTCTTTGCCTTCTACTGTGCGCAATAA  
ACAAGCATCTCAGACTGCTAAAAATAAATCCATGATTGAATTTATTGAGAAGATTCAGTCTAAAAATATTGTAGTT  
AGGCAAGAAGAAAGAGGTATTGTAATATCTCTTGCAGCAGATGCATTTTTTTGATTCTGCTAGTGCAGATGTTAAGC  
TTGAAGAGAATAGAGATTCTATTCAAAAAATAGCATCTTTTATTGGCTTTTTAAGTCCTAGAGGCTATAATTTTAA  
AATAGAAGGGCATAACAGATAATATTGATACTGATGTAAATGGACCTTGAAAAGCAATTGGGAACCTTTCGGCTGCT  
AGATCTGTTAATATGCTGGAACATATTTTGAACATTTTAGATCAATCTGATGTTAAAAGAATTGAAAATAATTTTG  
AAGTATCTGGTTTTTGGTGGAAAGTAGGCCTATTGCAACAGACGATACCCCTGAGGGTAGGGCTTATAATAGAAGAAT  
TGATATATTAACTTACTACAGATGCATCTTTAAGTTTCCCTAAGGAAATTAAGCAGTAA

f664.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MRMSVYTMGFAYIRSIMGYVVLFFFASLAVNFFVNIIQVGFFITFKSLEPRWDKISFNFSRWAKNSFFSAGAFFNL  
FKSLLKVVIICLIYYFIIENNIGKISKLSEYTLQSGISIVLVIAYKICFFSVMFLAIVGVFDYLFQRSQYIESLKM  
TKEEVKQERKEMEGDPLLRRIKERMVRILSTNLRVAIPQADVITNPEHFAVAIKWDSETMLAPKVLAKGQDEIA  
LTIKKIARENNVPLMENKLLARALYANVKVNEEIPREYWEIVSKILVRVYSITKKFN

t664.aa

FNVIQVGFFITFKSLEPRWDKISFNFSRWAKNSFFSAGAFFNLFKSLLKVVIICLIYYFIIENNIGKISKLSEYT  
LQSGISIVLVIAYKICFFSVMFLAIVGVFDYLFQRSQYIESLKM TKEEVKQERKEMEGDPLLRRIKERMVRILST  
NLRVAIPQADVITNPEHFAVAIKWDSETMLAPKVLAKGQDEIALTIKKIARENNVPLMENKLLARALYANVKVNE  
EIPREYWEIVSKILVRVYSITKKFN

f664.nt

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CATCTTTAGCTGTTAATTTTTTTGTTAATATTATTCAAGTAGGCTTTTTTATTACTTTTAAATCTTTGGAGCCAAG  
GTGGGATAAAATTAGTTTTTAATTTTTCCAGATGGGCACAAAATCTTTTTTTTTTCAGCAGGGGCTTTTTTCAATTTG  
TTTAAAAGTTTGT TAAAAGTTGTTATAATATGCTTGATATATTATTTTATTATAGAAAACAATATAGGCAAAATTT  
CTAAGCTTTTCGGAGTATACACTTCAATCTGGAATTTCTATTGTGTAGTGATTGCCTATAAGATATGTTTTTTTTTC  
AGTAATGTTTTTGGCAATTGTAGGGGTGTTTGATTATTTGTTTCAAAGATCTCAGTACATTGAGAGTTTGAAAATG  
ACAAAAGAAGAGGTAAAGCAGGAAAGAAAGGAAATGGAAGGTGATCCTTTACTTCGATCTAGAATAAAAGAGAGAA  
TGAGGGTTATTTTAAGTACCAATTTAAGAGTAGCTATTCTCAAGCAGATGTAGTAATTACAAATCCAGAACATTT  
TGCAGTTGCTATTAAATGGGATAGCGAAACAATGTTAGCTCCAAAGGTGCTTGCAAAGGTCAAGATGAAATAGCT  
CTCACAATTAATAAATGCAAGAGAAAATAATGTTTCCTTTAATGGAAAATAAGCTCCTTGCAAGAGCTCTTTATG  
CTAATGTTAAGGTTAATGAAGAGATTCCAAGAGAATATTGGGAGATTGTTTCAAAAATCTTGTGAGAGTATATTC  
TATTACTAAAAAGTTTAATTAG

t664.nt

TTTGTTAATATTATTCAAGTAGGCTTTTTTATTACTTTTAAATCTTTGGAGCCAAGGTGGGATAAAATTAGTTTTA  
ATTTTTCCAGATGGGCACAAAATCTTTTTTTTTTCAGCAGGGGCTTTTTTCAATTTGTTTAAAAGTTTGT TAAAAGT  
TGTTATAATATGCTTGATATATTATTTTATTATAGAAAACAATATAGGCAAAATTTCTAAGCTTTTCGGAGTATACA  
CTTCAATCTGGAATTTCTATTGTGTAGTGATTGCCTATAAGATATGTTTTTTTTTCAGTAATGTTTTTGGCAATTG  
TAGGGGTGTTTGATTATTTGTTTCAAAGATCTCAGTACATTGAGAGTTTGAAAATGACAAAAGAAGAGGTAAAGCA  
GGAAAGAAAGGAAATGGAAGGTGATCCTTTACTTCGATCTAGAATAAAAGAGAGAATGAGGGTTATTTTAAGTACC  
AATTTAAGAGTAGCTATTCTCAAGCAGATGTAGTAATTACAAATCCAGAACATTTTGCAGTTGCTATTAAATGGG  
ATAGCGAAACAATGTAGCTCCAAAGGTGCTTGCAAAGGTCAAGATGAAATAGCTCTCACAATTAATAAATTTGC  
AAGAGAAAATAATGTTCTTTAATGGAAAATAAGCTCCTTGCAAGAGCTCTTTATGCTAATGTTAAGGTTAATGAA  
GAGATTCCAAGAGAATATTGGGAGATTGTTTCAAAAATCTTGTGAGAGTATATTCATTACTAAAAAGTTTAATT  
AG

f680.aa

MFTLSFVLINFIITGILILMLEFNFLKVDKGNILLAGIFMGLMQGLGALPGISRSGITIFSASVIGFNRKSAFEI  
SFLSLIPIVFGAILLKHKEFYDIFMVLNFFEINLGALVAFVVGIF SINFFFKMLNNKKLYYFSIYLFALSIIVCYF  
VRI

t680.aa

ITGILILMLEFNFLKVDKGNILLAGIFMGLMQGLGALPGISRSGITIFSASVIGFNRKSAFEISFLSLIPIVFGA  
ILLKHKEFYDIFMVLNFFEINLGALVAFVVGIF SINFFFKMLNNKKLYYFSIYLFALSIIVCYFVRI

f680.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGTTTACATTGTCTTTCGTTTAAATTAATTTTATTATAACAGGGATTTTAATCTTGATGCTAGAAATTTAATTTTT  
TAAAAGTTGATTTTAAAGGTAATATTTTGTAGCAGGAATTTTATGGGGCTGATGCAAGGCTTGGGTGCGCTTCC  
AGGAATCTCTCGTTCAGGAATTACGATCTTTTCGGCATCGGTATTGGATTAAATAGAAAAAGTGCATTTGAAATT  
TCATTTTATCTTTAATCCCAATAGTTTTTGGAGCGATTTTATTAAACATAAAGAATTTTATGATATTTTATGG  
TTTTAAATTTTTTGAATAAACTTAGGAGCATTAGTTGCTTTTGTGTTGGTATTTCTCAATAAATTTCTTTTT  
TAAAATGCTTAATAACAAAAAACTGTATTATTTTCTATATATTTATTTGCACTTCAATTATAGTTTGTATTATT  
GTTAGAATATGA

t680.nt

ATAACAGGGATTTTAATCTTGATGCTAGAAATTTAATTTTTTAAAGTTGATTTTAAAGGTAATATTTTGTAGCAG  
GAATTTTTATGGGGCTGATGCAAGGCTTGGGTGCGCTTCCAGGAATCTCTCGTTCAGGAATTACGATCTTTTCGGC  
ATCGGTTATTGGATTAAATAGAAAAAGTGCATTTGAAATTTCAATTTTATCTTTAATCCCAATAGTTTTTGGAGCG  
ATTTTATTAAACATAAAGAATTTTATGATATTTTATGGTTTTAAATTTTTTGAATAAACTTAGGAGCATTAG  
TTGCTTTTGTGTTGGTATTTCTCAATAAATTTCTTTTTTAAATGCTTAATAACAAAAAACTGTATTATTTTTC  
TATATATTTATTTGCACTTCAATTATAGTTTGTATTATTGTTAGAATATGA

f688.aa

MIVLLISIGCANAVHIINEIFKLIKKEQLSKESIKATIKKLKTPILLTSFTTAFGFLSLTTSSINAYKTMGIFMSI  
GVIISMIISLTVLPGIITLIPFAKKKSFEKEKENKLNKISFLERLAKLNTQITKSILKRKYTSSIMVLIILGISFV  
GLLKIEINFDEKDYFKESTSVKKTNLNMQEMGGISIFKIEIEGRPGFEKNAKAMQILDITDKLDAFSAKTQSSS  
INGILKFTNFKIKKESPLEYKLPENKIIILNKLINLIDKSDWTKDNKRMVINDDWLSISIVRIEDNSTEGIKKFEK  
YAINITNEYMKNNKYHFSGVYDKVLIAKTMVKEQVINIITTLGSITLLLMFFFKSIKTGIIIAIPVAWSVFLNFAV  
MRLFGITLNPATATIASVSMGVGVDSYIHFNTFILQYQKNQIYKTALLESIPNVFNGIFANSISVGIGFLTTLTFS  
SYKIIISTLGAIIAFTMLTTSLASLTLLPLLIYLFKPRVKLASNNNFKKLKQZ

t688.aa

YKTMGIFMSIGVVIISMIISLTVLPGIITLIPFAKKKSFEKEKENKLNKISFLERLAKLNTQITKSILKRKYTSSIM  
VLIILGISFVGLLKIEINFDEKDYFKESTSVKKTNLNMQEMGGISIFKIEIEGRPGFEKNAKAMQILDITDKLD  
AFSAKTQSSSINGILKFTNFKIKKESPLEYKLPENKIIILNKLINLIDKSDWTKDNKRMVINDDWLSISIVRIEDN  
STEGIKKFEKYAINTINEYMKNNKYHFSGVYDKVLIAKTMVKEQVINIITTLGSITLLLMFFFKSIKTGIIIAIPV  
AWSVFLNFAVMRLFGITLNPATATIASVSMGVGVDSYIHFNTFILQYQKNQIYKTALLESIPNVFNGIFANSISV  
GIGFLTTLTSSYKIIISTLGAIIAFTMLTTSLASLTLLPLLIYLFKPRVKLASNNNFKKLKQZ

f688.nt

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AACTGCATTTGGATTTTATCTCTTACAACCTCTTCAATTAATGCCTACAAAACAATGGGTATTTTCATGTCAATT  
GGAGTAATTATCTCAATGATAATCTCATTAACCGTTTTTACCTGGAATAATAACATTAATCCCATTGCAAAAAAAA  
AGTCTTTTGAAGAAAGAAAAAGAAAAATAAACTAAATAAAATATCCTTCCTTGAAAGACTTGCCAACTAAATACGCA  
AATAACAAAATCTATATTAATAAGAAAAATACATCCTCTATAATGGTCCTCATCATACTGGGAATTTCTTTTGTA  
GGTCTTTTAAAAATCGAAATCAATTTTGATGAAAAAGATTACTTTAAAGAAAGCACAAGTGTAACAAAAACATTAA  
ACCTAATGCAAAAGAAATGGGGGGAATATCGATTTTCAAAATAGAAATGAAGGCAGGCCCGGTGAATTTAAAAA  
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TATGCTATTAACACAATTAATGAATATATGAAAAATAATAAATATCATTTCTCAGGTGTTTATGATAAGGTATTAA  
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TTTCTTTAAATCTATAAAAAACCGGAATAATTTATGCAATCCCAGTAGCATGGTCAGTGTTTTTAACTTTGCTGTA  
ATGAGATTATTTGGGATAACCTTAAACCCCGCAACGGCAACAATTGCATCTGTAAGCATGGGAGTAGGAGTAGATT  
ATTCAATTCATTTTTTCAATACATTTATTTTACAATACCAAAAAAATCAAATCTACAAAACCTGCACTTCTTGAATC  
AATACCAATGTATTTAATGGAATATTTGCAAATTCATTTCTGTTGGAATAGGATTTTTAACTCTAACATTTTCG

TABLE 1. Nucleotide and Amino Acid Sequences

TC TTATAAAATAATATCAACTCTTGGAGCAATAATTGCTTTTACAATGCTAACGACATCTCTTGCATCACTAACTC  
TTCTTCCATTATTAATTTATTTATTTAAACCTAGAGTAAAGCTAGCCTCAAACAACAATTTTAAAAAATTAAACA  
ATAA

t688.nt

TACAAAACAATGGGTATTTTCATGTCAATTGGAGTAATTATCTCAATGATAATCTCATTAAACCGTTTTACCTGGAA  
TAATAACATTAATCCCATTTGCAAAAAAAGTCTTTTGAAAAAGAAAAAGAAATAAACTAAATAAAATATCCTT  
CCTTGAAAGACTTGCCAACTAAATACGCAATAACAAAATCTATATTAAAAAGAAAAATATACATCCTCTATAATG  
GTCCTCATCATACTGGGAATTTCTTTTGTAGGTCTTTTAAAAATCGAAATCAATTTTGATGAAAAAGATTACTTTA  
AAGAAAGCACAAAGTGTAACAAAAACATTAACCTAATGCAAAAAGAAATGGGGGAATATCGATTTTCAAAATAGA  
AATTGAAGGCAGGCCCGGTGAATTTAAAAATGCTAAAGCAATGCAAAATATTAGACTTAATTACAGATAAGCTTGTAT  
GCATTTTCTGCAAAAACCTCAATCTAGTTCTATTAAATGGCATTTTTAAAATTTACAAATTTTAAAAATTAAGAAAT  
CCCCACTAGAGTATAAACTGCCTGAAAAATAAAATTATACTAAACAACTAATAAAATTTGATAGATAAAAGCGATTG  
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TCAACCGAAGGAATAAAAAAATTTGAAAAATATGCTATTAAACACAATTAATGAATATATGAAAAATAATAAATATC  
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CATCTGTAAGCATGGGAGTAGGAGTAGATTATTCAATTCATTTTTTCAATACATTTATTTTACAAATACCAAAAAA  
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TGCTAACGACATCTCTTGCATCACTAACTCTTCTCCATTATTAATTTATTTTAAACCTAGAGTAAAGCTAGC  
CTCAAACAACAATTTTAAAAAATTAAAAACAATAA

f704.aa

MNYTKFQEFISEFLGTFILLALGTGSVAMTVLFSSSPEIPGEI IKGGYTNIVFGWGLGVTFGIYTAARMSG AHLNP  
AVSIGLASVGKFPVSKLLHYIVAQILGAFTGALMTLVVFYPKWIEMDPGLENTQGIMATFFAVPGFLPGFIDQIFG  
TFLLMFLISVVGDFTKKHSNDNPFIPFIVGAVVLSIGISFGGMNGYAINPARDLGPRIILLFAGFKNHGFNNLSIVI  
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t704.aa

GEI IKGGYTNIVFGWGLGVTFGIYTAARMSG AHLNP AVSIGLASVGKFPVSKLLHYIVAQILGAFTGALMTLVVFY  
PKWIEMDPGLENTQGIMATFFAVPGFLPGFIDQIFGTFLMFLISVVGDFTKKHSNDNPFIPFIVGAVVLSIGISFG  
GMNGYAINPARDLGPRIILLFAGFKNHGFNNLSIVIVPIIGPIIGAILGATIYEFTLKNNKD

f704.nt

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CTGTTGCAATGACAGTATTATTTTCCCTCAAGTCCCGAAATACCAGGAGAAATAATAAAAGGAGGATATACAAATAT  
AGTATTTGGATGGGATTGGGTGTAACGTTTGGTATTTACACAGCAGCAAGAATGAGCGGAGCACACCTAAACCCA  
GCTGTTAGCATAGGATTAGCAAGTGTGGAAAGTTTCCCGTTTCAAACCTTTACATTACATTGTAGCACAAATAT  
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TTATTGTAGGAGCAGTGGTTTTATCAATAGGGATAAGTTTCGGAGGAATGAACGGTTATGCTATTAAATCCTGCAAG  
GGATCTGGGACCAAGAATTTTACTCTTATTTGCTGGATTTAAAAATCACGGATTTAAACAATCTAAGTATAGTTATT  
GTACCAATAATTGGCCCAATAATTGGAGCAATTTTGGGAGCTACAATTTACGAATTTACACTAAAAAATAACAAAG  
ACTAA

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GGAGAAATAATAAAAGGAGGATATACAAATATAGTATTTGGATGGGGATTGGGTGTAACGTTTGGTATTTACACAG  
CAGCAAGAATGAGCGGAGCACACCTAAACCCAGCTGTTAGCATAGGATTAGCAAGTGTGGAAAGTTTCCCGTTTC

TABLE 1. Nucleotide and Amino Acid Sequences

AAAACTTTTACATTACATTGTAGCACAAATATTAGGAGCTTTTACAGGTGCATTAATGACACTTGTCGTATTTTAT  
 CCTAAATGGATAGAAATGGATCCTGGCTTAGAAAATACTCAAGGAATAATGGCAACTTTCCCTGCTGTTCCCTGGAT  
 TTTTGCCTGGATTTATTGATCAAATTTTGGAACTTTTGTGCTAATGTTTTTAATTTCTGTTGTTGGAGATTTTAC  
 AAAAAACACAGCGACAATCCATTTATTCCTTTTATTGTAGGAGCAGTGGTTTTATCAATAGGGATAAGTTTTCGGA  
 GGAATGAACGGTTATGCTATTAATCCTGCAAGGGATCTGGGACCAAGAATTTTACTCTTATTTGCTGGATTTAAAA  
 ATCACGGATTTAACAATCTAAGTATAGTTATTGTACCAATAATTGGCCCAATAATTGGAGCAATTTTGGGAGCTAC  
 AATTTACGAATTTACACTAAAAAATAACAAAG  
 ACTAA

f707.aa

MRRLFLLYILCSFVFLNLFAQGSSSYIDKQKELAIIFYEVGQRYINVGKIKKGKLFQAKALKIYPDLKKGFEDIKLA  
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 FDLFDSVIADKVNVMQGFESKNDFISTLSSASSKADADELEYLSVDDYYDLKSLKISKSNDTSFAVNVNAKKNVDVT  
 KNFPFWKERQTLIFTTEDDNNWFLSSINZ

t707.aa

MRRLFLLYILCSFVFLNLFAQGSSSYIDKQKELAIIFYEVGQRYINVGKIKKGKLFQAKALKIYPDLKKGFEDIKLA  
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f707.nt

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 CCATAAATTGA

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 AATATATTGCTCAAAGAGAGAGAAGCAAAAATCAAGATAAAATTATTAAGTTTCAATTTGAAAGTTTGCAAGAGC  
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 AATTGGTTTTTGTCTTCCATAAATTGA

f709.aa

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 YVEEALMEWRNLKDQGYKVPYLRHLISTIEQRRGIFSNYELNFKLVKVASLDNSIYKRPHGYQITSLRADKYGGY  
 YAA NFVGNELIYFDVNNNVNALVKDGSYLLKSPYDVIEANNLLYVTLYSSDEIGVYDKVLGVKRKSGNKGTKDGE  
 LLAPQYMAIDKRNIIYVSEWGNKRVSKFLEGDFILHFGSRTSGYKGLLGPTGVTYLNENIYVADSLRNTIEVFDT



TABLE 1. Nucleotide and Amino Acid Sequences

SGNHLYSVFTSIEGIEGLSSDFVGNNVIVSSKDGVIKYSIAKKTITKILKADKMNSKISSSILDANNQMIVSDFNN  
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INIAVVFVKSSYMKKYDQIVGLNALMELSKNKNFSFINATSVPIIDNIESLTNSIRNTSSLGPYSTDAVKTDVS  
LKLAGSGLMSKSSRRVAVVYFSGGILNRKAFKEYSLDITVSYYKNNDIRFYLLILFGNDPINSKLQYLVNETGGAVIP  
FSSYEGVSKVYDLILEQKTGTLYLEYYYPGPQEPNKYFNLSVEANINQQTGRGEFAYFIN

t709.aa

QGIVTNKDAQEEFKWALNSYNGIYDDALLSFKKILSFDPNNDYHFWTGNVYYRLGYVEEALMEWRNLKDQGYKV  
PYLRHLISTIEQRRGIFSNYELNFKKLVKVASLDNSIYKRPHGYQITSLRADKYGGYYAANFVGNEILYFDVNNNV  
NALVKDGFSYLKSYPDVI EANNLLYVTLYSSDEIGVYDKVLGVKRKKSIGNKGTGDGELLAPQYMAIDKRNYIYVSE  
WGNKRVSKFGLGDFILHFGSRTSGYKGLLGPTGVTYLNIENIYVADSLRNTIEVFDTSGNHLYSVFTSIEGIEGLS  
SDFVGNNVIVSSKDGVIKYSIAKKTITKILKADKMNSKISSSILDANNQMIVSDFNNAKVSVYKSDASLYDSLNV  
VRRIRLGGPKIYVELNVSSKSGLPVVGKSENFSISNENYIYVNPKVAYNVNASKDINIAVVFVKSSYMKKYDQ  
QIVGLNALMELSKNKNFSFINATSVPIIDNIESLTNSIRNTSSLGPYSTDAVKTDVSLKLAGSGLMSKSSRRVAV  
FSGGILNRKAFKEYSLDITVSYYKNNDIRFYLLILFGNDPINSKLQYLVNETGGAVIPFSSYEGVSKVYDLILEQKT  
GTLYLEYYYPGPQEPNKYFNLSVEANINQQTGRGEFAYFIN

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TAAAAAATTTTAAGCTTTGATCCTAATAATCTTGATTATCATTTTTTGGACTGGCAATGTTTATTATAGACTGGGT  
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CCCTATCTTAGACATTTGATTTCTACTATTGAGCAAAGGAGAGGTATTTTTCAAATATGAACCTAATTTTAAAA  
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TGATAAGTACGGCGGATATTACGCTGCTAACTTTGTAGGCAATGAAATATTGTATTTTGATGTTAATAACAATGTT

TABLE 1. Nucleotide and Amino Acid Sequences

AATGCTTTAGTTAAAGATGGCTTTAGTTATTTAAATCACCTTATGATGTTATTGAAGCTAATAATCTGCTTTATG  
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TTACAAAAATTTTAAAAGCAGATAAAATGAATTCTAAAATTTCTTCATCTATTTTGGATGCCAATAATCAGATGAT  
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TTGTTGGGCTTAAAAGTGAAATTTTCAATTTCAAATGAAAATTATTACATTGTCAATCCCAAGGTGGCATATAA  
TGTAATGCTTCAAAAGACATTAATATAGCAGTTGTTTTTGATAAACTTCTTATATGAAAAAATATGATACAGAT  
CAATTTGTAGGGTTAAATGCCCTAATGGAGTTGTCAAAAAATAAAAACTTTAGTTTTATAAATGCAACAAGTGTGC  
CCATTATAGATAATATTGAAAGCTTAACAAATAGCATTAGAAATACAAGTTCTCTTGGTCTTATAGTACAGATGC  
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f730.aa

MIKSILDYLLTLHPVLLGLLGSTFTWFTTAFGAAVFFFRKVDNKIMDAMLGFSAGIMIAASFFSLIQPAIERAE  
LGYITWVPAVFGFLVGAFIYIVDVFPDLDKLTFIDEDLTKHGKKDFLLFTAVTLHNFPEGLAVGVAFGALASNP  
DIQTLVGAMLLTLGIGIQNIPEGAAISLPLRRGNVALAKCFNYGQMSGLVEIVGGLMGAYAVYSFTRILPFALAFS  
AGAMIYVSIEQLIPEAKRKDIDNKVPSIFGVIGFTLMMFLDVSLGZ

t730.aa

AVFFFRKVDNKIMDAMLGFSAGIMIAASFFSLIQPAIERAEELGYITWVPAVFGFLVGAFIYIVDVFPDLDKLT  
FIDEDLTKHGKKDFLLFTAVTLHNFPEGLAVGVAFGALASNPDIQTLVGAMLLTLGIGIQNIPEGAAISLPLRRGN  
VALAKCFNYGQMSGLVEIVGGLMGAYAVYSFTRILPFALAFSAGAMIYVSIEQLIPEAKRKDIDNKVPSIFGVIGF  
TLMMFLDVSLGZ

f730.nt

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GGTTTACTACAGCTTTTGGAGCAGCAGCAGTTTTTTCTTTAGAAAAGGTAGATAATAAAATAATGGACGCTATGCT  
TGGTTTTTTCAGCTGGCATTATGATAGCGGCCAGTTTTTTTTTCGCTTATTCAGCCTGCTATAGAAAGAGCTGAAGAG  
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GCAGGAGCTATGATTTATGTGTCAATTGAACAATTAATACCTGAAGCTAAGAGAAAAGACATTGACAATAAAGTGC  
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t730.nt

GCAGTTTTTTCTTTAGAAAGGTAGATAATAAAATAATGGACGCTATGCTTGGTTTTTTCAGCTGGCATTATGATAG  
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TGTTTTTGGATTTCTTGTGGGGCATTTTTTATATATATTGTAGATGTATTTGTTCCAGATCTGGATAAACTTACT  
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TABLE 1. Nucleotide and Amino Acid Sequences

GCTTCTTACGCTTGGTATTGGTATTCAAAATATTCCCGAAGGAGCAGCTATTTCTCTGCCTTTAAGAAGAGGTAAT  
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MLLKLKRYFVGFLLLFLIFILLFSTIFNFVLCGYLEDYYKQLTRAQVRRAAFSLQSFOLDLHVIINGAASNLALE  
 TISEFAMSENRGKDFSESELIDLRKNPKFVIDSVKVSKKYRQYLYNFMANLKNNDTLFEFAFFDFEGRVIVSTRHE  
 NNMDFGHSEANTNYFKKAVEDYRQNQLKFIGWYNSLSEGISA EVAIRSKQSEKKAFIIVPVYSPEDKLVCGYLAG  
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 LLALNAAIEAARAGDEGKGFVAVASEIRKLADLSKISALEIGELVEDNSKVATEAGVIFKEMPLPEI EETANLVKKI  
 SEGSSKQSDQIAQFKMALDQVGEVVQSSASSSEQLSSMSDKMLEKSKELRKS VLF FKKIKDSKIENPENDDYDFRLI  
 DCPENSFKDENQNLKSNGIS TSNASGHNNYSLDIESESSVRTINKRVDPKKAID IADKDLNFDDDFSEF

t197.aa

VLCGYLEDYYKQLTRAQVRRAAFSLQSFOLDLHVIINGAASNLALETISEFAMSENRGKDFSESELIDLRKNPKFV  
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 GWYNSLSEGISA EVAIRSKQSEKKAFIIVPVYSPEDKLVCGYLAGYLLNDIVADSFDRFRFGFYKRGNFIVDPN  
 NIAVNPFEYNETSRVSSKFLNVLKDVFSPFPSPNIASEVSVYTI DRILLSEMGEDCYAMLPIS SKLGEKSGVL  
 IARLPYKDIYGVISSLRFYIILYSVLGIIALSIVLSIRIDRIISFRLNAIRVLVQDMVKGNLKDQYALDDDDENTLD  
 ELGMLS LQVVKMKKAI SVAISSVLRNISYVNKASLEVASSSQNLSSSALQQASALEEMSANVEQIASGVNMSANN  
 SYETE QIALKTNENSQIGGRAVEESVIAMQDIVEKVS VIEE IARKTNLLALNAAIEAARAGDEGKGFVAVASEIRKL  
 ADLSKISALEIGELVEDNSKVATEAGVIFKEMPLPEI EETANLVKKI SEGSSKQSDQIAQFKMALDQVGEVVQSSAS  
 SSEQLSSMSDKMLEKSKELRKS VLF FKKIKDSKIENPENDDYDFRLIDCPENSFKDENQNLKSNGIS TSNASGHNNY  
 SLDIESESSVRTINKRVDPKKAID IADKDLNFDDDFSEF

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 TGAAGAATCTGTTATTGCTATGCAAGACATTGTGGAGAAAGTTAGTGTTATTGAAGAGATAGCTAGAAAAACCAAT  
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TABLE 1. Nucleotide and Amino Acid Sequences

AGATTAGAAAGTTGGCTGATTTGAGTAAAATTTCTGCTCTTGAGATTGGAGAGTTAGTTGAAGATAACTCTAAGGT  
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GATTGTCTTGAAAATTTCTTTTAAAGATGAAAATCAAAAATTTGAAAAGCAATGGAATTTCTACTTCAAATGCCAGTG  
GGCATAATAATTATTTCTTTAGATATTGAGAGCGAATCTTCTGTAAGAACTATTAATAAGCGAGTTGATCCTAAAAA  
AGCTATCGATATTGCTGATAAGGATTTAAATTTTGATGATGATTTTTCAGAGTTTTAG

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ATGTTTTCTCTAAGCCCCCTTTTCCATCAAACATTGCCAGTGAAAGTGTGCGTTTACACTATTGATAGAATACTTTT  
GTCCGAAATGGGAGAAGATTGTTATTATGCAATGTTGCCCATAAAGTAGTAAATTTGGGAGAAAAGAGTGGAGTACTT  
ATTGCTAGGCTTCCTTATAAGGATATTTACGGAGTAATATCTAGTCTAAGATTTTCAGTATATTTTATATTCAGTCT  
TAGGCATTATAGCATTAAAGTATTGTTCTTTCAATTAGAATAGACAGGATTATTAGTTTTCGTTTAAACGCAATTAG  
AGTTCTAGTTCAAGATATGGTTAAGGGCAATTTAGATAAAGATTATGCTCTTGATGATGATGAAAATACTCTTGAT  
GAACTTGGCATGTTAAGTCTTCAGGTTGTTAAATGAAAAAAGCTATTTCTGTAGCAATTTCTAGTGTGTTTGAGAA  
ATATTAGCTGTGTAAATAAGGCAAGTTTGAAGTTGCCAGTTCAAGTCAAAATTTAAGCTCTAGTGCATTAATGAACA  
GGCATTCTGCTCTTGAAGAAATGTCAGCTAATGTTGAGCAAAATAGCCCTCAGGTGTCACATGAGCGCAATAATCTCT  
TATGAAACAGAAACAAATAGCTTTAAAGACGAATGAAAATTTCTCAGATAGGTGGTAGGGCCGTTGAAGAATCTGTTA  
TTGCTATGCAAGACATTGTGGAGAAAAGTTAGTGTTATTGAAGAGATAGCTAGAAAAACCAATTTACTTGCTTTGAA  
TGCGGCTATTGAAGCTGCAAGAGCAGGAGATGAGGGAAAGGGATTGCTGTTGTGGCCAGTGAGATTAGAAAGTTG  
GCTGATTTGAGTAAAATTTCTGCTCTTGAGATTGGAGAGTTAGTTGAAGATAACTCTAAGGTAGCAACTGAAGCGG  
GAGTGATCTTTAAAGAAATGCTACCCGAAATTGAAGAAACGGCTAATCTTGTTAAGAAGATTTTCAAGAGGTAGCTC  
TAAGCAAAGCGATCAGATTGCTCAATTTAAAATGGCTTTAGATCAGGTTGGAGAAGTTGTTCAATCTTCAGCTTCA  
AGCAGTGAGCAGCTTTCTAGTATGTCCGATAAAATGTTAGAAAAGTCTAAGGAACTTAGAAAATCTGTATTATTTT  
TCAAAATTAAAGATTCTAAAATTGAAAATCCAGAAAATGATGATTATGATTTTCAGGTTAATAGATTGTCCTGAAAA  
TTCTTTTAAAGATGAAAATCAAAAATTTGAAAAGCAATGGAATTTCTACTTCAAATGCCAGTGGGCATAATAATTAT  
TCTTTAGATATTGAGAGCGAATCTTCTGTAAGAACTATTAATAAGCGAGTTGATCCTAAAAAAGCTATCGATATTG  
CTGATAAGGATTTAAATTTTGATGATGATTTTTCAGAGTTTTAG

f200.aa

MTISKNVFSKFLKFLNSSAFVSFALFVGLVFLVLMGLGHSPFRMYFIILEIIFSSPKHLGYVLSYSAPLIFT  
GLSIGISLKAGLFNIGVEGQFILGSIVALIASVLLDLPPILVITIFITFLASGSLGILIGYLKAKFNISEVISG  
IMFNWILFHLNNIILDFSFIKRDNDSFSKPIKESAYIDFLASWKLSPEGLAYRSSHPFVNELLKAPLHFGIILGII  
FAILIWFLLNKTIIGFKINATGSNIEASRCMGINVKAVLIFSMFLSAAVAGLAGAIQLMGVKNKAIKLSYMQGIGF  
NGIAASLMGNNSPIGIIIFSSILFSILLYGSSRVQSLMGLPSSIVSLMMGIIVLVISASYFLNKIVLKGVRVKYNN  
ILD

t200.aa

LVMGLGHSPFRMYFIILEIIFSSPKHLGYVLSYSAPLIFTGLSIGISLKAGLFNIGVEGQFILGSIVALIASVLL  
DLPPILVITIFITFLASGSLGILIGYLKAKFNISEVISGIMFNWILFHLNNIILDFSFIKRDNDSFSKPIKESA  
YIDFLASWKLSPEGLAYRSSHPFVNELLKAPLHFGIILGIIFAILIWFLLNKTIIGFKINATGSNIEASRCMGINV

TABLE 1. Nucleotide and Amino Acid Sequences

KAVLIFSMFLSAAVAGLAGAIQLMGVNKAIFKLSYMQIGIFNGIAASLMGNNSPIGIIFFSSILFSILLYGSSRVQS  
LMGLPSSIVSLMMGIIIVLVISASYFLNKIVLKGVKRVKYNIL

f200.nt

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CTCTATTTGTTGGATTTTAAATTGTTGGGCTAGTGGTGTATGGGGCTTGGTCATTCTCCTTTTAGAATGTATTTTAT  
AATATTAGAAATTTATTTTCTCTCCCAAACATTTAGGTTATGTTTAAAGTTATTCAGCTCCTTTGATTTTACA  
GGTCTTTCATTGGTATTTCTTTAAAGCGGGTCTTTTAAATATTGGGGTTGAAGGCCAGTTTATACTAGGATCTA  
TTGTTGCTTTAATAGCATCAGTTTACTTGATTTGCCTCCAATTTTACATGTAATTACTATTTTATTATTACTTT  
TTTAGCTTCAGGCAGTTTAGGAATTTTAAATCGGATATTTAAAGCCAAATTCATATTAGCGAAGTGATTTACAGGA  
ATAATGTTTAAATTGGATATTATTTCAATTTAAATAATATAATTTTAGATTTTAGTTTATTAAAGAGATAATAGTG  
ATTTTTCAAAACCCATTAAAGAAAGCGCATATATTGATTTTTTAGCTTCTTGAAGCTCTCACCAGAAGGTCTTGC  
TTATAGATCTTCTCATCCTTTTGTTAATGAGCTTTTAAAGCACCTCTTCATTTTGAATAATTTTAGGTATAAAT  
TTTGCTATTTTAAATATGGTTTTTACTTAATAAACTATTATTGGATTAAATAAATGCCACAGGAAGTAATATTG  
AAGCTTCAAGATGTATGGGTATTAATGTAAAGCTGTGCTAATTTTCAATGTTTCTCTCAGCAGCTGTTGCAGG  
TCTTGCTGGTGCTATTCAACTTATGGGTGTTAATAAAGCTATATTTAAGCTTCTTATATGCAAGGAATTGGTTTT  
AATGGGATAGCTGCTTCTCTTATGGGAAACAATTCGCCAATGGCATAATATTTCTAGCATTCTTTTTCTATAT  
TGCTTTATGGAAGCAGTAGAGTTCAAAGTTTAAATGGGCCCTCCATCTTCAATTGTATCTTTGATGATGGGAATAAT  
TGTTCTTGTAATTTCTGCTAGCTATTTTTTAAATAAAATGTTTTTAAAGGTGTTAAGCGTGTCAAATATAATAAT  
ATTCTTGATTAG

t200.nt

GGGCTAGTGGTGTATGGGGCTTGGTCATTCTCCTTTTAGAATGTATTTTATAATATTAGAAATTTATTTTCTCTC  
CCAAACATTTAGGTTATGTTTTAAGTTATTCAGCTCCTTTGATTTTACAGGTCTTCTATTGGTATTTCTTTAAA  
AGCGGGTCTTTTAAATATTGGGGTTGAAGGCCAGTTTATACTAGGATCTATTGTTGCTTTAATAGCATCAGTTTAA  
CTTGATTTGCCTCCAATTTACATGTAATTACTATTTTATTATTACTTTTATTTAGCTTCAGGCAGTTTAGGAATTT  
TAATCGGATATTTAAAGCCAAATTCATATTAGCGAAGTGATTTTACAGGAATAATGTTTAAATTGGATATTATTTCA  
TTTAAATAATATAATTTTAGATTTTAGTTTTATTAAAGAGATAATAGTGATTTTCAAACCCATTAAAGAAAGC  
GCATATATTGATTTTTTAGCTTCTTGAAGCTCTCACCAGAAGGTCTTGCTTATAGATCTTCTCATCCTTTTGTTA  
ATGAGCTTTTAAAGCACCTCTTCATTTTGAATAATTTTAGGTATAATTTTGTCTATTTTAAATATGGTTTTTACT  
TAATAAACTATTATTGGATTTAAATAAATGCCACAGGAAGTAATATTGAAGCTTCAAGATGTATGGGTATTAAT  
GTAAAGCTGTGCTAATTTTTTCAATGTTTCTCTCAGCAGCTGTTGCAGGTCTTGCTGGTGCTATTCAACTTATGG  
GTGTTAATAAAGCTATATTTAAGCTTCTTATATGCAAGGAATTGGTTTTAATGGGATAGCTGCTTCTCTTATGGG  
AAACAATTCGCCAATTTGGCATAATATTTTCTAGCATTCTTTTTCTATATTGCTTTATGGAAGCAGTAGAGTTCAA  
AGTTTAAATGGGCCCTCCATCTTCAATTGTATCTTTGATGATGGGAATAATGTTCTTGTAATTTCTGCTAGCTATT  
TTTTAAATAAAATGTTTTTAAAGGTGTTAAGCGTGTCAAATATAATAATATTCTTGATTAG

f208.aa

MVKKFSIFLKAIIFSIFELLIEELSIILFLPYKIRFALIFLGFLFDITIFIFIFLYKITKAYLSQRLEIYVRNNLF  
FDIIHCLIPAFYSSYQLKNIIVAHETILNPIMLSLFLKRLRLRLRFNDLIIIEIYNSKEKNLILIAFARTFSMSL  
LIPFTFFIISSSKIVNSIPEKQEFNIKNISIINEKAYIKEKYPFILIIEKDDIIYSKSDEIFVYSPSEYRVI  
EMEKTKFYIDKYLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFLNPIILMTKILQDPLEYRKIQIPFTLSEE  
KVYELAKSFNNLLKEKLSKRKSKIPIEIEKVKKIINKNQEI

t208.aa

IIIFSIFELLIEELSIILFLPYKIRFALIFLGFLFDITIFIFIFLYKITKAYLSQRLEIYVRNNLFFDIIHCLIPLA  
FYSSYQLKNIIVAHETILNPIMLSLFLKRLRLRLRFNDLIIIEIYNSKEKNLILIAFARTFSMSLLIPFTFFIIIS  
SSKIVNSIPEKQEFNIKNISIINEKAYIKEKYPFILIIEKDDIIYSKSDEIFVYSPSEYRVIEMEKTKFYIDK  
YLQRKSDSILGIFLFTLFASFTIFLMNFYKFFKASFLNPIILMTKILQDPLEYRKIQIPFTLSEEKVYELAKSFNN  
LLLKEKLSKRKSKIPIEIEKVKKIINKNQEI

f208.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGGTAAAAAATTTTCAATTTTCTTAAAAGCAATAATAATTTTTTCAATATTTGAACTTTTAATCGAAGAACTCT  
CAATAATTCTTTTTTTTACCATACAAAATACGATTTGCACATAATATTTCTTGGGTTTCTATTTGACACAATTTTTAT  
TTTCATTTTTTTTATACAAAATAACCAAGGCCTACCTTTCCCAAAGATTAGAAATCTACGTCAGAAACAATCTATTCT  
TTTCGATATAATCCACTGCCTTATTCCTTTAGCGTTTTATAGCTCATATCAGCTTAAAAACATAATTGTCGCCCATG  
AAACAATATTAAATCCAATAATGCTATCACTTTTCAAGTTAAGATTTTTTAAGACTTCTTAGGTTTAATGACCTAAT  
AATAGAAATATATTACAATTCAAAAGAAAAGAACCTAATACTAATAGCATTGCTAGGACATTTTCAATGAGCTTA  
TTAATACCATTTACATTTTTTTATAATAATATCAAGCTCAAAAATTGTAAATTCATACCAGAAAAACAAGAATTTA  
ATATCATTTAAAAATATATCAATAATAAATGAAAAAGCTTACATTAAAGAAAAATATCCCTTCATCTTAATAATCAA  
GGAAAAAGATGACATAATATACTCAAAATCAGACGAAATATTTGTTTACTACAGTCCCAGTGAATATAGAGTAATA  
GAAATGGAGAAAAACAAAATTTTATATAGATAAATATTTGCAAAGAAAAAGCGATTCTATTCTTGGAATTTTTCTAT  
TTACATTGTTTGCATCATTTACTATTTTTTAATGAATTTTTATAAATTTTTTAAAGCAAGCTTTTTAAATCCTAT  
TATTTTAATGACAAAAATTTTACAAGACCCATTAGAATATCGAAAAATTCAAATTCCTTTTACTTTAAGCGAAGAA  
AAAGTATATGAAGTTGCAAAATCATTTAACAATCTCTTGCTAAAAGAAAACTAAACTCAAAGCGAAAAAGCAAAA  
TACCTTTAGAAATTGAAAAAGTAAAAAAAATAATTAATAAAAACCAGGAAATAAAATGA

t208.nt

ATAATAATTTTTTCAATATTTGAACTTTTAATCGAAGAACTCTCAATAATTCTTTTTTTACCATACAAAATACGAT  
TTGCACATAATATTTCTTGGGTTTCTATTTGACACAATTTTTATTTTCATTTTTTTTATACAAAATAACCAAGGCCTA  
CCTTTCCCAAAGATTAGAAATCTACGTCAGAAACAATCTATTCTTCGATATAATCCACTGCCTTATTCCTTTAGCG  
TTTTATAGCTCATATCAGCTTAAAAACATAATTGTCGCCCATGAAACAATATTAAATCCAATAATGCTATCACTTT  
TCAAGTTAAGATTTTTTAAGACTTCTTAGGTTTAATGACCTAATAATAGAAATATATTACAATTCAAAAGAAAAGAA  
CCTAATACTAATAGCATTGCTAGGACATTTTCAATGAGCTTATTAATACCATTTACATTTTTTTATAATAATATCA  
AGCTCAAAAATTGTAAATTCATACCAGAAAAACAAGAATTTAATATCATTTAAAAATATATCAATAATAAATGAAA  
AAGCTTACATTAAAGAAAAATATCCCTTCATCTTAATAATCAAGAAAAAGATGACATAATATACTCAAAATCAGA  
CGAAATATTTGTTTACTACAGTCCCAGTGAATATAGAGTAATAGAAATGGAGAAAAACAAAATTTTATATAGATAAA  
TATTTGCAAAGAAAAAGCGATTCTATTCTTGGAATTTTTTACATTGTTTGCATCATTTACTATTTTTTTAA  
TGAATTTTTTATAAATTTTTTAAAGCAAGCTTTTTAAATCCTATTATTTTAAATGACAAAAAATTTACAAGACCCATT  
AGAATATCGAAAAATTCAAATTCCTTTTACTTTAAGCGAAGAAAAAGTATATGAAGTTGCAAAATCATTTAACAAT  
CTCTTGCTAAAAGAAAACTAAACTCAAAGCGAAAAAGCAAAATACCTTTAGAAATTGAAAAAGTAAAAAAAATAA  
TTAATAAAAACCAGGAAATAAAATGA

f210.aa

MKIQIIIMLLALLDFPLNARLLDISIEKRADEEIKKYSSYNLILEKEYYTNFPTSEIEKNIYKLTEHFVKSIMLNK  
TNYSLNSNYKEANKYLIQSELIDKKFLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNIT  
YFLKNLDKISNEMIFFPREKREVNMIQKTTIAADSSSKPRGINYDTGIPFNVLIVDSDSVFTVKQLTQIFTSEGFNI  
IDTAADGEEAVIKYKNHYPNIDIVTLTDITMPKMDGITCLSNIMEFDKNARVIMISALGKEQLVKDCLIKGAKTFIV  
KPLDRAKVLQVRMSVFK

t210.aa

RLDISIEKRADEEIKKYSSYNLILEKEYYTNFPTSEIEKNIYKLTEHFVKSIMLNKNTNYSLNSNYKEANKYLIQ  
SELIDKKFLKYKIFKIKNINGIFKSHSLIYTKKGFYKLELYIENNAEPLKIFNLNITYFLKNLDKISNEMIFFPRE  
KREVNMIQKTTIAADSSSKPRGINYDTGIPFNVLIVDSDSVFTVKQLTQIFTSEGFNIIDTAADGEEAVIKYKNHYP  
NIDIVTLTDITMPKMDGITCLSNIMEFDKNARVIMISALGKEQLVKDCLIKGAKTFIVKPLDRAKVLQVRMSVFK

f210.nt

ATGAAATTCAAATAATTATAATGCTGCTTGCATTGTTAGATTTTCCACTTAATGCCAGACTTTTGGACATTTCAA  
TTGAAAAAGAGCAGATGAAGAAATAAAAAAATATTCGTCTTATAATTTAATTTTAGAAAAAGAATACTATACCAA  
TTTTCCAACAAGCGAAATAGAAAAAATATTTATAAACTAACAGAACATTTTGTAAGAAAGCATAATGCTCAATAAA  
ACTAAGTACAGCTTATTAAATTCAACTACAAAGAAAGCAAAATAAATATCTAATTCAAAGCGAACTCATTTGATAAAA  
AATTTTTTAAATATAAAATATTTAAATCAAAAAATATAAATGGAATTTTTTAAAGCCATTCACTAATATATACAAA

TABLE 1. Nucleotide and Amino Acid Sequences

AAAAGGATTTTACAAATTAGAACTTTACATAGAAAATAATGCAGAACCTCTAAAAATATTTAACCTTAACATTACT  
TATTTTTTAAAGAATTTAGATAAAATAAGTAATGAAATGATTTTTTTTCCCAAGGGAATGA

t210.nt

AGACTTTTGGACATTTCAATTGAAAAAAGAGCAGATGAAGAAATAAAAAATATTCGTCTTATAATTTAATTTTAG  
AAAAAGAATACTATACCAATTTTCCAACAAGCGAAATAGAAAAAATATTTATAAACTAACAGAACATTTTGTA  
AAGCATAATGCTCAATAAACTAACTACAGCTTATTAAATTCAAACACAAAGAAGCAAATAAATATCTAATTCAA  
AGCGAACTCATTGATAAAAAATTTTAAAAATATAAAATATTTAAATCAAAAAATATAAATGGAATTTTAAAAAGCC  
ATTCACATAATATATACAAAAAAGGATTTTACAAATTAGAACTTTACATAGAAAATAATGCAGAACCTCTAAAAAT  
ATTTAACCTTAACATTACTTATTTTTTAAAGAATTTAGATAAAATAAGTAATGAAATGATTTTTTTTCCCAAGGGA  
TGA

f22.aa

MLKTLTKIITISCLIVGCASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSY  
KKENNDFAALLIMGNFPKIDIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKIDITAKDNMLTT  
KYIGEIEKNEMFFWIQDPTLLPNQIVSSKNLIPFSSGTLINSNLNQEYIFKSLIKTNNPPILKILSKKLIPTVL  
TNMTNLTISSHIKTTIKDQNTVEIEFNIQKSSVESLIEKLASNIQT

t22.aa

PYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNSLSPKYKSVLGLISNLYFSYKKENNDFAALLIMGNFPKIDIFW  
GIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKIDITAKDNMLTTKYIGEIEKNEMFFWIQDPTLL  
LPNQIVSSKNLIPFSSGTLINSNLNQEYIFKSLIKTNNPPILKILSKKLIPTVLTNMTNLTISSHIKTTIKDQNT  
VEIEFNIQKSSVESLIEKLASNIQT

f22.nt

ATGTTAAAAACATTAACAAAAATAATTACCATTTTCATGCCTCATAGTGGGATGCGCAAGCCTGCCTTACACTCCTC  
CAAAACAAAATCTAAATTACTTAATGGAACCTTTTACCTGGCGCAAATTTATACGCCCATGTAAATTTAATTA  
CAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCTTATAAGCAATTTATACTTTAGCTAT  
AAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAGATATTTTCTGGGGAATTCATA  
ATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAACTTAAAAATTCAAATATATACATTAT  
TCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGCAAAGACAATAATATGCTAACACA  
AAATATATTGGGGAAATAGAAAAAATGAAATGTTTTTTTGGATTCAAGATCCAACATTATTGCTCCCAACCA  
TAGTAAGCAGCAAAAATTTAATTCCTTTAGCAGTGGAACCTTTGTCTATAAACAGCTTAAATCAAGAAGATATAT  
TTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTCAAAAAAGTTAATTCCAACCGTCTTG  
ACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAATACGGTTGAAATAGAAT  
TTAATATTCAAAAATCTAGTGTGAAAGCCTTATAGAAAACTAGCTTCAAATATTCAAACCTAA

t22.nt

CCTTACACTCCTCCAAAACAAAATCTAAATTACTTAATGGAACCTTTTACCTGGCGCAAATTTATACGCCCATGTAA  
ATTTAATTA AAAACAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCTTATAAGCAATTT  
ATACTTTAGCTATAAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAGATATTTTCTGG  
GGAATTCATAAAAAATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAACTTAAAAATTCAA  
ATATATACATTATTCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGCAAAGACAATAA  
TATGCTAACACA AAAATATATTGGGGAAATAGAAAAAATGAAATGTTTTTTTGGATTCAAGATCCAACATTATTG  
CTCCCAACCAATAGTAAGCAGCAAAAATTTAATTCCTTTAGCAGTGGAACCTTTGTCTATAAACAGCTTAAATC  
AAGAAGAATATATTTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTCAAAAAAGTTAAT  
TCCAACCGTCTTGACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAATACG  
GTTGAAATAGAATTTAATATTCAAAAATCTAGTGTGAAAGCCTTATAGAAAACTAGCTTCAAATATTCAAACCT  
AA

f221.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MGITVFYLF SIFAS FVLGSSMDSVKENVLKSTIFYDVEEVEFPYARKQTLQFIAKTHLKYAVFNFDKNKMF SYTF  
VFDKKLISQYAIFIEVKKKFGEATLVTPNLNLWDLGDSIIVLNKNILRITLKSYSINYNK

t221.aa

SMSDVKENVLKSTIFYDVEEVEFPYARKQTLQFIAKTHLKYAVFNFDKNKMF SYTFVFDKKLISQYAIFIEVKKK  
FGEATLVTPNLNLWDLGDSIIVLNKNILRITLKSYSINYNK

f221.nt

ATGGGTATTACAGTTTTTTATTTATTTTCTATTTTTGCATCTTTTGTTCTGGGTCTAGCATGGATTCTGTAAAG  
AGAATGTTCTCAAGAGCACTATTTTTATTATGATGTTGAAGAAGTTGAATTCCTTATGCTAGGAAGCAGACTTT  
ACAATTTATTGCTAAAACCCATTTAAATATGCTGTTTTTAATTTTGACAAAAATAAAATGTTTTCTGACACTTTT  
GTTTTTGATAAAAAATTAATATCTCAGTATGCAATTTTTATTGAGGTAAAGAAAAAGTTGGCGAGGCTACACTAG  
TAACGCCTTTGAATTATTTATGGGATCTTGGTGATTCTATTATTGTTTTAAATAAAAAATTTTTAAGAATTACTTT  
AAAATCTTATATTTCAAATTATAATAAATGA

t221.nt

AGCATGGATTCTGTAAAGAGAATGTTCTCAAGAGCACTATTTTTTATTATGATGTTGAAGAAGTTGAATTCCTT  
ATGCTAGGAAGCAGACTTTACAATTTATTGCTAAAACCCATTTAAATATGCTGTTTTTAATTTTGACAAAAATAA  
AATGTTTTCTGACACTTTTGTTTTTGATAAAAAATTAATATCTCAGTATGCAATTTTTATTGAGGTAAAGAAAAAG  
TTTGGCGAGGCTACACTAGTAACGCCTTTGAATTATTTATGGGATCTTGGTGATTCTATTATTGTTTTAAATAAAA  
ATATTTAAGAATTACTTTAAATCTTATATTTCAAATTATAATAAATGA

f253.aa

MYMENIEVRGQPNFFGLIPFFVFIIYLG TGIYLG VIGVEMAFYQLPASVAMFFASIVCFLVFKGKPSDKIHIFIK  
GAAQYDIILMCLIFMLSGAFSSLCKEIGCVETVANLGIKYINPNWIVSGIFFVTCFLSFSAGTSVGSIVAIPIAF  
NIAVKSGINPNLIAASVMCGAMFGDNL SLISDTTIVSSRTQGSSILDVFISSSFYAFPSAILTFFSFFLSENLSN  
ATNFLHESSIDLKTVPYLMIIFSLAGMNVFIVLFLGILSICLISVLYGNLYFLDVMKNINKGFLNMADLIFLSI  
LTGGVSFAVIHNGGFKWLLIKLSLIRGKSSAEFSIGAFVSIVDVFLANNTIAILICGKVAKKIAFENNISVQRSA  
SILDMFSCIFQGIIPYGAQMIILVNFSNGLVSPISILPFLVYFGFLLFFVILSILGLDIKKVFLFLLKK

t253.aa

LVFKGKPSDKIHIFIKGAAQYDIILMCLIFMLSGAFSSLCKEIGCVETVANLGIKYINPNWIVSGIFFVTCFLSFS  
AGTSVGSIVAIPIAFNIAVKSGINPNLIAASVMCGAMFGDNL SLISDTTIVSSRTQGSSILDVFISSSFYAFPSA  
ILTFFSFFLSENLSNATNFLHESSIDLKTVPYLMIIFSLAGMNVFIVLFLGILSICLISVLYGNLYFLDVMKN  
INKGFLNMADLIFLSILTGGVSFAVIHNGGFKWLLIKLSLIRGKSSAEFSIGAFVSIVDVFLANNTIAILICGKV  
AKKIAFENNISVQRSASILDMFSCIFQGIIPYGAQMIILVNFSNGLVSPISILPFLVYFGFLLFFVILSILGLDIK  
KVFLFLLKK

f253.nt

ATGTATATGGAAAATATTGAAGTAAGAGGGCAGCCAAATTTTTTTGGGCTTATTCCTTTTTTTGTTTTTATTATTA  
TCTATTTAGGCACGGGATTTATTTGGGAGTTATTGGTGTAGAAATGGCCTTTTATCAACTGCCGGCTAGTGTTC  
AATGTTTTTTGCTTCCATTGTTTGTTTTTTGGTATTTAAAGGAAAATTTCCGACAAAATTCACATATTTATTA  
GGAGCAGCTCAGTACGATATTATACTAATGTGTCTTATTTTTATGCTTTCGGGAGCTTCTCTCTCTTTGTAAAG  
AAATAGGCTGCGTTGAAACTGTAGCAAATTTGGGAATTAAATATATTAATCCTAATTGGATTGTTTCTGGTATATT  
TTTTGTAACCTGCTTTCTTTCTTTTTCTGCCGGCACTTCTGTTGGATCTATCGTTGCAATTGCTCCTATTGCTTTT  
AATATTGCTGTTAAAGCGGCATTAATCCGAATTTAATAGCAGCATCTGTAATGTGTGGAGCTATGTTTGGAGATA  
ATCTTTCTTTAATATCAGATACAAC TATTGTTTCTAGTCGAACTCAAGGTAGTAGCATCTTAGATGTTTTTATTAG  
TAGCAGTTTTTTATGCTTTTCCATCCGCATACTAACTTTTTTTCTTTTTCTTTCTTTCTGAAAATTTGTCCAAT  
GCCACAACTTTTTACACGAAAGTTCAATAGATTTAGTGAAAACGTGCCTTATTTAATGATTATATTTTTCTCTT



TABLE 1. Nucleotide and Amino Acid Sequences

TAGCTGGAATGAATGTTTTTATAGTTCCTTTTTTAGGTATTCTTCTATATGTCTTATTAGCGTTTTGTATGGTAA  
TTTATACTTTCTAGATGTAATGAAAAACATTAATAAAGGGTTTTTAAATATGGCGGATTGATTTTTCTTTCAATT  
TTAACAGGGGGAGTTTTCTTTTGCCGTGATTCAATGGAGGCTTTAAATGGCTACTTATTAAATTAAATCCTTGA  
TTAGAGGAAAAAGTTCAGCGGAATTTTCTATTGGGGCTTTTGTTCATAGTTGATGTTTTCTTGCTAATAACAC  
AATTGCCATACTTATTTGCGGCAAAGTAGCAAAAAAGATAGCTTTTGAAAATAACATCAGTGTTCAAAGAAGTGCT  
TCTATTTTAGATATGTTCTCTTGTATTTTTCAAGGCATTATTCCTTATGGTGCGCAAATGATTATTTTAGTGAATT  
TTTCAAATGGACTTGTGTCGCCAATTAGTATTTTGCCATTTTATTTTGGATTTTTATTGTTTTTTGTTAT  
TTTATCTATTTGGGCCTTGATATAAAAAAAGTTTTTTTATTTTTTTTAAAAAATAA

t253.nt

TTGGTATTTAAAGGAAAATTTTCCGACAAAATTCACATATTTATTAAAGGAGCAGCTCAGTACGATATTATACTAA  
TGTGTCTTATTTTATGCTTTTCGGGAGCTTCTCTTCTCTTTGTAAAGAAATAGGCTGCGTTGAAACTGTAGCAAA  
TTTGGAATTTAAATATATTAATCCTAATTGGATTGTTTCTGGTATATTTTTTGTAACTGCTTTCTTTCTTTTTCT  
GCCGGCACTTCTGTTGGATCTATCGTTGCAATTGCTCCTATTGCTTTTAAATATGCTGTTAAAGCGGCATTAATC  
CGAATTTAATAGCAGCATCTGTAATGTGTGGAGCTATGTTTGGAGATAATCTTCTTTAATATCAGATACAACAT  
TGTTTCTAGTCGAACCTCAAGGTAGTAGCATCTTAGATGTTTTTATTAGTAGCAGTTTTTATGCTTTTCCATCCGCC  
ATACTAACTTTTTTTCTTTTTTCTTTCTTTCTGAAAATTTGTCCAATGCCACAACTTTTTTACACGAAAGTTCAA  
TAGATTTAGTGAAAAGTGTGCCTTATTTAATGATTATATTTTTCTCTTAGCTGGAATGAATGTTTTTATAGTTCT  
TTTTTTAGGTATTCTTTCTATATGTCTTATTAGCGTTTTGTATGGTAATTTATACCTTTCTAGATGTAATGAAAAAC  
ATTAATAAAGGGTTTTTAAATATGGCGGATTTGATTTTTCTTTCAATTTTAAACAGGGGGAGTTTCTTTTGCCGTGA  
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TATTGGGGCTTTTGTTCATAGTTGATGTTTTTCTTGCTAATAACACAATTGCCATACTTATTTGCGGCAAAGTA  
GCAAAAAAGATAGCTTTTGAAAATAACATCAGTGTTCAAAGAAGTGCTTCTATTTTAGATATGTTCTCTTGTATTT  
TTCAAGGCATTATTCCTTATGGTGCGCAAATGATTATTTTAGTGAATTTTCAAATGGACTTGTGTCGCCAATTAG  
TATTTTGCCATTTTATGTTTATTTTGGATTTTTATTGTTTTTTGTTATTTTATCTATTTTGGGCCTTGATATAAAA  
AAAGTTTTTTTATTTTTTTTAAAAAATAA

f265.aa

MRKCFVSLSLLLIFACSSNVEIELNDDISGIVSIFVNVNREFEKIRKELLTTLVGEEIANMPLFPVDEIKKYFKN  
GEEKLGLKLLSIKTQGDSINLVVKFDNLIKILGDYMKKPDISVFKIEKKDGKNI IELNINLENATKNINENKEYIS  
DALAALLPSDEIPMSAKEYKDVLYFLSDFTSKASELIDNSKLNLVVKTSRNVQEQFGFKQINSNTLRFEMDMVKG  
LSLETPIKLRLV  
Y

t265.aa

SNVEIELNDDISGIVSIFVNVNREFEKIRKELLTTLVGEEIANMPLFPVDEIKKYFKN GEEKLGLKLLSIKTQGDS  
INLVVKFDNLIKILGDYMKKPDISVFKIEKKDGKNI IELNINLENATKNINENKEYIS DALAALLPSDEIPMSAKE  
YKDVLYFLSDFTSKASELIDNSKLNLVVKTSRNVQEQFGFKQINSNTLRFEMDMVKLSLETPIKLRLVY

f265.nt

ATGAGAAAGTGTTTTGTAGCTTGAGTTTATTGTTGATTTTTTTTTGCTTGCTAGCTCTAATGTTGAAATTGAGTTAA  
ATGATGATATTAGTGGTATTGTTTCAATATTTGTTAATGTTAATAGAGAATTGAAAAAATTAGAAAAGAAGTCTT  
AACAACTTTGGTGGGAGAAGAAATTGCAATATGCCTCTTTTTTCTGCTAGATGAAATAAAAAAATACTTTAAAAAT  
GGAGAGGAAAAAGCTTGGGCTTAAGCTTTTGAGTATTAATAACCAAGGAGATTCTATTAATTTAGTTGTTAAGTTTG  
ATAATTTAATTAATAATTTTAGGCGATTATATGAAAAACCCGATATATCTGTGTTTAAAGATAGAAAAAAGATGG  
TAAAAATATTATTGAACCTAATATTAATTTGGAACGCTACTAAGAATATTAATGAAAATAAAGAATATATTAGT  
GATGCACTTGCTGCTCTTTTGCCATCGGATGAGATCCCAATGTCTGCCAAAGAATATAAAGATGTTTTGGTTTATT  
TTTTATCGGATTTTACTTCCAAAGCAAGTGAACCTTATTGACAATTCCAAACCTAATCTTGTTAGTTAAGACTTCTAG  
AAATGTTCAAGACAATTTGGATTCAACAAATTAACCTCAACACACTGCGGTTTGAGATGGATATGGTTAAAGGA  
TTAAGTCTTGAAACACCAATAAACTTAGATTAGTTTATTGA

t265.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TCTAATGTTGAAATTGAGTTAAATGATGATATTAGTGGTATTGTTTCAATATTTGTTAATGTTAATAGAGAATTTG  
AAAAAATTAGAAAAGAAGCTCTTAACAACCTTTGGTGGGAGAAGAAATTGCAAATATGCCTCTTTTCTCTGTAGATGA  
AATAAAAAAATACCTTTAAAAATGGAGAGGAAAAGCTTGGGCTTAAGCTTTTGAGTATTAAAACCCAAGGAGATTCT  
ATTAATTTAGTTGTTAAGTTTGATAATTTAATTAAAAATTTTAGGCGATTATATGAAAAAACCCGATATATCTGTGT  
TTAAGATAGAAAAAAGATGGTAAAAATATTATTGAACTTAATATTAATTTGGAAAACGCTACTAAGAATATTAA  
TGAAAATAAAGAATATATTAGTGATGCACCTTGCTGCTCTTTTGCCATCGGATGAGATCCCAATGTCTGCCAAAGAA  
TATAAAGATGTTTGGTTTATTTTTTATCGGATTTTACTTCCAAAGCAAGTGAACCTATTGACAATTCCAAACCTTA  
ATCTTGTTAGTTAAGACTTCTAGAAATGTTCAAGAACAATTTGGATTCAAACAAATTAACCTCAAACACACTGCGGTT  
TGAGATGGATATGGTTAAAGGATTAAGTCTTGAAACACCAATAAACTTAGATTAGTTTATTGA

f269.aa

MNIRKLLFCIFFMNISFLLFAGDYKGLDFKIKFFNQSIYRVNSNVFIEVSLSNASESVLTLEIGDINSFGDFDVT  
DTTNIKVKRPIEYVKKRSKNVAIPVRNMSLRPNEKFSVVINLNQFVKFSKDGVIYFVKGIFFPDIDSPSKKKESNII  
TLFLNDGFENPGSIDLVNLSENNNDIQDILKKKKLSPDEIVKYLLKALQLGKKEKFFLYLDIEGLLLNDKGKAYLY  
KQKLSPIPNKNVVEEYKEYLWNSNNSDISKAPNKFSSIIETTSYSDTSGKVIADLYFDDGQFYISKRYTFFFKKYDYY  
WIIYDIYVQNTGIKEK

t269.aa

GDYKGLDFKIKFFNQSIYRVNSNVFIEVSLSNASESVLTLEIGDINSFGDFDVTDTTNIKVKRPIEYVKKRSKNV  
AIPVRNMSLRPNEKFSVVINLNQFVKFSKDGVIYFVKGIFFPDIDSPSKKKESNIIITLFLNDGFENPGSIDLVNLS  
ENNNDIQDILKKKKLSPDEIVKYLLKALQLGKKEKFFLYLDIEGLLLNDKGKAYLYKQKLSPIPNKNVVEEYKEYLW  
NSNNSDISKAPNKFSSIIETTSYSDTSGKVIADLYFDDGQFYISKRYTFFFKKYDYYWIIYDIYVQNTGIKEK

f269.nt

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GCCTTGATTTTAAAATCAAGTTTTTTAATCAATCTATTTATCGTGTCAATAGTAATGTTTTTATTGAAGTTTCTCT  
TAGTAATGCGTCTGAGAGTGTTTTAACTTTAGAAAATAGGCGATATTAATTCTTTTGGCTTTGATTTTGTATGTTACT  
GATACCACCAATATTAAAGTTAAAAGACCTATTGAATATGTTAAAAAGAGATCTAAAAATGTTGCAATTCCTGTTA  
GAAATATGAGCTTGAGACCTAATGAAAAATTTTCTGTAGTTATTAACCTTAAATCAATTTGTTAAGTTTAGTAAAGA  
TGGAGTTTATTTTGTAAAGGTATTTTTTCCAGACATTTTCAGATCCATCTAAGAAAAAGAATCCAATATTATT  
ACGCTTTTTTTGAATGATGGTTTTGATGAAAATCCAGGTAGCATAGACCTTGTTAATTTGTCTGAAAATAATGATA  
TTCAAGATATCTTGAAAAGAAAAAATTATCTCCCGATGAAATTGTTAAATATTTGTTAAAGGCATTGCAGCTTGG  
GAAAAAGAAAAGTTCTTTTTATATCTTGATATTGAAGGTTTGTATTAAATGACAAGGGCAAGGCATACCTTTTAT  
AAGCAAAAGTTATCACCTATTTCCCAATAAAAATGTAGTTGAAGAGTATAAAGAATATTTGTGGAATTCATAAATT  
CGGATATTTCAAAGCACCAATAAATTTTCTATTATTGAACTACTTATTCTGATACTTCTGGCAAGGTGATTGC  
TGATTTATATTTTGACGATGGGCAATTTTATATTTCCAAAAGATATACTTTCTTCTTTAAAAAATATGATTATTAT  
TGGATAATTTATGATTACATTGTTCAAAATACTGGCATTAAGGAAAAGTAA

t269.nt

GGAGATTACAAGGGCCTTGATTTTAAAATCAAGTTTTTTAATCAATCTATTTATCGTGTCAATAGTAATGTTTTTA  
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ATCCAATATTATTACGCTTTTTTTGAATGATGGTTTTGATGAAAATCCAGGTAGCATAGACCTTGTTAATTTGTCT  
GAAAATAATGATATTCAAGATATCTTGAAAAGAAAAAATTATCTCCCGATGAAATTGTTAAATATTTGTTAAAGG  
CATTGCAGCTTGGGAAAAAGAAAAGTTCTTTTTATATCTTGATATTGAAGGTTTGTATTAAATGACAAGGGCAA  
GGCATACCTTTATAAGCAAAAGTTATCACCTATTTCCCAATAAAAATGTAGTTGAAGAGTATAAAGAATATTTGTGG  
AATTCATAAATTCGGATATTTCAAAGCACCAATAAATTTTCTATTATTGAACTACTTATTCTGATACTTCTG  
GCAAGGTGATTGCTGATTTATATTTTGACGATGGGCAATTTTATATTTCCAAAAGATATACTTTCTTCTTTAAAAA  
ATATGATTATTATTGGATAATTTATGATTACATTGTTCAAAATACTGGCATTAAGGAAAAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

f29.aa

MNWLSFFYVLLFLLIFPFELQSNKENIENLIKHLMLYDLTNNLSKELETINKIKNFDLEQHYLLITKYYLKIKKY  
KEANDFLKKINQKKIKNQKIKNEIISLKLRLINEDNINEEEIKKILNNEKNIDVKIYYQIFSLIKFKNKKLANKIKN  
IILTNPYSIYSYKIKRNE

t29.aa

NNKENIENLIKHLMLYDLTNNLSKELETINKIKNFDLEQHYLLITKYYLKIKKYKEANDFLKKINQKKIKNQKIKN  
EIISLKLRLINEDNINEEEIKKILNNEKNIDVKIYYQIFSLIKFKNKKLANKIKNIILTNPYSIYSYKIKRNE

f29.nt

ATGAACTGGCTATCCTTTTTTTATGTTTTATTATTTTTATTAATTTTTTCCTTTTGAATTACAGAGTAATAATAAAG  
AAAATATAGAAAATTTAATAAAGCTACATATGCTTTTATGATTTAACCAATAACCTGTCAAAAAGAAATTAGAAACAAT  
AAATAAAATTAATAAATTTTGAAGCTAGAACACATTATCTGCTAATTACAAAATATTATCTAAAAATAAAAAATAT  
AAAGAAGCTAATGATTTTTTAAAAAAAATAAACCAAAAAAAGATCAAAAATCAAAAAATAAAAAACGAAATCATTT  
CGCTAAAATTAAGAATAAATGAAGATAATATTAATGAAGAAGAAATCAAAAAATTTTAAATAACGAAAAAATAT  
AGATGTCAAAATAATTTATCAAAATATTCAGTCTTATAAAATTTAAAAATAAAAAATTAGCAAATAAAATTAAAAAC  
ATAATACTAACAACTATCCCAAAAGCATTATTTCTTATAAAATAAAAAAGAAATGAATAA

t29.nt

AATAATAAAGAAAATATAGAAAATTTAATAAAGCTACATATGCTTTTATGATTTAACCAATAACCTGTCAAAAAGAAAT  
TAGAAACAATAAATAAATTAATAAATTTTGAAGCTAGAACACATTATCTGCTAATTACAAAATATTATCTAAAAAT  
AAAAAATATAAAGAAGCTAATGATTTTTTAAAAAAAATAAACCAAAAAAAGATCAAAAATCAAAAAATAAAAAAC  
GAAATCATTTTCGCTAAAATTAAGAATAAATGAAGATAATATTAATGAAGAAGAAATCAAAAAATTTTAAATAACG  
AAAAAATATAGATGTCAAAATAATTTATCAAAATATTCAGTCTTATAAAATTTAAAAATAAAAAATTAGCAAATAA  
AATTAAAAACATAATACTAACAACTATCCCAAAAGCATTATTTCTTATAAAATAAAAAAGAAATGAATAA

f290.aa

MNSIYVIGKLLLTFLIFFPFCYNLFAVNLAEINKLSEYAKSIVLIDFDTKRILYSKKPNLVFPPASLTAKIVTIYT  
ALIEAEKRNIKLSIVPISDSASYYNAPPNSSLMFLEKGQIVNFEEILKGLSVSSGNDSSIAIAEFVVGNLNSFVN  
LMNINVLNLGLFNMHFVEPSGYSSSENKITALDMAFFVKYSYIEKFKFLNIHSLKYFIYPKSRNLGTALSSKFLNLK  
QRNANLLIYDYPYSDGIKTGYIKESGLNLVATAKKGERRLIAVVLGVEKGINGFGEKMRSSIANKLFEYGFNKYSK  
FPLIVKLKEKVYNGTVDTVLFSKEPFYIILTKDEFDKINISYTVDKLVAPLSGDMPPVGRAMIFLENEKIGDVALF  
SGKVKRLGFWQGLYKSFINLFSREY

t290.aa

VNLAEINKLSEYAKSIVLIDFDTKRILYSKKPNLVFPPASLTAKIVTIYITALIEAEKRNIKLSIVPISDSASYNA  
PPNSSLMFLEKGQIVNFEEILKGLSVSSGNDSSIAIAEFVVGNLNSFVNLMNINVLNLGLFNMHFVEPSGYSSSENK  
ITALDMAFFVKYSYIEKFKFLNIHSLKYFIYPKSRNLGTALSSKFLNLKQRNANLLIYDYPYSDGIKTGYIKESGL  
NLVATAKKGERRLIAVVLGVEKGINGFGEKMRSSIANKLFEYGFNKYSKFPLIVKLKEKVYNGTVDTVLFSKEPF  
YIILTKDEFDKINISYTVDKLVAPLSGDMPPVGRAMIFLENEKIGDVALFSGKVKRLGFWQGLYKSFINLFSREY

f290.nt

ATGAATAGTATCTATGTTATTGGGAAATTGTTATTAACCTTTATTTTTTAATTTTTTCCCGTTTTGTTATAATCTTT  
TTGCAGTTAATTTAGCTGAGATTAATAAATTATCAGAGTATGCAAAGTCAATAGTTTAAATAGATTTTGATACTAA  
GCGAATACTTTATTCTAAGAAGCCCAATTGCTTTTTTCCCTCCAGCATCTCTTACAAAGATTGTTACAATTTATACA  
GCTTTTAATTGAAGCTGAAAAGCGAAATATAAAATTAAAAAGCATAGTTCCTATTAGCGATTCTGCTTCATATTATA  
ATGCACCCCCCAATTCTTCTTTGATGTTTTTAGAAAAAGGTCAAATTGTTAATTTTGAAGAGATTTTAAAAAGGACT

TABLE 1. Nucleotide and Amino Acid Sequences

TTCAGTTTCTTCGGGTAATGATTCTTCTATTGCAATTGCTGAGTTTGTAGTAGGCAATTTAAATAGCTTTGTAAAT  
 TTAATGAATATTAATGTTTAAATTTAGGGCTTTTTAATATGCATTTTGTGTAACCTTCTGGATATAGCAGCGAGA  
 ATAAGATTACAGCACTAGATATGGCTTTTTTTGTGAAATCTTATATAGAAAAGTTTAAATTTATGCTTAATATTCA  
 TTCTTTAAAGTATTTTATTTATCCAAAGAGTAGAAATTTAGGAAGCTGCTTTGTTCATCAAAATTTTTTAAACTTAAAA  
 CAAAGAAATGCTAATTTATTAATATATGATTACCCTTATTCAGATGGCATTAAAACGGGATATATTAAGGAATCAG  
 GCTTAAATCTTGTGCTACTGCTAAAAAGGGTGAGAGAAGATTAATAGCAGTTGTATTGGGGGTGAAAAAGGAAT  
 TAATGGATTTGGAGAGAAAAATGAGATCTTCGATTGCAAAAAATTTATTTGAATATGGATTTAATAAATATTCTAAA  
 TTTCTTTAATAGTAAAAATTAAGAAAAAGTCTATAATGGTACAGTGGATACAGTTGCTCTTTTTTCTAAAGAGC  
 CTTTTTATTATATTTTAACTAAAGATGAATTTGATAAAATTAATATAAGTTATACTGTTGATAAATTGGTTGCTCC  
 ACTTAGTGGGGATATGCCTGTTGGGAGGGCTATGATTTTTTTAGAAAATGAAAAAATAGGGGATGTTGCTTTGTTT  
 AGTGGCAAGGTAAAAAGATTAGGGTTTTGGCAAGGTCTTTATAAGAGTTTTATAAATCTTTTTTCAAGAGAGTATT  
 AA

t290.nt

GTAAATTTAGCTGAGATTAATAAATTATCAGAGTATGCAAAGTCAATAGTTTTAATAGATTTTGATACTAAGCGAA  
 TACTTTATTCTAAGAAGCCCAATTTGGTTTTTCTCCAGCATCTCTTACAAAGATTGTTACAATTTATACAGCTTT  
 AATTGAAGCTGAAAAGCGAAATATAAAATTAAGCAATAGTTTCTTATTAGCGATTCTGCTTCATATTATAATGCA  
 CCCCCAATTCTTCTTTGATGTTTTTAGAAAAAGGTCAAATTGTTAATTTGAAGAGATTTTAAAAGGACTTTTCAG  
 TTTCTTCGGGTAATGATTCTTCTATTGCAATTGCTGAGTTTGTAGTAGGCAATTTAAATAGCTTTTGTAAATTTAAT  
 GAATATTAATGTTTTAAATTTAGGGCTTTTTAATATGCATTTTGTGTAACCTTCTGGATATAGCAGCGAGAATAAG  
 ATTACAGCACTAGATATGGCTTTTTTTTGTGAAATCTTATATAGAAAAGTTTAAATTTATGCTTAATATTCTATTCTT  
 TAAAGTATTTTATTTATCCAAAGAGTAGAAATTTAGGAAGTCTTTTGTTCATCAAAATTTTTTAACTTAAAACAAAG  
 AAATGCTAATTTATTAATATATGATTACCCTTATTCAGATGGCATTAAAACGGGATATATTAAGGAATCAGGCTTA  
 AATCTTGTGCTACTGCTAAAAAGGGTGAGAGAAGATTAATAGCAGTTGTATTGGGGGTGAAAAAGGAATTAATG  
 GATTTGGAGAGAAAAATGAGATCTTCGATTGCAAAAAATTTATTTGAATATGGATTTAATAAATATTCTAAATTTCC  
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 GTGGGGATATGCCTGTTGGGAGGGCTATGATTTTTTTAGAAAATGAAAAAATAGGGGATGTTGCTTTGTTTAGTGG  
 CAAGGTAAAAAGATTAGGGTTTTGGCAAGGTCTTTATAAGAGTTTTATAAATCTTTTTTCAAGAGAGTATTAA

f291.aa

MNSYDFITALVPIILIIIGLGIKKPAYVYVIPISLIATVAIVIFYKNLGIVNTSLAMLEGALMGIWPIATVIIAAI  
 FTYKMSDQKDIETIKNILSNVSSDRRIIVLLVWAGFGNFLEGVAGYGTAVAI PVSILIAMGFEPFFACLICLIMN  
 TSSTAYGSVGIPITSLAQATNLDVNIVSSEIAFQLILPTLTIPFVLVILTGGGIKGLKGVFLTLTLLSGMSMAISQV  
 FISKTLGPELPAILGSILSMTITIVYARFFGNKETTERQSKNTISLSKGIIACSPYILIVTFIVLVSPLFNKIHEY  
 LKTFQSTISIYPEANPLHFKWII SPGFLIILATTISYSIRGVPMLKQLKIFTLTLLKLMALSSFIIICIVAI SRLMT  
 HSGMIRDLANGISIIITGKFGPLFSPLIGAIGTFLTGS DTVSNVLFGLPQTQMAENIGANPYWLAAANTTGATGGKM  
 ISPQNITIATTTAGLIGQEGKLLSKTIIYALYYILATGLLVYL

t291.aa

QKDIETIKNILSNVSSDRRIIVLLVWAGFGNFLEGVAGYGTAVAI PVSILIAMGFEPFFACLICLIMNTSSTAYGS  
 VGIPITSLAQATNLDVNIVSSEIAFQLILPTLTIPFVLVILTGGGIKGLKGVFLTLTLLSGMSMAISQVFISKTLGP  
 ELPAILGSILSMTITIVYARFFGNKETTERQSKNTISLSKGIIACSPYILIVTFIVLVSPLFNKIHEY LKTFQSTI  
 SIYPEANPLHFKWII SPGFLIILATTISYSIRGVPMLKQLKIFTLTLLKLMALSSFIIICIVAI SRLMTHSGMIRDL  
 ANGISIIITGKFGPLFSPLIGAIGTFLTGS DTVSNVLFGLPQTQMAENIGANPYWLAAANTTGATGGKMISPQNITI  
 ATTTAGLIGQEGKLLSKTIIYALYYILATGLLVYL

f291.nt

ATGAATTCTTATGATTTTATAACAGCTTTGGTACCAATAATCCTAATAATTATTGGACTTGGCATAATAAAAAAGC  
 CAGCTTACTATGTAATACCCATATCATTAATAGCCACCGTTGCTATAGTTATATTTTATAAAAACCTGGGAATAGT  
 AAACACAAGTCTTGCAATGCTTGAGGCGCCCTTAATGGGGATATGGCCAATAGCAACTGTAATTATTGCTGCCATA

TABLE 1. Nucleotide and Amino Acid Sequences

TTTACATACAAAATGTCAGAAGATCAAAAAGATATAGAACTATTAAAAATATTTTATCAAACGTATCTTCTGATA  
GAAGAATTATAGTATTACTAGTTGCATGGGGATTTGGAAATTTTTTAGAAGGAGTTGCTGGATATGGAACGTCTGT  
TGCAATTCCTGTATCAATATTAATAGCAATGGGATTTGAACCATTTTTTGCTGCTTAATCTGTTTAATAATGAAC  
ACCTCATCAACCGCTACGGATCTGTGGGAATCCCTATAACATCTTTAGCTCAAGCAACTAACTTGGATGTTAACA  
TTGTTTCATCTGAGATTGCATTCCAACCTAACCTTCCAACCTTAACAATACCTTTTGTACTGGTAATCTTACAGG  
AGGGGGCATTAAAGGATTAAAAGGAGTATTCCTTCTTACCTTACTCTCAGGAATGTCAATGGCAATATCTCAAGTA  
TTTATATCAAAAACCTTTGGGTCCAGAACTTCCTGCAATCCTTGAAGCATTCTTCTATGACAATAACAATAGTTT  
ATGCAAGGTTTTTTGGAAATAAAGAACTACTGAGCGCCAAAGCAAAAACACAATATCCTTATCAAAAGGAATTAT  
TGCCTGCTCACCTACATTTTAATAGTAACCTTTTATAGTGTCTGTATCTCCTCTTTTAAACAAAATTCATGAATAC  
CTAAAACCTTTTCAAAGCACTATTAGCATTTATCCAGAAGCAAATCCCTTACACTTTAAATGGATTATCTCTCCGG  
GCTTCTTGATTATACCTTGCAACAACAATATCCTATTCAATACGGGGAGTTCCAATGTTAAACAGCTAAAAATATT  
TACATTGAACCTTGAAAAAATGGCATTATCTTCCCTTTTATAATCATATGCATTGTTGCAATATCAAGATTAATGACA  
CATAGTGAATGATAAGAGATCTTGCTAATGGAATCTCAATAATAACAGGTAAATTTGGACCATTATTTAGCCAC  
TAATTGGAGCTATTGGGACATTTTAAACAGGAAGTGATACGGTTTCAAATGTTCTTTTTGGACCCTTACAAACACA  
AATGGCAGAAAATATTGGAGCAAATCCTTACTGGCTTGACAGCAGCAAATACAACAGGAGCAACTGGAGGGAAAATG  
ATTTCTCCCCAAAACATCACAATAGCAACAACAACCTGCTGGATTAAATTGGACAAGAAGGCAAGCTTTTATCAAAA  
CAATAATTTATGCTTTTATACTACATTTTAGCAACAGGATTGCTAGTTTATTTAGTATAA

t291.nt

CAAAAAGATATAGAACTATTAAAAATATTTTATCAAACGTATCTTCTGATAGAAGAATTATAGTATTACTAGTTG  
CATGGGGATTTGGAAATTTTTTAGAAGGAGTTGCTGGATATGGAACGTCTGTTGCAATTCCTGTATCAATATTAAT  
AGCAATGGGATTTGAACCATTTTTTGCTGCTTAATCTGTTTAATAATGAACACCTCATCAACCGCTACGGATCT  
GTGGGAATCCCTATAACATCTTTAGCTCAAGCAACTAACTTGGATGTTAATCATGTTTTCATCTGAGATTGCATTCC  
AACTAATACTTCCAACCTTAACAATACCTTTTGTACTGGTAATCTTACAGGAGGGGGCATTAAGGATTAAAAGG  
AGTATTCCTTCTTACCTTACTCTCAGGAATGTCAATGGCAATATCTCAAGTATTTATATCAAAAACCTTTGGGTCCA  
GAACCTCTGCAATCCTTGAAGCATCTTTCTATGACAATAACAATAGTTTATGCAAGGTTTTTGGAAATAAAG  
AACTACTTGAGCGCCAAAGCAAAAACACAATATCCTTATCAAAGGAATTATTGCCTGCTCACCTACATTTTAAAT  
AGTAACTTTTTATAGTGCTTGATCTCCTCTTTTTAAACAAAATTCATGAATACCTAAAAACCTTTCAAAGCACTATT  
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TAACAGGAAGTGATACGGTTTCAAATGTTCTTTTTGGACCTTTACAAACACAAATGGCAGAAAATATTGGAGCAA  
TCCTTACTGGCTTGACAGCAGCAAATACAACAGGAGCAACTGGAGGGAAAATGATTCTCCCCAAAACATCACAATAG  
CAACAACAACCTGCTGGATTAAATTGGACAAG

f296.aa

MPSPIRVFFLVLLFIFIFNPVLIAMLFILFPFILILFSFLGVFRIYFTRDYSYSRSREFEFYKLSFLLMAKLLSIL  
GTVTGEQLNYVNFIIINSLNLSERKGSELYTIFHSAITKNNNADKILYTLKLGYPQHKDLFIWLFATLKEINRLSRY  
KNLEAEKFISYGVGFLELESDGYEAYKDINIKIVNPYSVLGLTYSASDDEVKKAYKSLVIKYHPDKFANDPVRQKD  
ANDKFIKIQDAYEKICKERNIR

t296.aa

IYFTRDYSYSRSREFEFYKLSFLLMAKLLSILGTVTGEQLNYVNFIIINSLNLSERKGSELYTIFHSAITKNNNADK  
ILYTLKLGYPQHKDLFIWLFATLKEINRLSRYKNLEAEKFISYGVGFLELESDGYEAYKDINIKIVNPYSVLGLTY  
SASDDEVKKAYKSLVIKYHPDKFANDPVRQKDANDKFIKIQDAYEKICKERNIR

f296.nt

ATGCCAAGCCCAATTAGAGTGTTTTTTTTTAGTGTTGTTGTTTATTTTTATTTTTAATCCCGTTTTAATAGCAATGC  
TTTTTATTTTTATTTCTTTTATTTTGATATTATTTAGTTTTTTAGGTGTTTTTAGAATATACTTTACAAGGGATTA  
CTCATATTCTAGATCTAGAGAGTTTGAATTTTATAAATTTCTTTTTTATTAATGGCTAAATTGCTATCTATTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

GGAAGTGTAACTGGGGAGCAGCTAAATTATGTCAATTTTATTATCAATTCTTTGAATTTGTCTGAACGTGGTAAAT  
CAGAATTGTATACCATTTTTCATTCTGCTATTACTAAAAATAATAATGCTGATAAAATTTTATATACCCTTAAGCT  
TGGTTATTTTTCAGCACAAAGATCTTTTATATGGCTTTTGGCCACTCTTAAAGAAATTAACAGGCTTTCTAGGTAT  
AAAAATTTAGAACTGAAAAATTTATTTCTTATGTTGGTGTTTTTTTAGAACTGAATCTGATGGTTATGAAGCTT  
ATAAAGATATTAATATTAAAAATTGTAAATCCTTATAGTGTTTTGGGGTTAACATATAGTGCTAGCGATGATGAGGT  
TAAAAAGGCGTATAAAAGCCTTGTATATAAAATATCATCCTGATAAGTTTGCAAATGATCCTGTAAGACAAAAAGAT  
GCAAATGATAAATTTATAAAAAATCAAGATGCTTATGAAAAATTTGCAAGGAAAGAAATATAAGGTAA

t296.nt

ATATACTTTACAAGGGATTACTCATATTTCTAGATCTAGAGAGTTTGAATTTTATAAACTTTCTTTTTTATTAAATGG  
CTAAATTGCTATCTATTTTAGGAAGTGTAACTGGGGAGCAGCTAAATTATGTCAATTTTATTATCAATTCTTTGAA  
TTTGTCTGAACGTGGTAAATCAGAATTGTATACCATTTTTCATTCTGCTATTACTAAAAATAATAATGCTGATAAA  
ATTTTATATACCCTTAAGCTTGGTTATTTTTCAGCACAAAGATCTTTTATATGGCTTTTGGCCACTCTTAAAGAAA  
TTAACAGGCTTTCTAGGTATAAAAAATTTAGAAGCTGAAAAATTTATTTCTTATGTTGGTGTTTTTTTAGAACTTGA  
ATCTGATGGTTATGAAGCTTATAAAGATATTAATATTAAAAATTGTAAATCCTTATAGTGTTTTGGGGTTAACATAT  
AGTGCTAGCGATGATGAGGTTAAAAAGGCGTATAAAAGCCTTGTATATAAAATATCATCCTGATAAGTTTGCAAATG  
ATCCTGTAAGACAAAAAGATGCAAATGATAAATTTATAAAAAATCAAGATGCTTATGAAAAATTTGCAAGGAAAG  
AAATATAAGGTAA

f3.aa

MKKKNLSIYMIMLISLLSCNTSDPNELTRKKMQDKNVKILGFLEKIQADNKEIVEKHIEKKEKQMVQAASVAPINV  
ESNFPYYLQEEIEIKEEELVPNTDEEKKAEKAISDGSLEFAKLVDENKLNKESAQLESSFN NVYKEILELADLIQ  
AEVHVAGRINSYIKKRKTTEKEYKKREIKNKIEKQALIKLFNQLLEKRGDIENLHTQLNSGLSERASAKYFFEKA  
KETLKAATERLNNKRKNRPWWARRTHSNLAIQAKNEAEDALNQLSTSSFRILEAMKIKEDVKQLLEEVKSFLDSS  
KSKIFSSGDRLYDFLETSK

t3.aa

NELTRKKMQDKNVKILGFLEKIQADNKEIVEKHIEKKEKQMVQAASVAPINVESNFPYYLQEEIEIKEEELVPNTD  
EEKKAEKKAISDGSLEFAKLVDENKLNKESAQLESSFN NVYKEILELADLIQAEVHVAGRINSYIKKRKTTEKEY  
KKREIKNKIEKQALIKLFNQLLEKRGDIENLHTQLNSGLSERASAKYFFEKAKETLKAATERLNNKRKNRPWWAR  
RTHSNLAIQAKNEAEDALNQLSTSSFRILEAMKIKEDVKQLLEEVKSFLDSSKSKIFSSGDRLYDFLETSK

f3.nt

ATGAAAAAAAAAATTTATCAATTTACATGATAATGCTAATAAGTTTATTATCATGTAATACAAGTGACCCCAATG  
AATTAAGTTCGTAATAAATGCAAGACAAGAAGCTGAAAATTTTAGGATTTT TAGAGAAAAATCAAGCAGATAATAA  
AGAAATTGTTGAAAAACATATAGAAAAAAGAAAAACAAATGGTGCAGGCTGCTTCTGTAGCACCTATTAATGTA  
GAGAGTAATTTCCCATATTATCTTCAAGAAGAAATAGAGATAAAGAAGAAGAGTTGGTTCCAAATACTGATGAAG  
AAAAGAAGGCAGAGAAGGCAATTAGCGATGGGAGTCTTGAATTTGCTAAATTAGTTGATGATGAAAATAAACTTAA  
AAATGAATCTGCGCAATTAGAATCTAGTTTTAATAATGTTTATAAAGAAATCTTAGAACTTGCAGATTTAATACAA  
GCAGAGGTGCATGTTGCAGGAAGGATAAATAGCTATATAAAAAAAGAAAGACCACTAAAGAAAAAGAATATAAGA  
AGAGAGAAATTAAGAATAAGATAGAAAAACAGGCTCTAATTAAGTTGTTCAATCAGTTATTAGAAAAAAGAGGCCGA  
TATTGAAAATCTTCATACTCAATTAAATAGTGGACTTAGCGAGAGAGCATCTGCAAAATACCTTTTTTGAGAAAGCC  
AAAGAACTTTAAAAGCTGCTATTACTGAAAGATTAAATAACAAACGTAAAAATCGGCCATGGTGGGCAAGAAGAA  
CACATAGTAATTTAGCAATACAGGCCAAAAATGAGGCAGAGGATGCTTTAAACCAATTAAGTACTTCTCTTTTAG  
GATACTTGAAGCAATGAAAAATAAGGAAGATGTAAACAGCTTCTTGAAGAAGTAAAAATCTTTTCTAGATTCTTCA  
AAGAGCAAAATCTTTTCTAGTGGCGATAGATTATATGATTTTTTTAGAGACGAGTAAATAA

t3.nt

AATGAATTAAGTTCGTAATAAATGCAAGACAAGAAGCTGAAAATTTTAGGATTTT TAGAGAAAAATCAAGCAGATA  
ATAAAGAAATTTGTTGAAAAACATATAGAAAAAAGAAAAACAAATGGTGCAGGCTGCTTCTGTAGCACCTATTA  
TGTAGAGAGTAATTTCCCATATTATCTTCAAGAAGAAATAGAGATAAAGAAGAAGAGTTGGTTCCAAATACTGAT

TABLE 1. Nucleotide and Amino Acid Sequences

GAAGAAAAGAAGGCAGAGAAGGCAATTAGCGATGGGAGTCTTGAATTTGCTAAATTAGTTGATGATGAAAAATAAAC  
TTAAAAATGAATCTGCGCAATTAGAATCTAGTTTAAATAATGTTTATAAAGAAATCTTAGAAGTTGCAGATTTAAT  
ACAAGCAGAGGTGCATGTTGCAGGAAGGATAAAATAGCTATATAAAAAAAGAAAGACCACTAAAGAAAAAGAATAT  
AAGAAGAGAGAAATTAAGAATAAGATAGAAAAACAGGCTCTAATTAAGTTGTTCAATCAGTTATTAGAAAAAGAG  
GCGATATTGAAAATCTTCATACTCAATTAAATAGTGGACTTAGCGAGAGAGCATCTGCAAAATACTTTTTTGAGAA  
AGCCAAAGAACTTTAAAGCTGCTATTACTGAAAAGATTAAATAACAAACGTAAAAATCGGCCATGGTGGGCAAGA  
AGAACACATAGTAATTTAGCAATACAGGCAAAAAATGAGGCAGAGGATGCTTTAAACCAATTAAGTACTTCTTCTT  
TTAGGATACTTGAAGCAATGAAAATAAAGGAAGATGTAAACAGCTTCTTGAAGAAGTAAATCTTTTCTAGATTC  
TTCAAAGAGCAAAATCTTTTCTAGTGGCGATAGATTATATGATTTTTTTAGAGACGAGTAAATAA

f30.aa

MNKKILTLLVLILSISSVLMLSKSITKSKYKIIRDYFINSNYVLVKIENKDLKFTISKPIYDKKLNNYFFKGQTT  
SHFLISNNVDIAINTSPYEVKQNMFFPKGLYIYNKKMISKQINNYGEIVIKHNKIIILNPKEDEIENCYDGFSGFFV  
LIKNGKYKKNFKETRHPRTIIGTDKNNKHLFLVTIEGRGVNNSKGASLNEAIDFALSYGMTNAINLDGGGSSTLVV  
KSNAPYKLNFTANIFGQERPVPFHLGIKLPN

t30.aa

LSKSITKSKYKIIRDYFINSNYVLVKIENKDLKFTISKPIYDKKLNNYFFKGQTTSHFLISNNVDIAINTSPYEV  
KQNMFFPKGLYIYNKKMISKQINNYGEIVIKHNKIIILNPKEDEIENCYDGFSGFFVLIKNGKYKKNFKETRHPRTI  
IGTDKNNKHLFLVTIEGRGVNNSKGASLNEAIDFALSYGMTNAINLDGGGSSTLVVKSNAPYKLNFTANIFGQER  
PVPFHLGIKLPN

f30.nt

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CCAAAAATCCAAATACAAAATTATTAGGGATTATTTTCATAAACAGCAATTATGTTCTGGTGAAAATTGAAAATAA  
AGATCTAAATTTTACCATATCAAAACCTATTTACGACAAAAAGCTAAATAATTACTTCTTTAAAGGCCAAACA  
AGCCATTTCTTAATTTCTAACAATGTTGACATTGCAATTAACACAAGTCCATACGAAGTTAAACAAAACATGTTTT  
TCCCAAAAGGACTATACATATATAATAAAAAAATGATTTCAAAACAAATAAATACTACGGAGAGATTGTAATAAA  
GCACAACAAAATATATTAATCCCAAGGAAGACGAAATAGAAAACGCGATTATGGATTTAGCGGATTTTTTGT  
TTAATCAAAAACGGAAAGTATAAAAAAATTTTAAAGAAACAAGGCACCCAAGAACAATAATAGGAACTGATAAAA  
ATAACAAGCATTTATTTCTTGTGTTACAATAGAAGGAAGGGGTGTCAATAATAGCAAAGGGGCTCTCTTAATGAAGC  
TATTGATTTTGCATTAAGCTACGGCATGACTAACGCTATTAATCTAGACGGGGGGGGCTCAAGCACTCTTGTGTA  
AAATCAAATAACGCTCCTTACAAATTAAACTTCACAGCAAACATCTTTTGACAGGAAAGACCTGTCCCATTTCATT  
TAGGAATAAACTTCCTAATTGA

t30.nt

CTGTCCAAATCAATCACCAAAAAATCCAAATACAAAATTATTAGGGATTATTTTCATAAACAGCAATTATGTTCTGG  
TGAAAATTGAAAATAAGATCTAAAATTTACCATATCAAAACCTATTTACGACAAAAAGCTAAATAATTACTTCTT  
TAAAGGCCAAACAACAAGCCATTTCTTAATTTCTAACAATGTTGACATTGCAATTACACAAGTCCATACGAAGTT  
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TAGCGGATTTTTTGTGTTTTAATCAAAAACGGAAAGTATAAAAAAATTTTAAAGAAACAAGGCACCCAAGAACAATA  
ATAGGAACTGATAAAAAATAACAAGCATTTATTTCTTGTGTTACAATAGAAGGAAGGGGTGTCAATAATAGCAAAGGGG  
CCTCTCTTAATGAAGCTATTGATTTTGCATTAAGCTACGGCATGACTAACGCTATTAATCTAGACGGGGGGGGCTC  
AAGCACTCTTGTGTGTAATCAAATAACGCTCCTTACAAATTAAACTTCACAGCAAACATCTTTTGACAGGAAAGA  
CCTGTCCCATTTCATTTAGGAATAAACTTCCTAATTGA

f308.aa

MQLLKKNYPFKRALLDLFLVYAIVYLASPFVNVNSEFWNVNENHFYFWISRSFLIIFIIYFFKLTSSYDDFRVEFF  
IPKFKFIFLWDSVLIFIKTILIAMIVIFLIAFLLEYLLPESVLVYVFQNNAGFNWKISSKKAFFLMTFTSFFTGAFF

TABLE 1. Nucleotide and Amino Acid Sequences

EELFYRAFVITKFTQMGPVAVATAILSSMFFAYGHLYYGILGLVTFILGIFFAFTYLRVKNVYVIFIHFSFYNIIVSSLLFLN

t308.aa

NSEFWNVNDENHFYFWISRSFLIIFIYFFKLTSSYDDFRVEFFIPKFKFIFLWDSVLIFIKTILIAMIVIFLIAFL  
LEYLLPESVLVYFQNNAGFNWKISSKKAFFLMTFTSFFTGAFFELFYRAFVITKFTQMGPVAVATAILSSMFFAY  
GHLYYGILGLVTFILGIFFAFTYLRVKNVYVIFIHFSFYNIIVSSLLFLN

f308.nt

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TGGCATCTCCTTTTGTAAATGTTAATTCAGAATTTTGAATGTTGATGAAAATCATTTTTATTGTTTGGATTTCAG  
ATCTTTTTTAATTATTTTTTATAATTTATTTTTTAACTTACCAGTTCTTATGATGATTTTAGAGTAGAGTTTTTT  
ATTCTAAATTTAAATTTATTTTTCTTTGGGATTCTGTTTAAATTTTATTAAAAACAATATTGATTGCAATGATAG  
TCATTTTTTAATAGCTTTTTTGCTTGAATATTTGTTGCCAGAATCGGTACTTGTCTATTATTTTCAAACAATGC  
TGGATTTAATTGGAAGATTAGCAGTAAAAAGCATTTTTTTTAATGACTTTTACCTCTTTTTTTACAGGAGCTTTT  
GAAGAACTTTTTTACAGGGCTTTTGTATTACTAAGTTTACACAAATGGGATTTCTGTGTAGCTACCGCCATTC  
TTAGTAGTATGTTTTTGTCTTATGGGCATTTATATTATGGAATTTTAGGATTTTGGTTACATTTATATTAGGGAT  
ATTTTTTGCTTTTACTTATTTAAGGTATAAAAATGTATATTATGTGATTTTATACATAGTTTTTATAATATTATT  
GTTAGCAGCTTGTGCTTTTTTTGAATTAA

t308.nt

AATTCAGAATTTTGAATGTTGATGAAAATCATTTTTATTGTTTGGATTTCAGATCTTTTTTAATTATTTTTATAA  
TTTATTTTTTTAACTTACCAGTTCTTATGATGATTTTAGAGTAGAGTTTTTATCTCTAAATTTAAATTTATTTT  
TCTTTGGGATTCTGTTTAAATTTTATTAAAAACAATATTGATTGCAATGATAGTCATTTTTTAATAGCTTTTTTG  
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TGTTATTACTAAGTTTACACAAATGGGATTTCTGTGTAGCTACCGCCATTCCTTAGTAGTATGTTTTTTGCTTAT  
GGGCATTTATATTATGGAATTTTAGGATTTTGGTTACATTTATATTAGGGATATTTTTTGCTTTTACTTATTTAA  
GGTATAAAAATGTATATTATGTGATTTTATACATAGTTTTTATAATATTATTGTTAGCAGCTTGTGCTTTTTTT  
GAATTAA

f31.aa

MKKYLFFILFLISSNNLIVSYPLSFGGGFSYQFTNYTDKTGATKFAPNFTRADHGINLNLFFDANYVLFEMSYKEA  
FVVTHNGRYFSLGLYGTYPVMVFKEQVRMLFPLIGFKYAFDLSSNNFNLFFLSMGLAADLFI PDL DGLYIRPLFMLS  
ISPFSNYKNFSGLTTEIMLGFNIGWRFFN

t31.aa

IVSYPLSFGGGFSYQFTNYTDKTGATKFAPNFTRADHGINLNLFFDANYVLFEMSYKEAFVVTHNGRYFSLGLYGT  
YPMVFKEQVRMLFPLIGFKYAFDLSSNNFNLFFLSMGLAADLFI PDL DGLYIRPLFMLSISPFSNYKNFSGLTTEI  
MLGFNIGWRFFN

f31.nt

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GTGGAGGTTTTCTTATCAATTTACTAATTATACTGATAAACAGGCGCCACTAAATTTGCTCCAAATTTTACCAG  
AGCAGATCATGGGATTAATTTGAATTTATTTTTTGATGCAAATTATGTACTTTTTGAAATGCTTTACAAAGAGGCT  
TTTGTTGTTACTCACAATGGGAGATATTCTCGCTTGGGCTTTATGGAACATATCCAATGGTTTTCAAAGAGCAGG  
TTAGAATGCTTTTCCCATTAATTGGGTTTAAATATGCTTTTGATTTAAGCTCTAATAACTTCAATCTCTTTTTTTT  
AAGCATGGGGCTTGCTGCTGATCTTTTTATTTCCCGATCTTGATGGTTTATATATTAGGCCTTGTTTATGCTTTCT  
ATTTCTCCATTTTCTAATTATAAAAATTTTCTGGGTTAACAACCTGAGATTATGCTTGGATTTAATATCGGTTGGA  
GATTTTTCAATTAG



TABLE 1. Nucleotide and Amino Acid Sequences

t31.nt

ATTGTTTCTTATCCACTTTCTTTTGGTGGAGGTTTTCTTATCAATTTACTAATTATACTGATAAAACAGGCGCCA  
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TTTTGAAATGTCTTACAAAGAGGCTTTTGTGTACTCACAATGGGAGATATTCTCGCTTGGGCTTTATGGAACA  
TATCCAATGGTTTTCAAAGAGCAGGTAGAAATGCTTTTCCCATTAATTTGGGTTTAAATATGCTTTTGATTTAAGCT  
CTAATAACTTCAATCTCTTTTTTTAAGCATGGGGCTTGCTGCTGATCTTTTTATTCCCGATCTTGATGGTTTATA  
TATTAGGCCTTGTATTGCTTTCTATTCTCCATTTTCTAATATAAAAAATTTTCTGGGTTAACAACAGATTT  
ATGCTTGGATTAAATATCGGTTGGAGATTTTCAATTAG

f939.aa

MKQKYENYFKRLILNLLIFLLLACSSSIFSQLGNLQIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGK  
IEKIDLSNSYEFINDIVNISGKTYLLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVGRDGVKEAYILAI  
NNREKIFDLQGS DKT PPQATENDKFYQISNEENLITGNSLKIWMNNNTYTNIDYQQAKEIMPIIKTSIRGSSEVL  
VMTGGYNNLDTKFKVYSNTNNYTTPIFIQDEVGEFSSYFAREFNDAILGSNNGFAEFTKNKEGIFALRAPSKSVE  
PGAYNGSQLSKTGLNDIIPVSNNTIYILTQGKGLWKLENRKLTK

f939.aa

CSSSIFSQLGNLQIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTY  
LLAQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVGRDGVKEAYILAIKNNREKIFDLQGS DKT PPQATENDK  
FYQISNEENLITGNSLKIWMNNNTYTNIDYQQAKEIMPIIKTSIRGSSEVLVMTGGYNNLDTKFKVYSNTNNYTT  
PIFIQDEVGEFSSYFAREFNDAILGSNNGFAEFTKNKEGIFALRAPSKSVEPGAYNGSQLSKTGLNDIIPVSNN  
TIYILTQGKGLWKLENR  
KLTK

f939.nt

ATGAAACAAAAATACGAAAACATTTTAAAAAAGATTAATTTTAAACCTATTAATATTTTTACTACTAGCATGCT  
CAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAACATGAATACAATATTTTGGGCAGTTCAAG  
TCCAAGAGGAATTTCTCTAGTAGGAGAACTCTCTACATTGCAGCCATGCATTTATTTAAAAAAGAAAACGGCAAG  
ATTGAAAAAATTGATTGAGCAATTCCTTATGAGTTTATAAACGACATTGTAATATATCTGGAAAAACCTATCTTT  
TAGCGCAAAACAAAGAAGAAGAAATAGAAAGTTTGCAGCTAAATGGAAAAGATTGGACATTAAAAATTTAAAAAAC  
GCTAAAAGCATATAAAATCTTAAATCCGTAGGAAGAGATGGCGTAAAAGAAGCATATATTTTAGCTATAGATAAA  
AATAATCGTGAGAAAATTTTGTATCTACAAGGATCTGACAAAACACCACCACAAGCTACTGAAAATGACAAAATTTT  
ATCAAAATATCAAAATGAAGAAAACCTTAATTACAGGAAATTCACCTCAAAATATGGCAAAATGAATAACAATACATAC  
AAACATAGACTATCAACAGGCCAAAGAAATAATGCCTATCATTAACCAAGCATTAGGGGCTCTTCTGAAGTTT  
GTAATGACTGGTGGTTACAATAATTTAGATACAAAATTTAAAGTTTACTCAAAATACAAATAATTACACAACGCCAA  
TATTTATTCAAGACGAAGTAGGCGAATTTAGCAGCTACTTTGCAAGAGAATTTAATGATGCGATATTAATCGGAAG  
TAATAATGGATTTCAGAAATTTACAAAAATAAAGAAGGAATTTTGCCTACGGGCACCTCAAAATCTGTAGAA  
CCTGGAGCTTATAACGGATCTCAGCTAAGCAAAACAGGCCTTAATGATATTATTCCTGTATCAAAACACAGATTT  
ACATATTAACCTAGGGCAAGGTTTGTGGAAATTGGAAAACAGAAAATTAACATAAAGATAA

t939.nt

TGCTCAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAACATGAATACAATATTTTGGGCAGTT  
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CAAGATTGAAAAAATTGATTGAGCAATTCCTTATGAGTTTATAAACGACATTGTAATATATCTGGAAAAACCTAT  
CTTTTAGCGCAAAACAAAGAAGAAGAAATAGAAAGTTTGCAGCTAAATGGAAAAGATTGGACATTAAAAATTTAAAA  
AACCGCTAAAAGCATATAAAATCTTAAATCCGTAGGAAGAGATGGCGTAAAAGAAGCATATATTTTAGCTATAGA  
TAAAAATAATCGTGAGAAAATTTTGTATCTACAAGGATCTGACAAAACACCACCACAAGCTACTGAAAATGACAAA  
TTTTATCAAAATATCAAAATGAAGAAAACCTTAATTACAGGAAATTCACCTCAAAATATGGCAAAATGAATAACAATACAT

TABLE 1. Nucleotide and Amino Acid Sequences

ACACAAACATAGACTATCAACAGGCCAAAGAAATAATGCCTATCATTTAAAACAAGCATTAGGGGCTCTTCTGAAGT  
TTTAGTAATGACTGGTGGTTACAATAATTTAGATACAAAATTTAAAGTTTACTCAAATACAAATAATTACACAACG  
CCAATATTTATTCAAGACGAAGTAGGCGAATTTAGCAGCTACTTTGCAAGAGAATTTAATGATGCGATATTAATCG  
GAAGTAATAATGGATTTGCAGAATTTACAAAAAATAAAGAAGGAATTTTGCCTACGGGCACCCCTCAAAATCTGT  
AGAACCTGGAGCTTATAACGGATCTCAGCTAAGCAAAACAGGCCTTAATGATATTATTCCTGTATCAAAACAACACG  
ATTTACATATTAACCTCAGGGCAAGGGTTTGTGGAAATTGGAACAGAAAATTAATAAAGAATAA

f739.aa

MQSGLKIKLILFFCCFACSCDINYPEIKELDYKINYYFTENRLDYSMSFDFAIKVINSKDVFKLSIENKNTNEFIQ  
VINNNYSSFFIDSSLGKDILYCKDLRFNFFDKTFEDFTSCVRLFDKGMRVYNRELVISLGMSKYDLDDVHNYVYKS  
KDMEMLNKLSNSKVFFVKTYKDKLHPVSSVVRIDSIDILEIDKAFDNYISFYVEKNSNLFFKVG

t739.aa

CCFACSCDINYPEIKELDYKINYYFTENRLDYSMSFDFAIKVINSKDVFKLSIENKNTNEFIQVINNNYSSFFIDS  
SLGKDILYCKDLRFNFFDKTFEDFTSCVRLFDKGMRVYNRELVISLGMSKYDLDDVHNYVYKSKDMEMLNKLSNSK  
VFFVKTYKDKLHPVSSVVRIDSIDILEIDKAFDNYISFYVEKNSNLFFKVG

f739.nt

ATGCAGAGCGGATTAAAAATTAAATTAATATTGTTTTTTGTTGTTTTGCTTGTTCTTGCGACATAAAATTATCCGG  
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TGCAATTAAAGTTATAAATTCAAAAGATGTTTTTAAATTATCAATAGAGAATAAGAACACTAATGAGTTTTATCAA  
GTGATTAATAATAATTATAGCTCTTTTTTTATTGATTCTAGCCTTGGAAGGATATTCTATATTGTAAGGATTTGA  
GGTTAATTTTTTTGATAAAACTTTTGAAGATTTTACCTCATGTGTTTCGTCTTTTTGATAAGGGCATGAGAGTATA  
CAATAGAGAGCTTGTTATTTCTTTGGGTATGTCAAAATATGATTTAGATGATGTTTACCAATTATGTATATAAGTCT  
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CGGTCTCTTCAGTTGTTAGAATTGATTCAATAGATATTCTAGAGATTGATAAAGCATTGATAATTACATAAGTTT  
TTATTATGTGCGAAAAAATTCAAATCTTTTTTTTAAAGTTGGCTGA

t739.nt

TGTTGTTTTGCTTGTTCTTGCGACATAAAATTATCCGGAGATAAAAGAGCTTGATTATAAGATAAAATTATTATTTTA  
CTGAAAATCGCTTAGATTACTCTATGAGTTTTGATTTTGCAATTAAAGTTATAAATTCAAAAGATGTTTTTAAATT  
ATCAATAGAGAATAAGAACACTAATGAGTTTATTCAAGTGATTAATAATAATTATAGCTCTTTTTTTATTGATTCT  
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CATGTGTTCTGCTTTTTGATAAGGGCATGAGAGTATACAATAGAGAGCTTGTTATTTCTTTGGGTATGTCAAAATA  
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GTATTTTTTGTAAAACTTATAAAGACAACTACATCCGGTCTCTTCAGTTGTTAGAATTGATTCAATAGATATTC  
TAGAGATTGATAAAGCATTGATAATTACATAAGTTTTTATTATGTGCGAAAAAATTCAAATCTTTTTTTTAAAGT  
TGGCTGA

f742.aa

MNKKHTNFSVLLLLIFLLILSFGGFGYIYQSKLNDKNREIMLNEVKNSVIDRNYKKAYSVAKLLQDKYPQONEDIA  
MLTNTLAEIANSSPFESKDLQORDSANQILDKIKQDNTKTNVNFNFIQDSTITENYSDRNDVVGIEDE  
DISEFKKSKIPEKIPNTNPKEEDQIIQSPNPKLSVNDQKNLNFLEKLNLSGKSNSENILNDSQKIENDKQNTN  
LSKEKNSENILKTPDNSKYSNNNNNTSLKKISSNSQKESELSPPSQTIIIGKIYRPYSYLIKKELEYEILDDINTGRV  
TLGKNRLKELIKKGLSNKFQVNELIENSKNKEASNNLLTLIKKDIEPNLINIPKDPYKKEIFQLDKEDKKPQYLE  
DLKSKVHSIKPIDLENTKSRQQAIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQ  
AIKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQ  
AQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQ  
IDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQ  
PNDQAASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQAIDLENTKSRQQ  
AENAYEKIILKLTNTQEDHYKLGIRFKLKKYEHSESFDQTIKLDPKHKKALHNKGIALLMMLNKNKKAIESFEKAI

TABLE 1. Nucleotide and Amino Acid Sequences

QIDKNYGTAYYQKGIAEEKNGDMQQAFASFKNAYNLDKNPNYALKAGIVSNNLGNFKQSEEYLNFFNANAKKPNEI  
 AIYNLSIAKFENNKLEESLETINKAIDLNPEKSEYLYLKASINLKKENYQNAISLYSLVIEKNPENTSAYINLAKA  
 YEKSGNKSQAISTLEKIINKNNKLALNNLGILYKKEKNYQKAIEIFEKAIINSIDIEAKYNLATTLIEINDNTRAKD  
 LLREYTKLKPNNPEALHALGII EYNENNNDQTLREL IKKFPNYKKNENIKKIIGI

t742 .aa

KLNDKNREIMLNEVKNSVIDRNYKKAYSVAKLLQDKYPQNEIDIAMLTNTLAEIANSSPFESKDLQRDSANQILDKI  
 KGQD  
 NTKTNVNFENFDIAFNPNRYIKDSTITENYSRNDVGVIEDIEDISEFKKSKIPEKIKPNTNPKEEDQIIQSPNPKLSV  
 NDQKNLFNLEKLKKNLSGKSNSENILNDSQKIENDKQNTNLSKEKNSENILKTPDNSKYNNNTTSLKKISSNSQ  
 KESELSPPSQTIIGKIYRPYSYLIKELYEILDDINTGRVTLGKNRLKELIKKGLSNKFQKVNELIENSKNKEASN  
 LLLTLIKKDIENPLINIPKDPYKKEIFQLDKEDKKPQYLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPN  
 DAQASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKS  
 KVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDK  
 LNEFXKNNPNDAQASKTLAQANKIQHLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFXKNNPNDAQASKTLAQAN  
 KIQHLEDLKSQVHSIKPIDLENTKSRQQAIDKDLNEFLKNNPNDAQASKTLAQANKIQHLEDLKSQVHSIKPIDLEN  
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 SFDQTIKLDPKHKKALHNKGIALMMLNKNKKAIESFEKAIQIDKNYGTAYYQKGIAEEKNGDMQQAFASFKNAYNL  
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 KNYQKAIEIFEKAIINSIDIEAKYNLATTLIEINDNTRAKDLLREYTKLKPNNPEALHALGII EYNENNNDQTLREL  
 IKKFPNYKKNENIKKIIGI

f742 .nt

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 TAATAGATACATTAAAGACAGCACAATAACAGAAACTACTCTGACAGAAACGATGATGTTGGCATTGAAGATGAA  
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 ACCTTTGGAATAACAGATTAAAAGAATTAATTAAAAAAGGTCTAAGCAACAAATTTCAAAAAGTAAATGAATTGA  
 TTGAAAATTCAAAAATAAAGAAGCTTCAAATTTACTATTAACTTAATAAAAAAGATATTGAACCAATCTCAT  
 TAATATACCAAAAGATCCTTACAAAAAGAAATTTTCAATTAGATAAAGAAGACAAAAAGCCTCAGTACCTAGAG  
 GACCTTAAATCTAAAGTTCATTCAATAAAACCCATTGATCTTGAAAACACAAAATCACGCCAACAAAGCCATTAAGG  
 ATCTAAACGAATTCTTGAAAAACAATCCCAATGACGCTCAGGCCTCTAAACCTTAGCTCAAGCTAATAAAATACA  
 ACACCTAGAGGACCTTAAATCTAAGGTTCAATCAATAAAACCCATTGATCTTGAAAACACAAAATCACGCCAACAA  
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 ACGCCAACAAGCCATTAAGGATCTAAACGAATTCTTAAAAACAATCCCAATGACGCCCAGGCCTCTAAACCTTTA  
 GCTCAAGCTAATAAAATACAACACCTGGAGGACCTTAAATCTAAGGTTCAATCAATAAAACCCATTGATCTTGAAA  
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 CTTGAAAACACAAAATCACGCCAACAAAGCCATTAAGGATCTAAACGAATTCTTAAAAACAATCCCAATGACGCCAG  
 GCCTCTAAACCTTAGCTCAAGCTAATAAAATACAACACCTAGAGGACCTTAAATCTAAGGTTCAATCAATAAAAC  
 CCATTGATCTTGAAAACACAAAAT  
 CACGCCAACAAAGCCATTAAGGATCTAAACGAATTCTTAAAAACAATCCCAATGACGCCCAGGCCTCTAAACCTTT  
 AGCTCAAGCTAATAAAATACAACACCTGGAGGACCTTAAATCTAAGGTTCAATCAATAAAACCCATTGATCTTGAA  
 AACACAAAATCACGCCAACAAAGCCATTAAGGATCTAAACGAATTCTTAAAAACAATCCCAATGACGCCCAGGCCTC

TABLE 1. Nucleotide and Amino Acid Sequences

TAAAACTTTAGCTCAAGCTTATGAAAACAATGGAGATTTGCTAAAAGCAGAAAATGCATACGAAAAAATTATCAAA  
CTCACAAATACCCAAGAAGATCACTATAAACTTGAATCATTTAGATTCAAGCTTAAAAAGTATGAACACTCAATAG  
AATCATTTGATCAAACAATAAACTCGACCCAAAACATAAAAAAGCACTTCATAACAAAGGAATAGCTTTAATGAT  
GCTAAATAAAAAACAAAAAGCAATAGAATCTTTTGAGAAAGCAATACAAATTGATAAAAAATTATGGCACCGCCTAC  
TACCAAAAAAGGAATAGCAGAAGAAAAAATGGCGATATGCAACAAGCATTGTGCAAGCTTTAAAAATGCCTACAATC  
TCGACAAAAACCCCAATTATGCATTAAGAGCAGGAATAGTATCAAAATAACTTGGGCAACTTCAAACAAAGTGAAGA  
GTATTTAAATTTTTTTAATGCCAATGCAAAAAACCTAACGAAATTGCTATTTACAACCTATCAATAGCAAAATTT  
GAAAAACAATAAACTTGAAGAATCTCTTGAAACAATAAACAAAGCCATAGATTTAAATCCAGAAAAAAGTGAATATT  
TATATTTAAAAGCATCTATAAATCTTAAAAAAGAAAATTACCAAAATGCTATATCACTTTACAGCTTAGTAATTGA  
AAAAACCCCTGAAAATACCTCAGCCTATATAAACCTGGCAAAAGCATATGAAAAATCAGGAAATAAAAGTCAAGCA  
ATCTCAACTCTTGAAAAGATAATAAACAAAAATAATAATTAGCCTTAAACAATCTTGGGATACTTTACAAAAAAG  
AAAAAATTATCAAAAAGCAATTGAAATTTTGA AAAAGCAATAATCAATTCAGATATTGAAGCAAAATATAATCT  
TGCAACCCTCTAATTGAAATTAATGATAACACAAGAGCTAAAAGACCTTCTAAGAGAATATACAAAATTAAAAACCA  
AACAAATCCAGAGGCCTTACATGCACTAGGAATAATAGAATATAATGAAAATAACAATGATCAAACTAAGAGAAC  
TTATAAAAAAATTTCCAAATTACAAAAAATGAAAATATTAAAAAATAATAGGAATATAA

t742.nt

AAATTAAATGACAAAAATCGAGAAATAATGCTAAACGAAGTTAAAAATAGCGTAATAGATCGAACTATAAAAAAG  
CATATTCTGTTGCAAAACCTTCTGCAAGACAAATACCCCCAAATGAAGACATTGCAATGCTTACAAATACACTAGC  
AGAAATTGCCAACAGTAGTCCTTTTGAATCAAAAAGACTTGCAAAAGAGATTCTGCTAATCAAATCTTAGACAAGATC  
AAAGGTCAAGACAATACAAAAACAAATGTAAACGAAAATTTTGATATAGCATTTAATAATAGATACATTAAAGACA  
GCACAATAACAGAAAACTACTCTGACAGAAACGATGATGTTGGCATTGAAGATGAAGACATATCTGAATTTAAAAA  
AAGCAAAATCCCAGAAAAAATAAACCAAAATACAAACCCAAAAAGAAAGACCAAAATAATACAATCTCCAAATCCG  
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GTGAAAAATATTTTAAACGATTCTCAAAAAATAGAAAATGATAAGCAAAACACAAATTTATCCAAAGAAAAAATTC  
GGAGAATATTTTAAAAAATCCGGACAACAGTAAATATTCAAACAATAACAATACTACATCTTTAAAAAATTTCT  
TCAAATTTCCCAAAAAGAAAGTGAGCTTTCTCCACCCAGTCAAAACAATAATAGGGAAAATTTATAGGCCATATAGCT  
ACTTGATAAAAAAAGAGCTCTATGAAATATTAGACGATTAATAACCGGAAGAGTCACACTTGGAAAAACAGATT  
AAAAGAATTAATTTAAAAAAGGTCTAAGCAACAAATTTCAAAAAGTAAATGAATTGATTGAAAATTCAAAAATAAA  
GAAGCTTCAAATTTACTATTAACTTAAATAAAAAAAGATATTGAACCAAAATCTCATTAAATATACCAAAAGATCCTT  
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TTCAATAAAACCCATTGATCTTGAAAACACAAAATCACGCCAACAAGCCATTAAGGATCTAAACGAATTTCTTGAAA  
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CTAAGGTTCAATCAATAAAACCCATTGATCTTGAAAACACAAAATCACGCCAACAAGCCATTAAGGATCTAAACGA  
ATTCTTGAAAAACAATCCCAATGACGCTCAGGCCTCTAAACTTTAGCTCAAGCTAATAAAATACAACACCTAGAG  
GACCTTAAATCTAAGGTTTCAATTAATAAAACCCATTGATCTTGAAAACACAAAATCACGCCAACAAGCCATTAAGG  
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GCCATTAAGGATCTAAACGAATTTCTTAAAAACAATCCCAATGACGCCAGGCCTCTAAACTTTAGCTCAAGCTAAT  
AAAATACAACACCTGAGGACCTTAAATCTAAGGTTTCAATTAATAAAACCCATTGATCTTGAAAACACAAAATCACG  
CCAACAAGCCATTAAGGATCTAAACGAATTTCTTAAAAACAATCCCAATGACGCCAGGCCTCTAAACTTTAGCTCA  
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GCATTTAAAGCAGGAATAGTATCAAATAAATTTGGGCAACTTCAAACAAAGTGAAGAGTATTTAAATTTTTTTAATG  
CCAATGCAAAAAACCTAACGAAATTGCTATTTACAACCTATCAATAGCAAAATTTGAAAAACAATAAACTTGAAGA  
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AATCTTAAAAAAGAAAATTACCAAAATGCTATATCACTTTACAGCTTAGTAATTGAAAAAACCCCTGAAAATACTT

TABLE 1. Nucleotide and Amino Acid Sequences

CAGCCTATATAAACCTGGCAAAAGCATATGAAAAATCAGGAAATAAAAGTCAAGCAATCTCAACTCTTGAAAAGAT  
AATAACAAAAATAATAATTAGCCTTAAACAATCTTGGGATACCTTTACAAAAAGAAAAAATTATCAAAAAGCA  
ATTGAAATTTTGGAAAAGCAATAATCAATTCAGATATTGAAGCAAAATATAATCTTGCAACCACTCTAATTGAAA  
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TGCACTAGGAATAATAGAAATATAATGAAAATAACAATGATCAAACTAAGAGAATAAAAAAATTTCCAAATT  
ACAAAAAATGAAAATATTAAAAAATAATAGGAATATA

f743.aa

MRIYFLNKNYKIFILFLILILNSKLAYSQRLIRIGKEEMKNKNYIQAIETLSDAIKKYPKVQLGYYFLSIAYREN  
NQLTEAEGALLDGIAGVGEIDYILYYELGNIMFNREGGYPLAIKYYSNSIKSRPNYDSALLNRANAYVQGGKITS  
KEKEYQKAWDSYTMAIHDYSQFITLRSKTEKKDSILLIISYLRNEKINLEQLDKSLKGRTEHIVYAKEDKNQILKD  
SFKDNLETNSLIELEKLNWQEELYIDE

t743.aa

YSQRLIRIGKEEMKNKNYIQAIETLSDAIKKYPKVQLGYYFLSIAYRENNQLTEAEGALLDGIAGVGEIDYILYYE  
LGNIMFNREGGYPLAIKYYSNSIKSRPNYDSALLNRANAYVQGGKITSKEKEYQKAWDSYTMAIHDYSQFITLRS  
KTEKKDSILLIISYLRNEKINLEQLDKSLKGRTEHIVYAKEDKNQILKDSFKDNLETNSLIELEKLNWQEELYIDE

f743.nt

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TGGC  
ATATTCTCAAAGGCTAATTAGAATTGGCAAAGAAGAGATGAAAAACAAAAATTACATTCAGCAATCGAAACACTA  
AGTGATGCTATTAAAAAATATCCAAAAGTACAACCTCGGCTATTACTTTTATCAATAGCATACAGAGAAAAATAATC  
AATAACAGAAAGCAGAAGGAGCATTGCTCGATGGAATTGCAGTAGGGGGTGAAATCGACTACATACTATATTATGA  
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GACAAAAGTTTGAAGGGGCGAACCAGCATATTGTATACGCAAAAGAAGATAAAAAATCAAATACTTAAAGATAGTT  
TTAAAGACAACCTAGAAACAAATTCCTTAAATTGAGCTAGAAAACTTAATTGGCAAGAGGAGTTATACATAGATGA  
ATAA

t743.nt

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GTGATGCTATTAAAAAATATCCAAAAGTACAACCTCGGCTATTACTTTTATCAATAGCATACAGAGAAAAATAATCA  
ACTAACAGAAAGCAGAAGGAGCATTGCTCGATGGAATTGCAGTAGGGGGTGAAATCGACTACATACTATATTATGAA  
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AAAACAGAAAAAAGACAGCATTTTGCTTATAATAAGCTATTTAAGAAATGAAAAAATTAATCTTGAACAACCTTG  
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TAAAGACAACCTAGAAACAAATTCCTTAAATTGAGCTAGAAAACTTAATTGGCAAGAGGAGTTATACATAGATGAA  
TAA

f748.aa

MKFIINLLSTIKIITFTVIVCLTILSIFQPIYILKENEISITTRLGKIQRTEENLAGLKYKIPLIENVQIFPKIIL  
RWDGEPQRIPTGGEKQLIWIDTTARWKIADINKFYTTIKTMSRAYVRIDAAIEPAVRGVIAKYPLLEIIRSSNDP  
IQRLSNGILTPQETKINGIYKITKGRKIEKEIIRIANNNTKDIGIEIVDVLIRKVITYDPSLIESVNNRMISERQQ  
IAEEQRSIGLAEKTEILGSIEKEKLKILSEAKATAAKIKAEGDREAAKIYSNAYGKNIEFYKFWQALESYKAVLKD  
KRKIFSTDMDFQYLHKN

TABLE 1. Nucleotide and Amino Acid Sequences

t748.aa

IFQPIYILKENEISITTRLGKIQRTEENLAGLKYKIPLIENVQIFPKIILRWDGEPQRIPTGGEEKQLIWIDTTARW  
KIADINKFYTTIKTMSRAYVRIDAAIEPAVRGVIAKYPLLEIIRSSNDPIQRLSNGILTPQETKINGIYKITKGRK  
IEKEIIRIANNNTKDIGIEIVDLIRKVTDPSLIESVNNRMISERQQIAEEQRSIGLAEKTEILGSIEKEKLKI  
LSEAKATAAKIKAEGDREAAKIYSNAYGKNIEFYKFWQALESYKAVLKDGRKIFSTDMDFFQYLHKRN

f748.nt

ATGAAATTTATAATAAATCTTTTATTATCTACTATAAAGATTATAACCTTTACAGTAATAGTTTGCTTGACTATTT  
TGTCTATTTTCCAGCCAATTTTATATTTTGAAAGAAAAATGAAATTTCAATAACCACTCGACTTGGAATAATCAAAG  
AAGTGAATAATTTAGCTGGACTTAAATATAAAATACCATTAATTGAAATGTGCAATATTTCCCAAAATCATTCTT  
AGATGGGATGGAGAACCTCAAAGAATCCCAACAGGAGGGGAAGAAAAGCAATTAATATGGATTGATACAACTGCTA  
GATGGAAAAATTGCAGACATAAATAAATTTTACACAACAATAAAAAACAATGAGTAGAGCTTACGTTAGAATTGATGC  
AGCAATTGAACCTGCTGTTAGGGGGGTATTGCAAAAATACCCTTTGCTTGAAATTATAAGAAGCTCAAACGATCCT  
ATTCAACGTTTGTCTAATGGAATACTCACCCACAAGAAACAAAAATTAACGGTATTTATAAAATAACAAAAGGAC  
GAAAGATAATCGAAAAAGAAATAATTCGTATAGCAACAACAATACCAAAGATATTGGAATTGAAATTGTAGACGT  
ACTAATAAGAAAAGTTACTTATGACCCAAGCCTTATTGAATCTGTAAACAACAGAATGATCTCAGAAAGACAACAA  
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AAATGCATATGGCAAAAATATTGAATTTTACAAATTCTGGCAGGCATTAGAAAGCTATAAAGCAGTATTAAGAT  
AAAAGAAAAATTTTCTCAACAGACATGGATTTCTTTCAATATCTTCACAAAAGAAATTGA

t748.nt

ATTTTCCAGCCAATTTTATATTTTGAAAGAAAAATGAAATTTCAATAACCACTCGACTTGGAATAATCAAAGAAGTGA  
AAAATTTAGCTGGACTTAAATATAAAATACCATTAATTGAAATGTGCAATATTTCCCAAAATCATTCTTAGATG  
GGATGGAGAACCTCAAAGAATCCCAACAGGAGGGGAAGAAAAGCAATTAATATGGATTGATACAACTGCTAGATGG  
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ATAATCGAAAAAGAAATAATTCGTATAGCAACAACAATACCAAAGATATTGGAATTGAAATTGTAGACGTAATA  
TAAGAAAAGTTACTTATGACCCAAGCCTTATTGAATCTGTAAACAACAGAATGATCTCAGAAAGACAACAAATCGC  
AGAAGAACAAGAAAGCATAGGATTAGCTGAAAAAACAGAAATTCCTTGGAAGCATAGAAAAAGAAAACTGAAATA  
TTAAGTGAAGCAAAAGCCACTGCTGCAAAAATAAAAGCCGAAGGGGATAGAGAAGCCGCAAAAATTTATTCAAATG  
CATATGGCAAAAATATTGAATTTTACAAATTCTGGCAGGCATTAGAAAGCTATAAAGCAGTATTAAGATATAAG  
AAAATTTTCTCAACAGACATGGATTTCTTTCAATATCTTCACAAAAGAAATTGA

f764.aa

MSGPKKLAIALLVISIQGCKESSIIIEKQFNIAIIFSDATEYFFEIQTTPIKNEILFINDKNLEIIKDKLKTTHK  
ILLTHKSNNEILNNEILKEKIFYLSKIKFSLKKSIDFLNEKSIDLQKTLFRDKSLNNEIDLEYLEKKGKEKNVNI  
TLNEKNISYIQTFITSQIKTIILFSLRDNNIILKKILNSPFSKNIKFVLIGNTRKDLKIIKLKYIITLKEPDLIK  
IAKDVEKDFQYEFNIYKQ

f764.aa

EKQFNIAIIFSDATEYFFEIQTTPIKNEILFINDKNLEIIKDKLKTTHKILLTHKSNNEILNNEILKEKIFYLSK  
IKFSLKKSIDFLNEKSIDLQKTLFRDKSLNNEIDLEYLEKKGKEKNVNITLINEKNISYIQTFITSQIKTIILF  
LRDNNIILKKILNSPFSKNIKFVLIGNTRKDLKIIKLKYIITLKEPDLIKIAKDVEKDFQYEFNIYKQ

f764.nt

ATGTCTGGCCCTAAAAAAGTTGCTATAATAGCGCTCTTAGTAATTTCAATACAAGGATGCAAAGAATCTTCTATTA  
TTGAAAAACAATTTAATTATGCAATAATTTTTTCAGATGCAACTGAATATTTTTTGAAATTCAAACAACCTCCATT  
CATAAAAAACGAAATACTATTTATAAATGACAAAAATTTAGAAATTATAAAGACAAGCTTAAAAACAACAAAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

ATACTATTAACTCATAAATCAAATAATGAAATTCCTAAATAACGAAATTCCTAAAAGAGAAAATTTTTTATCTATCAA  
AAATAAAATTTTCTCTAAAAAAATCTATTGACCTTCTGCTTAACGAAAAATCAATAGATTTGCAAAAAACATTACT  
ATTTAGAGACAAATCTCTAAATAACGAAGACCTTGAATACTTGGAAAAAAAAGGCAAAGAAAAAAATGTCAATATT  
ACTCTAATAAACGAAAAAAACATATCCTATATTCAAACATTCATTACTTCTCAAATAAAAAACAATAATATTATTCT  
CTTTAAGAGATAATAATATTATTTTAAAAAAGATACTAAATTCGCCTTTTCTAAAAATATAAAATTTGTATTAAT  
TGGCAATACAAGAAAAGACTTAAAAATTATTAAGCTAAAATATATAATCACCCCTAAAGAGCCTGATTTGATAAAA  
ATAGCAAAAGATGTTGAAAAAGATTTTCAATATGAATTTAACATTTATAAACAATAA

t764.nt

GAAAAACAATTTAATTATGCAATAATTTTTTCAGATGCAACTGAATATTTTTTTTGAAATTCAAACAACCTCCATTCA  
TAAAAACGAAATACTATTTATAAATGACAAAAATTTAGAAATTATAAAAGACAAGCTTAAAAACAACAAAAAAAT  
ACTATTAACCTCATAAATCAAATAATGAAATTCCTAAATAACGAAATTCCTAAAAGAGAAAATTTTTTATCTATCAAAA  
ATAAAATTTTCTCTAAAAAAATCTATTGACCTTCTGCTTAACGAAAAATCAATAGATTTGCAAAAAACATTACTAT  
TTAGAGACAAATCTCTAAATAACGAAGACCTTGAATACTTGGAAAAAAAAGGCAAAGAAAAAAATGTCAATATTAC  
TCTAATAAACGAAAAAAACATATCCTATATTCAAACATTCATTACTTCTCAAATAAAAAACAATAATATTATTCTCT  
TTAAGAGATAATAATATTATTTTAAAAAAGATACTAAATTCGCCTTTTCTAAAAATATAAAATTTGTATTAATTG  
GCAATACAAGAAAAGACTTAAAAATTATTAAGCTAAAATATATAATCACCCCTAAAGAGCCTGATTTGATAAAAAT  
AGCAAAAGATGTTGAAAAAGATTTTCAATATGAATTTAACATTTATAAACAATAA

f770.aa

MINFSKSFYPLPIGKIFVLSGDMGSGKTSFLKGLALNLGISYFTSPTYNIVNVYDFINFKFYHIDLYRVSSLEEF  
ELVGGLEILMDLDSIIAIEWPQIALSIVPKDRLFSLTFKIVGSGRVVELNG

t770.aa

KTSFLKGLALNLGISYFTSPTYNIVNVYDFINFKFYHIDLYRVSSLEEFELVGGLEILMDLDSIIAIEWPQIALSI  
VPKDRLFSLTFKIVGSGRVVELNG

f770.nt

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TGTTAATGTTTATGATTTTATAAATTTTAAATTTTATCATATTGATTTATATCGGGTGTCTTCTTTGGAAGAATTT  
GAGCTTGTTGGGGGATTGGAAATACTTATGGATCTTGACTCGATTATTGCTATTGAATGGCCACAAATTGCTTTGA  
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TTAA

t770.nt

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GTTCCAAAAGATAGATTATTTTCTTTAACTTTTAAAATAGTAGGTTTCAGGCAGGGTTGTAGAACTTAATGGTTAA

f790.aa

MNTKATTPLLLLFLIQSLAFSSEIFEFKYIKGSKFRLEGTDNQKIYFNHYNSSSNTNIQISSEIKDIKENFASIK  
AFFRILKRENINEPYLLNEEFEEIFSVNKQGEYTIGANQKRPSVRGIPRFPKTPIKINEKWSYLAEEYIEASKIDK  
SIKDFVVKFNVNYEYKGKEEHNGKHYHIILSNYESQYNVKNISFYQKVDQKIYFDNEIGNTYKYSKYIFEINQNN  
NQHFKMIGNSLGRIVSIELPNDNLIETEVENYIREKKIKAEVEKNNKGINLSFDIEFYPSNFQILQKEYKKIDLI  
AKLLEKFKNNILIEGHTEQFGLEEEMHELSEKRARAIGNYLIKMKVKDKDQILFKGWGSQKPKYPKSSPLKAKNR  
RVEITILNN

t790.aa

TABLE 1. Nucleotide and Amino Acid Sequences

SEIFEFKYIKGSKFRLEGTDNQKIYFNHYNSSSNTNIQISSEIKDIKENFASIKAFFRILKRENINEPYLLNEEF  
EEIFSVNKQGEYTIGANQKRPSVRGIPRFPKTPIKINEKWSYLAEEYIEASKIDKSIKDFVVKFNVNYEYKGKEEH  
NGKHYHIILSNYESQYNVKNISFYQKVDQKIYFDNEIGNTYKYSDKYIFEINQNNNQHFKMIGNSLGRIVSIELPN  
DNLIETEVENYIREKKIKAIEVEKNNKGINLSFDIEFYPSNFQILQKEYKKIDLIKLLKFKKNNILIEGHTEQF  
GLEEEMHELSEKRARAIGNYLIKMKVKDKDQILFKGWSQPKPKSSPLKAKNRRVEITILNN

f790.nt

ATGAATACCAAGGCGACTACACCATTGTTGTTATTATTTTAAATTCAAAGCTTAGCTTTTTCTTCTGAAATCTTTG  
AATTTAAATACATTAAAGGTTCAAAGTTTAGATTAGAAGGCACAGATAATCAAAAAATATATTTCAATGGCCATTA  
TAATTCAGCTCTAATACCAATATTCAAATTTCAAGTGAAATAAAAAGACATAAAAAGAAAACCTTTGCAAGCATTA  
GCTTTTTTTTGAATCTTAAAAAGAGAAAATATTAATGAACCTTACCTATTAAATGAAGAGTTTGAAGAAATCTTCA  
GCGTAAATAAGCAAGGAGAATATACAATAGGAGCAAATCAAAAAAGACCTTCTGTTAGAGGTATTCCAAGATTCCC  
AAAAACACCAATCAAAATAAATGAAAAATGGTCATATCTTGCAGAAGAATATATAGAAGCGTCAAAAAAGACAAA  
AGTATAAAAGATTTTCGTTGTAAAATTTAATGTAACTACGAATATAAAGGCAAAGAAGAGCACAATGGCAAGCAT  
ACCACATAATTTCTTTCGAATTATGAATCACAATACAATGTAAAAACATCTCTTTCTATCAAAAAGTAGACCAAAA  
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CGAGTAGAAATTACAATATTAAATAACTAA

t790.nt

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TGCAAGCATTAAGCTTTTTTTTGAATCTTAAAAAGAGAAAATATTAATGAACCTTACCTATTAAATGAAGAGTTT  
GAAGAAATCTTCAGCGTAAATAAGCAAGGAGAATATACAATAGGAGCAAATCAAAAAAGACCTTCTGTTAGAGGTA  
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GGATTGGAAGAAGAGATGCACGAGCTATCTGAAAAAGAGCTCGTGCAATTGGAAATTTTAAATAAAATGAAAG  
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GGCTAAAAATAGGCGAGTAGAAATTACAATATTAAATAACTAA

f792.aa

MKIFIYVWVIFFFSVFKVFSIYSLTDEEFFKKYSLFFVHKGFLSKNVNGKITKVQVNGINSRWVYPFYKLVP  
SIYEDVYSSSSFLTSSNNLYVSVDYSKNFRKLVGIDKFNSGAYITSSAFSQGDYKRIAIGTAIHGIYLSVNGA  
ISFKNLNRLIPQIYLGAGYYDIISAIEFSKEETNNLYFSSGVYGDIFLISQKSGFIKKISFPFKKQIIRILD  
LSSKNVEKILVRTYDNHFYSYINGQWVFIGKLSLQDQDFEKSQRMQLAKNKGSIYLTAYTLRNKKAVDERFK  
FIKDSGMNAVVIDFKDDNGNLTYSSKLSLPNKLRSVKNFIDVPYILKKAKELGIYVIARC VVFKDSKLYYD  
NFKHALWNKKTNKPWAHLIKKVDSSGLVKYVQVEHWVDIFSPATWEYNI  
SIAKEIQSFGVDEIQFDYIRFPSDGPVSLAISRMNKYEMQPVDALESFLIMAREQLYVPISVDIYGYNGW  
FPTNSIGQNISMLSDYVDVISPMFYPSHYTDDFLPSNFYYTKRAYRIYKEGSDRALAFSLDG  
VVIRPYVQAFLLGKERLVDDEIYLEYLFQKLGIKESFGSGFSLWNASNVYYMIKGS  
LKEYLDSF



TABLE 1. Nucleotide and Amino Acid Sequences

t792.aa

IYSLTDEEFFKKYSLFFVHKGFLSKNVNGKITKVQVNGINSRWVYPFYKLVPSRITSIYEDVYSSSSFLTTSNNLY  
VSYDYSKNFRKLVGIDKFNSGAYITSSAFSQGDYKRIAIGTAIHGIYLSVNGAISFKNLNRLIPQIYLGAGYYDII  
SAIEFSKEETNNLYFSSGVYGDIFLISQKSGFIKKISFPFKQIIRILDLSKKNVEKILVRTYDNHFYSYINGQWV  
FIGKLSLQDQDFFEKSQRMQLAKNKGSIYLTAYTLRNKKAVDERFKFIKDSGMNAVVIDFKDDNGNLTYSSKLSLP  
NKLRSVKNFIDVPYILKKAKELGIYVIARCVVFKDSKLYYYDNFKHALWNKKNKPAWHLIKKVDSSGLVKYVQVE  
HWVDIFSPATWEYNISIAKEIQSFGVDEIQFDYIRFPSDGPVSLAISRMNKYEMQPVDALESFLIMAREQLYVPIS  
VDIYGYNGWFPTNSIGQNISMLSDYVDVISPMFYPSHYTDDFLPSNFYFYTGRAYRIYKEGSDRALAFSLDGVVIRP  
YVQAFLLGKERLVDDEIYLEYLFKQLKGIKESFGSGFSLWNASNYYMIKGSLSKEYLDSF

f792.nt

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AACCAAAGTTCAAGTCAATGGGATAAATCTAGGTGGGTTTACCCTTTTTATAAGCTTGTTCCTAGTCGAATTACT  
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GTTGATGCACCTGAATCTTTTTTGATTATGGCAAGAGAACAGCTTTATGTTCTTATTTCTGTTGATATTTATGGGT  
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t792.nt

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AATAAGTTGAGATCTGTTAAAAAATTTATTGATGTTCTTATATTTCTTAAAAAAGCAAAAGAGCTTGGAATTTATG  
TTATTGCTAGATGTGTTGATTTAAAGATTCAAAATTTGTATTATTATGATAATTTTAAACACGCCCTTTGGAATAA  
AAAAACCAATAAACCTTGGGCTCATTTGATTAAAAAAGTTGATTCTAGTGGTCTTGTGAAATATGTACAAGTAGAG

TABLE 1. Nucleotide and Amino Acid Sequences

CATTGGGTAGATATTTTCTCCTGCTACTTGGGAATATAATATTTCTATCGCAAAAGAAATTCAATCTTTTGGAG  
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TTGACGTCATATCTCCTATGTTTTATCCTTCGCATTATACTGATGATTTTTTGCCAAGCAATTTTTATTACACAAA  
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TATGTTCAAGCTTTTTTATTAGGAAAAGAAAGATTGGTGGATGACGAGATTTATTTGGAGTATTTAAAGTTTCAGC  
TTAAAGGAATTAAAGAGTCATTTGGTAGTGGCTTTAGCCTTTGGAATGCATCTAATGTTTATTATATGATTAAAGG  
TAGTTTAAAGAATATTTAGATTCTTTTTTAA

f797.aa

MSIKKFILTLIILSLAKNSFSENEINIFENENYIVKENIKTEIKKLKQSFLLASVDVAISQPYIELADLNGEPIKE  
LEGISYSFINVFSKIGSSAIISFDLSNEASKKYKIIKLEFLSPDKGNFINQLSSLTSGKQQSKKELAKDAYSFGLT  
RTESLSKTIAEYYKDNWYYILAAITVENNINKETEKYEIRINPKIYNDFQKKLRLHFKNQIKKFPIPIIE

t797.aa

KNSFSENEINIFENENYIVKENIKTEIKKLKQSFLLASVDVAISQPYIELADLNGEPIKELEGISYSFINVFSKIG  
SSAIISFDLSNEASKKYKIIKLEFLSPDKGNFINQLSSLTSGKQQSKKELAKDAYSFGLT  
RTESLSKTIAEYYKDNWYYILAAITVENNINKETEKYEIRINPKIYNDFQKKLRLHFKNQIKKFPIPIIE

f797.nt

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ACTTGATCTGTGATGTCGCCATTAGCCAACCCCTACATAGAATTGGCAGATTTAAATGGAGAACCGATAAAAGAA  
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CAAACGAAGCTTCCAAGAAAATACAAAATCATAAAATTAGAATTTTAAAGTCCAGATAAAGGCAATTTTATTAACCA  
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AGAAGTGAATCTCTTTCAAAAACAATTGCAGAATATTACAAAGATAACAACTGGTATTATATTTTAGCAGCAATAA  
CAGTAGAAAATAATATAAATAAAGAACTGAAAAATACGAAATTAGAATTAACCCATAAATATATAATGATTTTCA  
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t797.nt

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AGATTTAAATGGAGAACCGATAAAAGAACTTGAAGGGATTAGTTATTCATTTATAAATGTATTTTCAAAAATTGGA  
TCTTCTGCTATTATTTTCATTTGACCTATCAAACGAAGCTTCCAAGAAATACAAAATCATAAAATTAGAATTTTAA  
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AACTGGTATTATTTTAGCAGCAATAACAGTAGAAAATAATATAAATAAAGAACTGAAAAATACGAAATTAGAA  
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AATACCCATTATAGAATAA

f799.aa

MKKHIIIGIIFVAILLFFKILLIPRIQNHENNKNNIKMIIISYQDKNRLSLKINIKTKKTTNLGKAKLDIYDSKL  
IESNLLYISSKNFTTYANIYYQNESLLSIILKSNGNNNVFYSKRIPRGKI

t799.aa

HENNKNNIKMIIISYQDKNRLSLKINIKTKKTTNLGKAKLDIYDSKLIIESNLLYISSKNFTTYANIYYQNESLLS  
IILKSNGNNNVFYSKRIPRGKI

TABLE 1. Nucleotide and Amino Acid Sequences

f799.nt

ATGAAAAACATATCATTATTGGGATAATCTTTGTTGCAATTCTTTTATTTTTTAAATTTTATTAATCCCAGAA  
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AAAGATAAACATAAAAAACAAAAAACTACCAACCTGGGAAAAGCCAACTAGATATTTATCTAGACAGTAAATTA  
ATTGAAAGCAATTTGCTTTATATAAGCAGCAAAAACCTTTACAACATATGCTAATATAATCTATCAAAATGAAAGTT  
TATTAAGTATAATATTAAAGAGTAATGGCAATAATAATGTCTTTTATAGTAAAAGAATAAAACCTAGAGGTAAAT  
ATGA

t799.nt

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CAATTTGCTTTATATAAGCAGCAAAAACCTTTACAACATATGCTAATATAATCTATCAAAATGAAAGTTTATTAAGT  
ATAATATTAAAGAGTAATGGCAATAATAATGTCTTTTATAGTAAAAGAATAAAACCTAGAGGTAAATATGA

f800.aa

MKKHYKALILSLLFAIISCNTKTLNELGEEQFKIPFGTLPGAIMPLNNKFTNSKFDIKTYNGLVYIAEIKTNKLM  
FNSYGLIKIQTQNGIFKTNPD LKIKKIDFEGIQAIYPLKDFIIVADKLNNKSKFNQKENIAYFMRILILNKNSSV  
EILGQEGNLGMPFPQIYDVNV DENGNI AIIISYSEGYIIYSYNKEFSPLYKIYVNKNLLKTIDNQKKYNISIDKV  
FFEVNKKTLYVKTTYENIGDNENINDLGIKIKDQYIYKMSLKKNKELEVINKIALPKNLLDDKQESFINI IKIQK  
DKIIASTNMKNLSNNLIWKLD SKGSIKEQIALIEPPNLMFLSESLSKDGILSILYGGKTGVS VYWWNLNALLKL

t800.aa

KTLNELGEEQFKIPFGTLPGAIMPLNNKFTNSKFDIKTYNGLVYIAEIKTNKLMIFNSYGLIKIQTQNGIFKTNPD  
LKIKKIDFEGIQAIYPLKDFIIVADKLNNKSKFNQKENIAYFMRILILNKNSSVEILGQEGNLGMPFPQIYDVNV  
DENGNI AIIISYSEGYIIYSYNKEFSPLYKIYVNKNLLKTIDNQKKYNISIDKVFFEVNKKTLYVKTTYENIGD  
NENINDLGIKIKDQYIYKMSLKKNKELEVINKIALPKNLLDDKQESFINI IKIQKDKIIASTNMKNLSNNLIWKLD  
SKGSIKEQIALIEPPNLMFLSESLSKDGILSILYGGKTGVS VYWWNLNALLKL

f800.nt

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AAAATCAAAATTC AACCAAAAAGAGAATATTGCCTACTTCATGAGAATACTAATACTAAACAAAAACTCATCTGTA  
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ACATTGCAATAATATCAATATATAGCGAAGGATATATAATATATTCTTACAATAAAGAATTTTCCCCGCTTTATAA  
AATTTACGTCAACAAAAACCTGTTAAAAACAATAGACAATCAAAAAGAAAAAATACAACATTTCAATAGATAAGGTT  
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AAATAAAATTGCTCTTCTTAAAACTTACTAGATGATAAACAAGAAAGCTTTATAAACATTATAAAAAATACAAAA  
GACAAAATAATAGCATCTACTAATATGAAAAATTTATCTAACAATTTAATATGGAAATTAGACAGCAAGGGCTCAA  
TTAAAGAACAATAGCTTTAATTGAGCCTCAAATTTAATGTTTCTCTCTGAGAGTTTATCTAAAGATGGAATACT  
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t800.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

AACTAAATAATAAAAAATCAAAATTCAACCAAAAAGAGAATATTGCCTACTTCATGAGAATACTAATACTAAACAA  
AAACTCATCTGTAGAAATTTTGGGTCAAGAAGGTTTAAACGGAATGCCATTTCCACAAATTTATGATGTTAATGTT  
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CCCCGCTTTATAAAATTTACGTCAACAAAAACCTGTTAAAAACAATAGACAATCAAAAGAAAAAATACAACATTTT  
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AAAAATACAAAAAGACAAAATAATAGCATCTACTAATATGAAAAATTTATCTAACAATTTAATATGGAATTAGAC  
AGCAAGGGCTCAATTAAAGAACAATAAGCTTTAATTGAGCCTCCAAATTTAATGTTTCTCTCTGAGAGTTTATCTA  
AAGATGGAATACTTAGTATACTTTATGGCGGAAAACTGGTGTTAGTGTTTACTGGTGGAATTTAAATGCATTATT  
AAAATTATAA

f810.aa

MYKLFLFFIIFMFLSCDEKKSSKNLKS VKIGYVNWGGETAATNVLKVVF EKMGYN AEIFS VTTSIMYQYLASGKID  
GTVSSWVPTADKFYYEKLKTKFVDLGANYEGTIQGFVPSYVPISSISELKKGDKFKNKMIGIDAGAGTQIVTEQ  
ALNYYGLSKEYELVPSESVM LASLDSSIKRNEWILVPLWKPHWAF SRYDIKFLDDPDLIMGGIESVHTLVRLGLE  
NDDFDAYYVFDHFYWSDDLILPLMDKNDKEPGKEYRNAVEFVEKNKEIVKTWVPEKYKTLFD

t810.aa

CDEKKSSKNLKS VKIGYVNWGGETAATNVLKVVF EKMGYN AEIFS VTTSIMYQYLASGKIDGTVSSWVPTADKFYY  
EKLKTKFVDLGANYEGTIQGFVPSYVPISSISELKKGDKFKNKMIGIDAGAGTQIVTEQALNYYGLSKEYELVP  
SSESVM LASLDSSIKRNEWILVPLWKPHWAF SRYDIKFLDDPDLIMGGIESVHTLVRLGLEND DFDAYYVFDHFYW  
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f810.nt

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t810.nt

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CGTGCACTCTTGTTAGACTTGGTCTTGAAAATGATGATTTTGATGCATATTATGTTTTTGATCATTTTTTATTGG  
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TTGTTGAAAAGAATAAAGAGATTGTAAAGACGTGGGTTCCAGAAAAATATAAGACCTTATTTGATTAA

f814.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MLVKRIVGKPITMLILFSLLLMISLYTFSRLKVDLLPGIDIPQISIHVYPGASPREVEESVSRVLESGLSSVKNL  
KNIYSVSSKESSTVSLEFYHGTDLDLVLNEIRDALELVKSSLPKSKQTPRIFRYNLKNIPVMEIVINSVRPVSELK  
RYADEIIKPGLERLDGVAIVTVNGGSKRVLIEVSQNRLESYGLSLSRISIIASQNLSELSAGNILENNLEYLVEV  
SGKFKSIEEIGNVVIAYKIPDISSGINLSPIEIKLKDIANIKTDFEDLSEYVEYNGLPSISLSVQKRSDSNSIAVS  
NVVMNEIEKLKLSMPKDMKLEIASDSTDFIKASISTVNSAYFGAMLAIFVIFFLRSFRATIIIGISIPAIIVLT  
FCLMYFVNISLNIMSLAGLALGIGMVVDCSIVVIDNIYKYRQKGAKLISSSILGAQEMMLPITSSTFTSICVFGPF  
LIFKSELGVYGDFFKDFTFITIVISLGVSLLVAFILVPLVSSHVGLYTSFQKNIKNAFIRKIDAFFASIYYFLEFL  
YINLLNIVLNHKLIFGLIVFFSFIGSLLGLLDVTTFTTRGKENSITINLNFPHKTNLEYAKFYSNRFLEIVKSEA  
KGYKSIIATLRADRIITFNVLFPLKEESRDNLTSVDYDSIKYKIMNRIGNLYPEFNIEPSISGNALGGGDSIKIKI  
SANDFEYIKDYGKILVSMMLKKEIPELVNPRLSISDFQLQIGVEIDRALVYNYGIDMNTILNELKANINGVVAGQYV  
EKGLNYDIVLKLDRMDVKNLKDLEKIFITNSSGVKIPFSSSIATFEKTNKAESYRENQALTIYLNAGISPDNDLTQ  
VTAKVVDFINNKPVPHKEGITLKVEGEYNEFSNIMNQFKIIIMMAIIVVFGIMASQFESFLKPFIIIFTIPLTAIGV  
VLIHFLAGEKLSIFAAIGMLMLVGVVVNTGIVLVDYTGLLIKRGFGLREAIIESCRSRLRPILMSSLTSIIGLIPM  
AFSSSGSNELLKPIAFTFIGGMTASTFLTFLFIPMLFEIFPTCFKFQI

t814.aa

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EIRDALELVKSSLPKSKQTPRIFRYNLKNIPVMEIVINSVRPVSELKRYADEIIKPGLERLDGVAIVTVNGGSKR  
VLIEVSQNRLESYGLSLSRISIIASQNLSELSAGNILENNLEYLVEVSGKFKSIEEIGNVVIAYKIPDISSGINLS  
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LVAFILVPLVSSHVGLYTSFQKNIKNAFIRKIDAFFASIYYFLEFLYINLLNIVLNHKLIFGLIVFFSFIGSLL  
GLLDVTTFTTRGKENSITINLNFPHKTNLEYAKFYSNRFLEIVKSEA KGYKSIIATLRADRIITFNVLFPLKEESRD  
NLTSVDYDSIKYKIMNRIGNLYPEFNIEPSISGNALGGGDSIKIKISANDFEYIKDYGKILVSMMLKKEIPELVN  
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NSSGVKIPFSSSIATFEKTNKAESYRENQALTIYLNAGISPDNDLTQVTAKVVDFINNKPVPHKEGITLKVEGEYNE  
FSNIMNQFKIIIMMAIIVVFGIMASQFESFLKPFIIIFTIPLTAIGVVLIHFLAGEKLSIFAAIGMLMLVGVVVNT  
GIVLVDYTGLLIKRGFGLREAIIESCRSRLRPILMSSLTSIIGLIPMAFSSSGSNELLKPIAFTFIGGMTASTFLT  
LFFIPMLFEIFPTCFKFQI

f814.nt

ATGTTGGTAAAGAGAATAGTTGGCAAACCAATAACAATGTTGATTTTATTTTCATTGTTATTGATGATAAGTTTGT  
ATACCTTTTCAAGATTAAGAGTAGATCTTTTGCCGGAATTGACATTCCTCCAAATAAGTATTCACACTGTTTATCC  
TGGCGCTTCTCCTAGAGAAGTTGAAGAGAGTGTCTTAGAGTCCTTGAGAGTGGCTTGAGTTCGGTAAAGAATTTA  
AAAAATATATATAGTGTATCTTCCAAAGAAAGCAGCACCGTTTCACTTGAATTTTATCATGGAACCGATTAGATT  
TGGTTTTAAATGAAATTCGAGATGCTCTTGAATTTGGTAAAATCTTCATTGCCCAGCAAATCACAGACCCCAAGAAT  
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TAAATTTATCTCCTATTGAGATAAAACTCAAGATATTGCTAATATTAACCGATTTTGAAGATTTGTCTGAATA  
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GTGTTTCTCTTTTAGTTGCAATTTTTTGGTTCCTGTTTTATCAAGCCACTATGTCGGTTTTATACACAAGTTTCCA  
AAGAATATTAAGAATGCTTTTATTAGGAAAATCGATGCCTTTTTTTGCTAGTATTTATTATTTTTTAGAGTTTTTG

TABLE 1. Nucleotide and Amino Acid Sequences

TATATCAATTTATTAAATATAGTTTAAATCACAAATTGATTTTTGGGTTGATTGTTTTTTTAGTTTTATTGGCA  
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GCATTTTCTAGCGGAAGTGGAAATGAACCTCTAAAACCAATTGCATTTACTTTTATTGGCGGAATGACAGCTAGCA  
CATTTCTTACTTTGTTTTTTATTCCCATGCTTTTTGAAATTTTCCAACATGTTTCAAGTTTCAAATCTAG

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AGATTAAAAGTAGATCTTTTGCCGGGAATTGACATTCCCCAAATAAGTATTCACACTGTTTATCCTGGCGCTTCTC  
CTAGAGAAGTTGAAGAGAGTGTCTTAGAGTCCCTTGAGAGTGGCTTGAGTTCGGTAAAGAATTTAAAAAATATATA  
TAGTGATCTTCCAAAGAAAGCAGCACCGTTTCACTTGAATTTTATCATGGAACCGATTAGATTGGTTTTAAAT  
GAAATTCGAGATGCTCTTGAATTGGTAAATCTTCAATTGCCAGCAAATCACAGACCCCCAAGAATTTTATAGATACA  
ATCTTAAAAACATCCCTGTAATGGAAATGTTATTAAATCTGTAAGGCCAGTTTCTGAGCTTAAAAAGATATGCCGA  
TGAAATCATTAACCTGGGCTTGAAAGGCTTGATGGAGTTGCAATTGTTACTGTAAATGGTGGAAAGTAAAAAGCGT  
GTTTTAATTGAAGTTTCTCAAAACAGGCTGGAGTCTTATGGGCTTCTTTGTCAAGAATATCTTCAATTATAGCAT  
CCCCAAATTTGGAACCTTTCAGCTGGCAATATATTGGAGAACAACTTGAATATTTGGTTGAAGTTTCTGAAAAAT  
TAAATCAATTGAAGAGATAGGTAATGTGGTCATAGCTTATAAGATACCCGACATTTCTTCTGGCATAAATTTATCT  
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GAATGAAATAGAAAAATTGAAATTATCTATGCCTAAAGATATGAAATTGGAGATTGCTTCTGATAGTACTGATTTT  
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GAGAAAAATCAAGCTTTAACCATTATCTTAATGCGGGTATTTCTCCAGATGATAATTTAACCCTAAGTAACCGCAAA  
AGTTGTAGATTTTATTAATAATAAGGTGCCCCATAAAGAAGGCATAACTCTTAAGGTTGAAGGAGAATATAATGAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTTTCAAATATCATGAATCAGTTTAAAATAATCATTATGATGGCTATTATTGTTGTGTTTGGTATTATGGCTTCTC  
AATTTGAATCTTTTTTAAAACCCCTTTATTATTATTTTACAAATTCCTTTAACGGCAATAGGGGTTGTGCTTATACA  
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GGAATTGTTCTTGTAGACTATACTGGTTTATTGATCAAGAGGGGATTGGCCTAAGAGAAGCAATTATGAATCTT  
GTCGTTCAAGGCTTAGGCCAATTTTAATGTCTTCTTTGACCTCAATAATAGGGCTTATTCCAATGGCATTTTCTAG  
CGGAAGTGGAATGAACCTCTAAAACCAATTGCATTTACTTTTATTGGCGGAATGACAGCTAGCACATTTCTTACT  
TTGTTTTTTATTCCCATGCTTTTTGAAATTTTCCAACATGTTTCAAGTTTCAAATCTAG

f818.aa

MLKNHSLKLIQLKVMMIYLKKMGNDMTKFYNYRIEIVSNLSLELDVFECIEKIEQELGESIYYSKIGNVYGKGKK  
GEKHGNGVWPEENFILIIYTSNQSIVERLKDIDVDDLNRSYPTEGINLFLVRNS

t818.aa

KKMGNDMTKFYNYRIEIVSNLSLELDVFECIEKIEQELGESIYYSKIGNVYGKGKKGEKHGNGVWPEENFILIIYT  
SNQSIVERLKDIDVDDLNRSYPTEGINLFLVRNS

f818.nt

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AAATTCCTAA

t818.nt

AAGAAGATGGGGAATGATATGACTAAATTTTATAATTATAGGATTGAAATAGTTTCTAACTTATCTTTAGAGCTTG  
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TCCAATCAGTCTATTGTTGAGCGATTAAAGGATATTGTGGATGATTTGAATCGTTCTTACCCTACAGAAGGGATTA  
ATCTTTTTGTTTTGAGAAATTCCTAA

f820.aa

MLNNTYRIKTILTIFLAITLLTIYKYFTLMAFNNSPDNTISLKSNDIAKRGTIYDRNGKPIAFSSKSYSIGTNPQK  
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NITGFVGTDLNLGLEIEFSLNSILGKDKTKQQLNEEPETNNIHLTIDMDIQQGVSKI AKKYFKENNPESLITLVM  
NSQNGEILSMVQFPQYDANFYSKYPEEIRKNLSSSLTYEPGSINKIFTVAII LESGKLNLEEKFLDNIGIYQKQFPS  
GEKITIKTLNPPYKHIDSTEILYSSNVGIAYITEKVSNEYFYKLLDFGFGKVGVPFPGETKGLLNHYSKWSGR  
SKATIGFGQEIGVSAVQILQAASILSNNGIMLKPRI IKKISNDKGENIKEFDKEEIRKVISKNSAQKVLKMMREVV  
NKG GIPNLKIKNLDISAKSGTSQAIDRKTGKYSEEDYTSSILAIYPTEQPKYIIYIVYRYPKKIIYGTRIAAPMAK  
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SPNTKLEDITELELYLK

t820.aa

FNNSPDNTISLKSNDIAKRGTIYDRNGKPIAFSSKSYSIGTNPQK IENIVSTSETLGAILQINSRILKEKLSSNKG  
FLYIKRKIKREESDLIKRIQAEGRLSNITLYPDYTRIYPFRNTTSNITGFVGTDLNLGLEIEFSLNSILGKDKTKQ  
QQLNEEPETNNIHLTIDMDIQQGVSKI AKKYFKENNPESLITLVMNSQNGEILSMVQFPQYDANFYSKYPEEIRKN  
LSSSLTYEPGSINKIFTVAII LESGKLNLEEKFLDNIGIYQKQFPSGEKITIKTLNPPYKHIDSTEILYSSNVGIA  
YITEKVSNEYFYKLLDFGFGKVGVPFPGETKGLLNHYSKWSGRSKATIGFGQEIGVSAVQILQAASILSNNGIM  
LKPRI IKKISNDKGENIKEFDKEEIRKVISKNSAQKVLKMMREVVNKG GIPNLKIKNLDISAKSGTSQAIDRKTGK



TABLE 1. Nucleotide and Amino Acid Sequences

YSEEDYTSSILAIYPTEQPKYIIYIVYRYPKKIIYGTRIAAPMAKEIIIEFIEHQONTIAYKKIKMPSKIKIPKAET  
NYKNKTYLPNFINLSKREAIIDILKYKNTMKIKINGDGFVYKQSI SPNTKLEDITELELYLK

f820.nt

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AACAAATTTATGATAGAAATGGCAAACCAATAGCATTCCTCTTCAAAATCCTACTCAATTGGTACAAATCCTCAAAAA  
ATAGAAAATATTGTAAGCACATCTGAAACTCTTGGTGCAATACTTCAAATTAATTCAAGAATTTTAAAGGAAAAGC  
TTTCTCTAACAAGGGTTTTTATATATAAAAAAGAAAAATAAAAAAGAGAAGAATCAGATTTAATAAAAAAGAAATTC  
AGCTGAAGGCAGGCTTTCAAACATCACTTTATATCCTGATTACACAAGAATTTATCCCTTCAGGAATACCACAAGC  
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CAATGTTGGAATAGCTTACATTACTGAAAAAGTTAGCAATGAATACTTTTATAAAAAAATTTTAGATTTTGGCTT  
TGGGGAAGAAAGTTGGAGTTCCATTTCCCGGAGAAACAAAAGGACTGCTAAATCATTATTCAAAATGGTCAGGACGA  
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GCAATAATGGAATAATGCTAAAACCTAGAATAATAAAAAAATAAGCAACGATAAAGGAGAAAATATTAAAGAATT  
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GAAATAATAGAATTTATTGAGCACCAACAAAATACAATAGCATATAAAAAAATTAATATGCCATCAAAAAATCAAGA  
TCCCTAAAGCTGAAACTAATTACAAAAACAAAACATACTTACCAATTTTATCAACCTTTCTAAAAGAGAAGCAAT  
AGACATACTAAAATACTATAAAAAATACTATGAAAATAAAAAATAATGGCGATGGATTTGTTTACAAGCAAAGTATA  
TCCCCCAATACAAAATTAGAAGATATAACAGAGCTTGAAGTGTATTTAAATAA

t820.nt

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CAATTTTAAATGAGGAGCCAGAAACAAACAACATCCACTTAACAATAGACATGGATATACAACAAGGTGTTAGCA  
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AATTACAAAAACAAAACATACTTACCAATTTTATCAACCTTTCTAAAAGAGAAGCAATAGACATACTAAAATACT



TABLE 1. Nucleotide and Amino Acid Sequences

ATAAAAAATACTATGAAAATAAAAATAAATGGCGATGGATTTGTTTACAAGCAAAGTATATCCCCCAATACAAAATT  
AGAAGATATAACAGAGCTTGAAGTGTATTTAAAATAA

f831.aa

MAKNLLVFFIAIIFVFSIIIVFYNSLGKDYVKS GGEIVENLEKDLNDYLNKENDAKEREKIFLRIRELISKEKEI  
SSYFISR FYLARAVYFQSQAQYDEAIKDLDIVIKAKGIESEIAFLNKAAYEKMGLKEDALLVYEDLINSTSLDFL  
KVRALLSKAILIEEKDELAVKVYEEIVKFPYENNLINMANNKILELKQN

t831.aa

YNSLGKDYVKS GGEIVENLEKDLNDYLNKENDAKEREKIFLRIRELISKEKEISSYFISR FYLARAVYFQSQAQYDE  
AIKDLDIVIKAKGIESEIAFLNKAAYEKMGLKEDALLVYEDLINSTSLDFLKVRALLSKAILIEEKDELAVKVY  
EEIVKFPYENNLINMANNKILELKQN

f831.nt

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TTAA

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AAAATTAA

f843.aa

MKAIGNAILLNMPILFSIGISIGVARMGQGTAAALGGLIGYLT FNITENYFIEAFSGLVEAETMSSVGRINFFGVQT  
LNTGIAGSLAVGLLVGYLHNKFYNM KLPKPVFFSECHFVPIV IILPFCVFLAIFFLIWSSFDDLIASLGLFVFR  
FEYFGSFLYGFLNRLLLPLGLHSILSFPFEFTSLGGVEIVNGDTVRLKNIFYAQLLDPSLGKFSSGFAKISSGFY  
LSIMFGLPGAALGVYKGI VHEDKNKVAALLFSGALTAFLTGIT EPLEFLFIFTAPLLYFVHAAYSGFALLLANFFN  
VTIGNSFSTGFLDFFMF GILQNSKTNWISVLPLGAMFFALYYFTFSWLYRYFDFQIFVTD DPFEGQEGKLES LG  
IAHLLIQGLGGFDNITKLDVCSTRLHVDV VNTLVDNLLKEAGVLKIGLVNGKVQLFYGSNVYIKN AIDTYSK  
SLFEASVMVAVDNVKKGFKTYIEMKEDKKLEKQKSGKTYKLSELED

t843.aa

RMGQGTAAALGGLIGYLT FNITENYFIEAFSGLVEAETMSSVGRINFFGVQTLNTGIAGSLAVGLLVGYLHNKFYNM  
KLPKPVFFSECHFVPIV IILPFCVFLAIFFLIWSSFDDLIASLGLFVFRFEYFGSFLYGFLNRLLLPLGLHSIL  
SFPFEFTSLGGVEIVNGDTVRLKNIFYAQLLDPSLGKFSSGFAKISSGFYLSIMFGLPGAALGVYKGI VHEDKNK  
VAALLFSGALTAFLTGIT EPLEFLFIFTAPLLYFVHAAYSGFALLLANFFNVTIGNSFSTGFLDFFMF GILQNSK  
TNWISVLPLGAMFFALYYFTFSWLYRYFDFQIFVTD DPFEGQEGKLES LGIAHLLIQGLGGFDNITKLDVCSTRL

TABLE 1. Nucleotide and Amino Acid Sequences

HVDVVTNELVDNLLKEAGVLKIGLVNGKVQLFYGSNVYYIKNAIDTYSPKSLFEASVMVAVDNVKKGFKTYIEMK  
EDKKLEKQKSGSKTYKLSELED

f843.nt

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TTGCAGCACTTCTTTCTCTGGGGCCTTGACAGCTTTTTTAAACAGGAATAACTGAGCCTTTAGAATTTTTATTTAT  
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CAAATTGGATTAGTGTATTACCTTTGGGGGCAATGTTTTTGTCTTTTATTATTTTACTTTTAGTTGGCTTTTATAG  
ATACTTTGATTTTTCAGATATTTGTTACAGACGATCCATTTTTTGAAGGCCAAGAAGGAAAGCTAGAGAGTCTCGGA  
ATTGCGCATCTTTTAAATCAAGGCTCTGGTGGATTTGATAATATTACAAAGCTTGATGTTTGTCTACAAGATTGC  
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TAATGGCAAGGTTTCACTTTTATGGATCTAATGTTTATTATATTAAAAATGCCATTGATACCTATTCTCCAAAG  
AGTCTTTTTGAAGCTAGTGTATGGTTGCAGTTGATAATGTAAAAAAGGTTTAAACTTATATTGAAATGAAAG  
AAGACAAAAAAGCTTGAAGCAAGGTAAATCAGGAAAAACCTATAAGCTTAGCGAATTAGAAGAAGATTAG

t843.nt

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TTGAGGCTTTTTTCAGGGCTTGTGTAAGCAGAGACAATGTCTTCTGTTGGGCGTATAAATTTTTTTGGTGTTCAAAC  
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TGTTACGATTGGCAATAGCTTTTCTACTGGATTTTGGATTTTTTTATGTTTGGGATACTTCAAGGAAATCTTAAG  
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GATACTTTGATTTTTCAGATATTTGTTACAGACGATCCATTTTTTGAAGGCCAAGAAGGAAAGCTAGAGAGTCTCGG  
AATTGCGCATCTTTTAAATCAAGGCTCTGGTGGATTTGATAATATTACAAAGCTTGATGTTTGTCTACAAGATTG  
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GAGTCTTTTTGAAGCTAGTGTATGGTTGCAGTTGATAATGTAAAAAAGGTTTAAACTTATATTGAAATGAAA  
GAAGACAAAAAAGCTTGAAGCAAGGTAAATCAGGAAAAACCTATAAGCTTAGCGAATTAGAAGAAGATTAG

f850.aa

MRFKKIFLIIFIISNLKVYSYNYAIQYKNEGIDKYYFEILNDGFGFSLSDFFDDLRSGLIFTYVSKYNFIIINLEA  
HMLTYRGYKDSPKSLISRTDLIEIGFMYFFPILLILINGKNFGEIDLIGIVKNLLFGDWGGHLMQSIHILINQHRP  
IPSIKSYDSYNYRGFLSFALNYSYMNFLNLNENYMDLSYFADYFIKNSIGITLKNNIGFDIKLYSQIQNQIKSLKT  
YSKTQEAETGIGINYQFYSKNFFITNNLNINNFSTKENFLSVGGFGIIITPEEYKKISESNNEFNVISNNFYFGFD  
IMIPLKIRNSLFYKINENINHYFSISTNYTYNETNSFTNQLSSGIMYEFLPQKTFNPYLISGLFFAYNQNNKDI  
KSISRPIRIKNIQVGIENELGFLFKMLKYRNTHEYIFKIYSKVNYIPIAYNLDEKKLEKHSINFNYLGIGIVVK

TABLE 1. Nucleotide and Amino Acid Sequences

t850.aa

YSYNYAIQYKNEGIDKYYFEILNDGFGFSLSDFFDDLRSGLIFTYVSKYNFIINLEAHMLTYRGYKDSPKSLISR  
TDLIEIGFMYYPILLLLINGKNFGEIDLIGIVKNLLFGDWGGHLMQSIIHLILNQHRPIPSIKSYDSYNYRGFLSF  
ALNYSYMNFLNLNENYMDLSYFADYFIKNSIGITLKNENIGFDIKLYSQIQNQIKSLKTYSKTQEAETGIGINYQFY  
SKNFFITNNLNIKNFSTKENFLSVGGFGIIITPEEYKKISESNNEFNVISNNFYFGFDIMIPKIRNSLFYKINEN  
INHYFSISTNYTNYNETNSFTNQLSSGIMYEFLPQKTFNPYLISGLFFAYNQNNKDIKSISRPIRIKNIQVQIE  
NELGFLFKMLKYRNTHEYIFKIIYSKVNYIPIAYNLDEKKLEKHSINFNYLGIGIVVK

f850.nt

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TTTTGATGACTTGAGAAGTGGTTCTCTTATTTTACCTATGTTTCAAATACAATTTTATAATAAATTTAGAAGCA  
CACATGTTAACCTATAGGGGTATAAAGACTCTCCGAAATCTTTAATTAGTAGAACAGACTTAATTGAAATAGGCT  
TCATGTACTATTTTCCAATTTTATTGCTAATTAATGGAAGAAATTTTGGAGAAATAGACTTGGAATTGGAGTTAA  
AACTTATTATTTGGAGACTGGGGAGGGCATTAAATGCAAAGCATAATTCACCTCATTTTAAATCAACACCGTCCA  
ATTCCAAGTATAAAAAAGCTACGACAGCTACAATTATAGAGGATTTTAAAGCTTGTCTCTAAATTACTCTTACATGA  
ATTTTTTAAATTTAGAAAATTATATGGACTTATCTTATTTTGCAGATTATTTTATTAACAGTATTGGAATTAC  
CTTAAAAAATGAAAAATTTGGATTGATATAAACTTTATTTCCCAAAATTCAAAATCAAATCAAAGCCTCAAAACA  
TATTCAAAAACACAAGAAGCAGAAACAGGAATTGGAATAAATTATCAATTTTACTCTAAAAATTTTTTCATAACCA  
ATAATTTAAACATTAAAAATTTTCAACCAAAGAAAATTTCTTAAGCGTTGGGGGATTTGGAATAATCATTACACC  
TGAAGAATACAAAAAATATCAGAATCAAATAATGAATTTAATGTTATAAGTAATAATTTTACTTTGGATTGAT  
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CAACAAATTATTACACTAATTATAATGAACTAATAGCTTTACAAATCAATTATCATCAGGCATCATGTATGAATT  
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AAAAGCATCTCAAGACCAATAAGAATAAAAAACATTCTTCAAGTTGGAATTGAAAATGAATTAGGATTTTGTTC  
AAATGCTAAAATACCGCAACACTGAGTATATTTTCAAATATATTCAAAAGTTAACTATATTCCTATAGCTTATAA  
CTTAGATGAAAAAAATTAGAAAAACATTCTATTAACCTTAAATTATTTAGGAATTGGAATAGTCGTTAAATAA

t850.nt

TATTCTTATAATTATGCAATCCAATATAAAAAATGAAGGTATTGACAAATATTATTTTGAAATACTAAATGATGGAT  
TCGGATTTTCATTAAGCGATTTTTTTGATGACTTGAGAAGTGGTTCTCTTATTTTACCTATGTTTCAAATACAA  
TTTTATAATAAATTTAGAAGCACACATGTTAACCTATAGGGGTATAAAGACTCTCCGAAATCTTTAATTAGTAGA  
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TAATTTTTTACTTTGGATTGATATTATGATCCCATTAATAAAGAAATTCATTATTTTATAAAATAAATGAAAAC  
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TAATCAAAACAATAAAGATATCAAAGCATCTCAAGACCAATAAGAATAAAAAACATTCTTCAAGTTGGAATTGAA  
AATGAATTAGGATTTTGTTCAAAATGCTAAAATACCGCAACACTGAGTATATTTTCAAATATATTCAAAGTTA  
ACTATATTCCTATAGCTTATAACTTAGATGAAAAAAATTAGAAAAACATTCTATTAACCTTAAATTATTTAGGAAT  
TGAATAGTCGTTAAATAA

f853.aa

MKSFLFWVILGTVGISSFAQNTPVAIINLYKNEIITKTGFDSKVDIFKKTQGRDLTDAEKKQVLQVLIADVLFSQE  
ASKQGIKISDDEVMQTIRTQFGLVNFTDEQIKQMIKQGTNWGELLSSMKRSLSSQKLVLKQAQPKFSEIKTPSEK  
EIVEYYEANKTKFVNPDISRVSHIFFSTKDKKRSVDLDQAKNILSQIRSKKITFEEAVRKYSNDESSKAKNGDLGF

TABLE 1. Nucleotide and Amino Acid Sequences

LSRGDQNAQNLLGADVFVKEVFNFNKGDISSPIASKEGFHIVKVTEKYAQRFLGLNDKVSPTADLIVKDAIRNNMIN  
VQQQQIVVQVQQDMYGKLNKSANIQLDSSLK

t853.aa

QNTPVAIINLYKNEIITKTGFDSKVDIFKKTQGRDLTDAEKKQVLQVLIADVLFSSQEASKQGIKISDDEVMTIRT  
QFGLVNFTDEQIKQMIKQGTNWGELLSSMKRSLSSQKLVLKQAQPKFSEIKTPSEKEIVEYYEANKTKFVNPDIS  
RVSHIFFSTKDKKRSVDLDQAKNILSQIRSKKITFEEAVRKYSNDESSKAKNGDLGFLSRGDQNAQNLLGADVFKE  
VFNFNKGDISSPIASKEGFHIVKVTEKYAQRFLGLNDKVSPTADLIVKDAIRNNMINVQQQQIVVQVQQDMYGKLN  
KSANIQLDSSLK

f853.nt

ATGAAGAGTTTTTTATTTTGGGTAATATTGGGAACTGTAGGGATTAGCTCTTTTGCTCAAAAATACTCCTGTTGCTA  
TTATTAATTTATATAAGAATGAAATTATTACTAAAACCTGGTTTTGATTCTAAGGTTGATATATTTAAAAAGACCCA  
AGGTAGAGACTTAAGTATGCTGAGAAAAAGCAAGTTCTGCAAGTTTAAATAGCAGATGTTCTTTTAGTCAAGAG  
GCTTCAAAGCAAGGAATTTAAATCTCAGATGATGAGGTTATGCAAACAATTAGAACTCAATTTGGGCTTGTGAATT  
TTACTGATGAACAAATCAAGCAAATGATAGAAAAACAAGGTACAAATTGGGGCGAGCTTTTGTCTTCAATGAAAAG  
ATCTCTGTCTTCTCAAAAGCTTGTTTTAAAGCAAGCTCAGCCTAAGTTTTCTGAAATTTAAACTCCTAGTGAGAAA  
GAAATTGTTGAGTATTATGAGGCTAATAAACTAAGTTTGTAAATCCCGATATTTCAAGAGTTAGTCATATCTTTT  
TTTCTACTAAAGATAAAAAAGATCAGATGTTTTAGATCAAGCAAAAAATATTTTAAGCCAAATAAGATCAAAAAA  
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TTATCAAGAGGTGATCAAAATGCTCAAAATCTTCTTGGAGCCGATTTTGTGAAAGAGGTTTTTAATTTTAATAAGG  
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GTTCAACAACAGCAAATTGTTGTTCAAGTACAGCAAGATATGTATGGTAAGCTTAACAAGTCTGCAAAATATACAAA  
TCTTGGATTCTAGTCTAAAAATA

t853.nt

CAAAATACTCCTGTTGCTATTATTAATTTATATAAGAATGAAATTATTACTAAAACCTGGTTTTGATTCTAAGGTTG  
ATATATTTAAAAAGACCCAAGGTAGAGACTTAAGTATGCTGAGAAAAAGCAAGTTCTGCAAGTTTAAATAGCAGA  
TGTTCTTTTTTAGTCAAGAGGCTTCAAAGCAAGGAATTTAAATCTCAGATGATGAGGTTATGCAAACAATTAGAACT  
CAATTTGGGCTTGTGAATTTTACTGATGAACAAATCAAGCAAATGATAGAAAAACAAGGTACAAATTGGGGCGAGC  
TTTTGTCTTCAATGAAAAGATCTCTGTCTTCTCAAAAGCTTGTTTTAAAGCAAGCTCAGCCTAAGTTTTCTGAAAT  
TAAACTCCTAGTGAGAAAGAAATTGTTGAGTATTATGAGGCTAATAAACTAAGTTTGTAAATCCCGATATTTCA  
AGAGTTAGTCATATCTTTTTTTCTACTAAAGATAAAAAAGATCAGATGTTTTAGATCAAGCAAAAAATATTTTAA  
GCCAAATAAGATCAAAAAAATTACTTTTGAAGAAGCTGTAAGAAAAATATTCAAATGACGAATCTTCTAAGGCTAA  
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GTTTTTAATTTTAATAAGGGTGATATATCTTCGCCTATTGCTTCAAAGGAAGGGTTTCATATTGTTAAAGTTACAG  
AAAAATATGCTCAGAGATTTTLAGGTTTGAATGATAAAGTGCTCTCTACTGCAGATTTGATTGTCAAAGATGCAAT  
AAGAAATAACATGATTAATGTTCAACAACAGCAAATTGTTGTTCAAGTACAGCAAGATATGTATGGTAAGCTTAAC  
AAGTCTGCAAAATATACAAATCTTGGATTCTAGTCTAAAAATA

f859.aa

MKLPKLYKLILLFLFTTRLFSVKDEKSDNKLELFSNVETKIKKNSKNYDSNSNSKKIKKESILKRD TNSEKNINSN  
IYIQSKSKINYPNRLGNNINQKTANDVNFTKTSYVKVYPNYKDDNFQEIKNANKFPAKTEKTHMLIGPILKDNLG  
IIIKMLKTKGYTLIEYIEDNN

t859.aa

VKDEKSDNKLELFSNVETKIKKNSKNYDSNSNSKKIKKESILKRD TNSEKNINSNIYIQSKSKINYPNRLGNNIN  
QKTA

f859.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAATTACCAAACTTTACAAATTAATACTACTCTTTCTTTTACAACAAGATTGTTTTTCAGTAAAAGATGAAA  
AATCAGACAATAAATTGGAATTATTTTCAAACGTAGAAAACAAAAATCAAAAAAATTCTAAAAATTACGACTCAAA  
TTCAAACAGCAAAAAGATCAAAAAAGAATCAATTTTAAAAAGAGATACAAACAGCGAAAAAATATAAATTCCAAT  
ATATACATACAAAAATCAAAAAAATTAATTACCCCAACAGAAATTTAGGCAATAATATCAATCAAAAACTGCAA  
ATGATGTAAATTTTACAAAACTAGTTATGTTAAAGTTTATCCCAACTATAAAGACGATAACTTTCAAGAAATTAA  
AAATGCTAATAAATTTCCAGCTAAAACCGAAAAAATCACAATGCTAATCGGCCCAATATTAAAAGATAATCTAGGA  
ATAATAATTAAAATGCTAAAAACAAAGGGATACACTTTAATAGAATACATAGAGGACAATAATTAA

t859.nt

GTAAAGATGAAAAATCAGACAATAAATTGGAATTATTTTCAAACGTAGAAAACAAAAATCAAAAAAATTCTAAAA  
ATTACGACTCAAATTCAAACAGCAAAAAGATCAAAAAAGAATCAATTTTAAAAAGAGATACAAACAGCGAAAAA  
TATAAATTCCAATATATACATACAAAAATCAAAAAAATTAATTACCCCAACAGAAATTTAGGCAATAATATCAAT  
CAAAAACTGCAATGATGTAAATTTTACAAAACTAGTTATGTTAAAGTTTATCCCAACTATAAAGACGATAACT  
TTCAAGAAATTAAAAATGCTAATAAATTTCCAGCTAAAACCGAAAAAATCACAATGCTAATCGGCCCAATATTAA  
AGATAATCTAGGAATAATAATTAAAATGCTAAAACAAAGGGATACACTTTAATAGAATACATAGAGGACAATAAT  
TAA

f861.aa

MKNFKEVIIIFDSGIGGLSYFKYIKSRIGGCQYVYVADNKNFPYGEKSPEYLLLEAVLFLIEKLKKIYNIGALVLAC  
NTISVSVYNKLNLFVFPVYVTLDPVSSVSDLVLKRVLLIATNTTLESKFVKDQVNIHNDLIVKAAGELVNFVEYGEN  
YKKYALRCLEALKFEVNTGREIVFLGCTHYLHLKVMIEDFLKIPVYENRELVVKNLIRSMNFSEHKGNYYKNDFFD  
FVDDEFYLTENKNLTFYQNFCKKYNLRFKGMIV

t861.aa

RIGGCQYVYVADNKNFPYGEKSPEYLLLEAVLFLIEKLKKIYNIGALVLACNTISVSVYNKLNLFVFPVYVTLDPVSS  
VSDLVLKRVLLIATNTTLESKFVKDQVNIHNDLIVKAAGELVNFVEYGENYKKYALRCLEALKFEVNTGREIVFL  
GCTHYLHLKVMIEDFLKIPVYENRELVVKNLIRSMNFSEHKGNYYKNDFFD FVDDEFYLTENKNLTFYQNFCKKYNL  
RFKGMIV

f861.nt

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AATACAATTTCTGTTAGTGTATACAATAAATTAAATTTTGTGTTTTCCAGTAGTCTATACTTTGCCAGATGTAAGTT  
CAGTTTCAGATCTTGTTTTAAAAAGAGTTCTTTTGATTGCAACAAATACTACTCTTGAAAGCAAATTTGTTAAGGA  
TCAAGTAAATATACATAATGATTTGATTGTAAAGCTGCTGGAGAGCTTGTAATTTTGTTGAATATGGAGAGAAT  
TACAAAAAATATGCTCTTAGATGTTTAGAAGCTTTAAATTTGAAGTTGTAAATACTGGTAGAGAAATGTTTTTTC  
TTGGATGCACGCATTATTTGCATCTTAAGGTAATGATAGAAGATTTTTTAAAAATTCCTGTTTATGAGAATCGTGA  
ATTAGTGGTAAAAAATCTTATTAGATCAATGAATTTTTCTGAACACAAAGGTAATTATTATAAGAATGATTTTGAT  
TTTGTAGATGATGAGTTTTATTGACCGAAAATAAAAATTTGACTTTTTATCAAAATTTTGCAAAAAATATAATC  
TTCGCTTTAAGGGAATGATAGTTTGA

t861.nt

AGAATAGGGGGATGCCAATATGTTTATGTTGCCGATAATAAAAAATTTCCCTTATGGAGAAAAAAGTCCTGAATATC  
TTCTAGAAGCAGTTTGTGTTTTGATTGAGAAGCTTAAAAAATCTATAATATTGGTGCAATTAGTTTTGGCTTGTA  
TACAATTTCTGTTAGTGTATACAATAAATTAAATTTTGTGTTTTCCAGTAGTCTATACTTTGCCAGATGTAAGTTCA  
GTTTCAGATCTTGTTTTAAAAAGAGTTCTTTTGATTGCAACAAATACTACTCTTGAAAGCAAATTTGTTAAGGATC  
AAGTAAATATACATAATGATTTGATTGTAAAGCTGCTGGAGAGCTTGTTAATTTTGTTGAATATGGAGAGAATTA  
CAAAAAATATGCTCTTAGATGTTTAGAAGCTTTAAATTTGAAGTTGTAAATACTGGTAGAGAAATGTTTTTCTT  
GGATGCACGCATTATTTGCATCTTAAGGTAATGATAGAAGATTTTTTAAAAATTCCTGTTTATGAGAATCGTGAAT

TABLE 1. Nucleotide and Amino Acid Sequences

TAGTGGTAAAAAATCTTATTAGATCAATGAATTTTTCTGAACACAAAGGTAATTATTATAAGAATGATTTTGATTT  
TGTAGATGATGAGTTTTATTGACCGAAAATAAAAAATTTGACTTTTTATCAAAATTTTTGCAAAAAATATAATCTT  
CGCTTTAAGGGAATGATAGTTTGA

f363.aa

MIRLKVLI LCLFGIFVLNGFADTNFEFNFGGGVAFVSPFSSFYNEALEINAKLKQNLPSDLSPIEKEEIVQNFS  
DLANIAGIRYGTYAQFGAKFDDFVSIGFELLFNINLLKAIKRS DGTANENFSFIMAITPRFYTKLDFFVLALAFF  
TGP KINIATSSADSVLAE LGTMGWDIGARLSFSFLILEGYVWNINPKFSDFKFGIGFEFGIV

t363.aa

DTNFEFNFGGGVAFVSPFSSFYNEALEINAKLKQNLPSDLSPIEKEEIVQNFSDLANIAGIRYGTYAQFGAKF  
DDFVSIGFELLFNINLLKAIKRS DGTANENFSFIMAITPRFYTKLDFFVLALAFFTGP KINIATSSADSVLAE LGT  
MGWDIGARLSFSFLILEGYVWNINPKFSDFKFGIGFEFGIV

f363.nt

ATGATTAGGCTTAAAGTTTTAATTTTGTGTTTATTTGGGATTTTTGTGTAAATGGTTTTGCAGATACTAATTTTG  
AATTC AATTTTGGTGGTGGGGTTGCTTTTCCTGTAGTCCCTTTTCAAGCTTTTACAATGAGGCTTTAGAGATTAA  
TGCAAAGCTTAAGCAAAATTTGCCTTCAGATTTATCCCCAATAGAAAAAGAAGAGATAGTCCAAAATTTTCCGAT  
TTAGCCAATATTGCTAAAGCTGGAATAAGATATGGAACCTACGCTCAATTTGGCGCTAAATTTGATGATTTTGT  
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GAATTGTGTAG

t363.nt

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CTGCAAAATGAAAATTTCTCGTTTATTATGGCAATAACACCAAGATTTTATACAAAATTAGATTTTTTGTTTTAGC  
TTTAGCGTTTTTCACAGGTCCTAAGATCAATATAGCGACTTCTTCTGCGGATTCTGTTT TAGCAGAACTGGGAACA  
ATGGGCTGGGATATTGGTGCTAGACTTTCATTTTCTTTTTTAATCTTGAAGGGTACTATGTTTGAATATTAAAA  
ACCCTAAATTTTCTGATTTCAAGTTTGAATAGGTTTTGAATTTGAATTTGTGTAG

f368.aa

MIDL TQEQEILIKNKFLAKVFLMSIGLLISAVFAYATSENQTIKAIIFSNSMSFMAMILIQFGLVY AISGALNK  
ISSNTATALFLLYSALTGVTLSSIFMIYTQGSIVFTFGITAGTFLGMSVYGYTTTDLTKMG SYLIMGLWGIIIAS  
LVNMFRRSSGLNFLISILGVVIFTGLTAYDVQNI SKMDKMLQDDTEIKNRMAVVASLKLYLDFINFLYLLRFLGQ  
RRND

t368.aa

TSENQTIKAIIFSNSMSFMAMILIQFGLVY AISGALNKISSNTATALFLLYSALTGVTLSSIFMIYTQGSIVFTFG  
ITAGTFLGMSVYGYTTTDLTKMG SYLIMGLWGIIIASLVNMFRRSSGLNFLISILGVVIFTGLTAYDVQNI SKMD  
KMLQDDTEIKNRMAVVASLKLYLDFINFLYLLRFLGQRRND

f368.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGATCGATTTAACACAAGAAAAACAAGAAATACTAATAAAAAACAAGTTTTAGCCAAAGTTTTCGGGCTTATGT  
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AAATTCAATGTCATTTATGGCTATGATACTTATACAATTTGGACTTGTATATGCAATAAGTGGTGCTCTTAATAAA  
ATATCAAGCAATACTGCAACAGCTCTTTTCTTGCTCTACTCAGCACTAACAGGAGTAACATTATCTTCTATATTTA  
TGATTTACACACAAGGATCAATAGTATTCACATTCGGAATTACTGCTGGAACATTTCTTGGAATGTCTGTTTATGG  
ATACACTACAACAACAGATCTAACAAAAATGGGAAGCTATTTAATAATGGGCTTATGGGGAATCATTATTGCATCT  
CTTGTTAATATGTTTTTTAGAAAGCTCAGGTCTTAATTTCTTATATCTATTTTGGGCGTAGTTATATTTACAGGCT  
TAACAGCTTATGATGTTCAAAATATTTCTAAAAATGGACAAAATGCTACAAGACGACACTGAAATAAAAAACAGAAT  
GGCGGTTGTAGCCTCACTTAACTTTATTTAGATTTTATAAATTTATTCTTATATCTTCTAAGATTTTGGGCCAA  
AGAAGAAACGATTAA

t368.nt

ACCTCAGAAAATCAAACAATCAAAGCAATAATATTCTCAAATTCATGTCATTTATGGCTATGATACTTATACAAT  
TTGGACTTGTATATGCAATAAGTGGTGCTCTTAATAAAATATCAAGCAATACTGCAACAGCTCTTTTCTTGCTCTA  
CTCAGCACTAACAGGAGTAACATTATCTTCTATATTTATGATTTACACACAAGGATCAATAGTATTCACATTCGGA  
ATTACTGCTGGAACATTTCTTGGAATGTCTGTTTATGGATACACTACAACAACAGATCTAACAAAAATGGGAAGCT  
ATTTAATAATGGGCTTATGGGGAATCATTATTGCATCTCTTGTTAATATGTTTTTTAGAAAGCTCAGGTCTTAATTT  
CCTTATATCTATTTTGGGCGTAGTTATATTTACAGGCTTAACAGCTTATGATGTTCAAAATATTTCTAAAAATGGAC  
AAAATGCTACAAGACGACACTGAAATAAAAAACAGAATGGCGGTTGTAGCCTCACTTAACTTTATTTAGATTTTA  
TAAATTTATCTTATATCTTCTAAGATTTTTGGGCCAAAGAAGAAACGATTAA

f371.aa

MKFFFLQIALILLSNSSLLFGQSPPEKEDSLLLYKEGKFKEAILNTLEEIRLNPSNLDARTILIWSLIAIGEYK  
RAEKEAIIIGLGIKKHDIRIIQALGEAYFFQKNYDNALKYFQEYISLDSKGARI IKVYNLIADSFYELKRYNEADFA  
YEHALRFSPNNQNLLIKLARSINAKNKILAEALIKILTISPNNLEAKNLLEELKKSNNKP

t371.aa

EDSLLLYKEGKFKEAILNTLEEIRLNPSNLDARTILIWSLIAIGEYKRAEKEAIIIGLGIKKHDIRIIQALGEAYFF  
QKNYDNALKYFQEYISLDSKGARI IKVYNLIADSFYELKRYNEADFAYEHALRFSPNNQNLLIKLARSINAKNKI  
LAEEALIKILTISPNNLEAKNLLEELKKSNNKP

f371.nt

ATGAAATTTTTTTTTCTATTACAAATAGCTTTAATTCTACTATCCAATTCAAGCTTGTTATTTGGACAATCACCGC  
CTAAAGAAAAAGAAGACTCTCTTCTTCTATATAAAGAAGGAAAATTTAAAGAAGCTATTTTAAACACGTTAGAAGA  
AATTCGACTAAATCCTAGTAACCTTAGATGCTAGGACAATATTGATATGGAGCTTAATAGCCATAGGAGAATACAAG  
AGAGCTGAAAAAGAGGCGATTATAGGACTTGGCATTAAAAAACATGACATAAGAATTATTCAAGCACTAGGAGAAG  
CTTATTTCTTTCAAAAAAATTATGACAATGCATTAAAAATCTTTCAAGAATACATTAGCCTTGATTCTAAAGGAGC  
AAGAATAATAAAAGTTTATAATTTAATTGCAGATTCTTTTATGAGCTAAAAAGATATAATGAAGCCGATTTTGCA  
TACGAACATGCATTACGTTTTTCTCCTAATAACCAAAATCTATTAATAAAATTAGCAAGATCAAGAATAAATGCAA  
AAAATAAAATATTAGCAGAAGAAGCACTAATTAAAATCTTACAATCTCTCCTAATAATCTAGAGGCAAAAAATTT  
ACTAGAAGAATTAAAAAAAGCAACAACAACCTTGA

t371.nt

GAAGACTCTCTTCTTCTATATAAAGAAGGAAAATTTAAAGAAGCTATTTTAAACACGTTAGAAGAAATTCGACTAA  
ATCCTAGTAACCTTAGATGCTAGGACAATATTGATATGGAGCTTAATAGCCATAGGAGAATACAAGAGAGCTGAAAA  
AGAGGCGATTATAGGACTTGGCATTAAAAAACATGACATAAGAATTATTCAAGCACTAGGAGAAGCTTATTTCTTT  
CAAAAAAATTATGACAATGCATTAAAATACTTTCAAGAATACATTAGCCTTGATTCTAAAGGAGCAAGAATAATAA  
AAGTTTATAATTTAATTGCAGATTCTTTTATGAGCTAAAAAGATATAATGAAGCCGATTTTGATACGAACATGC  
ATTACGTTTTTCTCCTAATAACCAAAATCTATTAATAAAATTTAGCAAGATCAAGAATAAATGCAAAAAATAAATA  
TTAGCAGAAGAAGCACTAATTAATTTCTTACAATCTCTCCTAATAATCTAGAGGCAAAAAATTTACTAGAAGAAT  
TAAAAAAGCAACAACAACCTTGA

TABLE 1. Nucleotide and Amino Acid Sequences

f502.aa

MKKANFLSTNFLILLVCFVNVNLFSDKDIFKFKLVDQFFPFYKNNKGEYEGLIIFSILDKWAKDNNADIMVEHIDN  
LNESEIEDEAIYLGITYNVKLNDFYFYSKSELARSISILFFKNSNKKYKNTHSTFLSNFNIGVIKNTIYEDILRLKN  
VNTIFLADNSQELVLALKNKVDYIYGDKTLHYIANNFLSEDLVIFTGDVFYSIKNRVAISRNAPEIVKLNLDL  
FSYLMKMPPELVFSFLDSNAKGSFVDVGLYNDYPPLSFINSQKLSGILVDLWNLLSRQHIFKPIFKGFSKEDIKK  
SLDGKSVGIFGGIISNDSVLENNVYVVSPIYPLNFKFYSKDLSNDAGPINSQFIDFNFNNIQLNKNKDIVNNFID  
IVNNSYGFIEENSITTKYLLKLNGYNGRLKSYDSIFNKNRFLVLAIDNRIYKVIKYLNSIFDDISFESLLQIDKNW  
LDKEEINSSRINSYKIMNKVKFNIEEKIWLKSKNNKLNLA VKNWYPIDYVEANNYKGINQFLDKIRMFSGLRFNII  
KVHSSLDLKKLIKSGKIDMLNTNATDSNLDNVFNILKNSRIPLYIFSNKKRVLPSRSLEKFAILDFLYSKNLASNI  
KSKLILVSSFNALLLLKYGKVDGIIISDEYTAAAVFEELNIDDVEKIPTFRDLAFDLSLAIYNQDYILKEIIQKV  
MRSNVDSQMYLNDWKFDIYYKRSIRFKNFKFLVITFIIFYFTFLGFVFIIFMFRLSFEQKRRYSFVMNEKKIAEAA  
NAAKTIFIANVSHDIRTPINGIMAATELLDITLTDVQKDYVRMINYSSDLSLLSIDDILYLSKIDVNELYVESQE  
IDLESEMVLKAFQSQCAKKNIDLFSYSKSIFFNNYIKGDIVKIKQVLINLIGNAFKFTDDGVIVLNYEEVCRTRT  
DGNRVLVTVEFKVIDTGKIEKENFSKIFEIFKQEDDSSSRVHEGAGLGLSISRELIRLMGGLGIAVDSKVGEGETT  
FSFMLPFLGSELKSKLSINRFQSVNGDNKVLNVLLSQKSIKIFEHCSILLGCSSNVRYVASFEDAYKVFKKYP  
YNFVYINVNNNDNIQEGIRLANNIERLNSDVQIIFLFYYLDNKALKNLKYGYVKKPLMGLGICSIYKKEFNPEMDF  
EDLVPIDSALRIKEPINVLIAEDNQVNQVKLDILVVIGINENFIDVDDGVKALKSLKDKKYTISFIDIRMPRYD  
GFSVAKEIRKFEKAKNLKPCVLVAVTAHALQEYKDKCLASGMNDYISKPIHISSIKTILKKYLQFEVDDIGENENL  
NQLVKFPNLDVNRALKELNLSYVSSELCRGLVDFISINIIDLEKAFDEEDLSLIKDISHSISGALSNNRSELYKD  
FQKIETSKDSISELKKMYSFVKDDLFQLISDIKENILFESEIVSENKLYFKNNDQFLNLLNKLKLIKTRKPREYK  
EILESINKYVLDDNIQVLFSDLRRLRLYRFAESSKILEEIIEMLNKRY

t502.aa

CFVNVNLFSDKDIFKFKLVDQFFPFYKNNKGEYEGLIIFSILDKWAKDNNADIMVEHIDNNESEIEDEAIYLGITY  
NVKLNDFYFYSKSELARSISILFFKNSNKKYKNTHSTFLSNFNIGVIKNTIYEDILRLKNVNTIFLADNSQELVLAL  
KNDKVDYIYGDKTLHYIANNFLSEDLVIFTGDVFYSIKNRVAISRNAPEIVKLNLDLFSYLMKMPPELVFSFLD  
SNAKGSFVDVGLYNDYPPLSFINSQKLSGILVDLWNLLSRQHIFKPIFKGFSKEDIKKSLDGKSVGIFGGIISND  
SVLENNVYVVSPIYPLNFKFYSKDLSNDAGPINSQFIDFNFNNIQLNKNKDIVNNFIDIVNNSYGFIEENSITTKY  
LLKLNGYNGRLKSYDSIFNKNRFLVLAIDNRIYKVIKYLNSIFDDISFESLLQIDKNWLDKEEINSSRINSYKIM  
NKVKFNIEEKIWLKSKNNKLNLA VKNWYPIDYVEANNYKGINQFLDKIRMFSGLRFNIIKVHSSLDLKKLIKSGKI  
DMLNTNATDSNLDNVFNILKNSRIPLYIFSNKKRVLPSRSLEKFAILDFLYSKNLASNIKSKLILVSSFNALLLL  
YKGVKGVDGIIISDEYTAAAVFEELNIDDVEKIPTFRDLAFDLSLAIYNQDYILKEIIQKVVMRSNVDSQMYLNDWKFD  
IYYKRSIRFKNFKFLVITFIIFYFTFLGFVFIIFMFRLSFEQKRRYSFVMNEKKIAEAAANA AAKTIFIANVSHDIRT  
PINGIMAATELLDITLTDVQKDYVRMINYSSDLSLLSIDDILYLSKIDVNELYVESQEIDLESEMVLKAFQSQ  
CAKKNIDLFSYSKSIFFNNYIKGDIVKIKQVLINLIGNAFKFTDDGVIVLNYEEVCRTRTDGNRVLVTVEFKVIDTG  
KIEKENFSKIFEIFKQEDDSSSRVHEGAGLGLSISRELIRLMGGLGIAVDSKVGEGETTFSFMLPFLGSELKSKK  
LSINRFQSVNGDNKVLNVLLSQKSIKIFEHCSILLGCSSNVRYVASFEDAYKVFKKYPYNFVYINVNNNDNIQEGI  
RLANNIERLNSDVQIIFLFYYLDNKALKNLKYGYVKKPLMGLGICSIYKKEFNPEMDFEDLVPIDSALRIKEPIN  
VLIAEDNQVNQVKLDILVVIGINENFIDVDDGVKALKSLKDKKYTISFIDIRMPRYDGFSAKEIRKFEKAKNL  
KPCVLVAVTAHALQEYKDKCLASGMNDYISKPIHISSIKTILKKYLQFEVDDIGENENLNQLVKFPNLDVNRALKE  
LNLSYVSSELCRGLVDFISINIIDLEKAFDEEDLSLIKDISHSISGALSNNRSELYKDFQKIETSKDSISELKKM  
YSFVKDDLFQLISDIKENILFESEIVSENKLYFKNNDQFLNLLNKLKLIKTRKPREYKEILESINKYVLDDNIQV  
LFSDLRRLRLYRFAESSKILEEIIEMLNKRY

f502.nt

ATGAAAAAAGCAAAC TTTTAAAGTACTAATTTTTTAATTTTACTTTTGGTTTGCTTTGTCAACGTCAATTTATTTT  
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TTCAACATTTTTATCCAATTTTAAATATAGGAGTTATTAAAAATACAATATATGAAGATATCTTAAGGTTAAAAAAC  
GTTAACACCATTTTTTTGGCTGATAATTCTCAAGAGTTAGTATTGGCCTTAAAAACGATAAAGTTGATTATATAT



TABLE 1. Nucleotide and Amino Acid Sequences

ATGGTGATTGCAAGACTTTACATTATATTGCAAATAACTTTTTAAGTGAAGATCTTGTGATTTTTACCGGGGATGT  
TTTTTATAGTATCAAAAATAGAGTGGCTATTAGTAGAAATGCTCCTGAGATAGTAAAGAATTTGAATTTAGATTTG  
TTTTCATATTTAATGAAAATGCCTGAGGAACCTGTTTTTCTTTTTTAGATAGCAATGCTAAGGGAAGTTTGTG  
ATGTTGGTTTATATAATGATTATCCTCCTTAAAGTTTATTAATTCACAGGGAATTTGTCTGGCATTTTAGTGA  
TTTGTGGAATCTTCTCTCAAGACAACATATCTTTAAACCTATTTTTAAGGGATTTTCCAAAGAGGATATTAAGAAA  
TCATTAGATGGAAAATCAGTAGGTATTTTTGGAGGAATTATTAGCAATGATAGTGTGTTGGAAAATGTTAATTATG  
TAGTAAGTAAGCCAATATATCCTCTTAATTTTAAATTTTATTCATAAGACCTAAGCAATGATGCTGGTCCAATAAA  
TTCTCAGTTTATTGATTTTAATTTTAATAATATTCAATTAAATAAGAATAAAGATATTGTTAATAACTTTATAGAT  
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GTAGATTAAAATCTTACGATTCGATTTTAAATAAAAAATAGGTTTTTAGTATTAGCCATTGATAATAGGATTTATAA  
GGTTATTAAATATATCTCAATTCATATTGATGATATTCATTGTAATCTTTGCTTCAAATAGATAAAAAATG  
TTGGATAAAGAAGAGATTAAATAGTTCTAGATAAAATAGTTATAAAAATTATGAATAAGGTTAAATTTAATATAGA  
AAAAAATTTGGTTATCAAAAAATAATAAATTAAATCTTGCTGTTAAAAATTTGGTATCCAATAGATTATGTTGAGGC  
AAATAATTATAAAGGAATAAATCAATTTTTGCTTGATAAGATTAGAATGTTTTCAGGTTTGAGATTTAACATAATT  
AAAGTACACAGCAGTTTAGATCTTAAAAAATTAATCAAACTCGGAAAAATCGATATGCTAAATACTAATGCAACCG  
ATTCAAATTTAGATAATGTTTTCAACATAAAATTAATTCGCAATTCACCTTTATATTTTTTCAAATAAGAAAAG  
GGTGCTTCCATCTAGATCTTTAGAAAAGTTTGCTATACTTGATTTTTTATATAGTAAAAATTTGGCTTCTAATATT  
AAATCAAAGCTTATCTGGTAAGCAGTTTTAATGAAGCGTTGCTTCTTCTTTATAAGGGAAAGGTAGATGGGATTA  
TTAGCGATGAGTATACAGCTGCTGCTGTTTTTGAGGAATTAATATTGATGATGTTGAAAAAATTCCTACTTTTAG  
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ATGCGTTCAAATGTTGACAGTCAGATGTATTTAAATGATTGGAAATTTGATATTTATTATAAATCCAGAAGTATCA  
GGTTTAAAAATTTCAAATTTTTAGTGATAACATTCATTATATTTTATTTTACTTTTTTAGGATTTGTAATTATATT  
TATGTTTCAGATTATCATTGAGCAGAAAAGAAGATATTCCTTTGTGATGAATGAAAAAAGATTGCGGAAGCCGCT  
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CTGAGCTTTTGGATACAACATATCTTACAGATGTTCAAAAAGATTATGTTAGGATGATAAATTATTCATCTGATTC  
TTTGCTTCTTTAATTGATGATATATTGTATTTGTCTAAAAATAGATGTCATGAATTATATGTTGAGAGTCAAGAG  
ATTGATTTAGAGAGTGAAATGGAAATGGTTTTAAAGGCTTTTCAATCTCAATGTGCAAGAAAAAATATTGATTTAT  
TCTCTTATTCTAAATCTATTTTTAATAATTATATAAAGGGTGATTTGTAAAAATTAACAAGTTTTAATTAAATTT  
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GATGGTAATAGGGTTTTTGGTTACAGTTGAATTTAAGGTAATAGATACAGGCAAAGGGATTGAAAAAGAAAATTTTT  
CTAAGATATTTGAAATATTTAAACAAGAGGATGATTCTTCTTCAAGGGTTCATGAAGGTGCAGGATTGGGATTGTC  
AATATCTAGAGAGCTTATAAGACTAATGGGTGGTCTTGGTATTGCTGTTGATAGCAAGGTGGGAGAGGGTACAAC  
TTTTCAATTTATGTTGCCCTTTTTATTTGGGTAGTGAGCTTAAAGTAAAAAATTTGTCAATCAATAGATTTCAATCAG  
TAAATGGTGACAATAAAGTATTAAATGTGCTTTTAAAGTCAAAAATCTATTAAATTTTTGAGCACTGTTTCGATTTT  
ATTGGGATGCTCTTCTAATGTGCGCTATGTAGCGTCTTTTGAGGATGCTTATAAAGTCTTCAAGAAATACCCCTCT  
TATAATTTTGTTTATATAAATGTAAATAACGATAATATTCAAGAGGGTATTCGACTTGCCAATAATATTGAAAGAC  
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CAGCGCATGCTTTGCAAGAGTATAAAGACAAGTGTCTTGCAAGTGGTATGAATGATTATATCTCAAAACCAATACA  
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AATCAACTTGTTAAGTTTCCCTAATTTAGATGTTAATAGGGCTTTAAAGAATTAAATCTTTTATATGATCATATT  
CTGAATTATGTAGAGGGCTTGTGATTTTATCTCTATTAATATTTGATTTGGAAGAAAGCTTTTGTATGAGGAAGA  
TTTGTCTTTAATTAAGGATATATCTCATTCATATCTGGAGCTCTTTCTAATATGCGTAGCGAATTGTATAAAGAT  
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TTCAACTAATAAGCGACATAAAGGAAAATATTTTGTGTTGAGTCTGAGATTGTTAGTGAGAACAAGCTATATTTTAA  
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GAAATCTTGAGAGCATTAAATAATATGTTTTAGACGATAATATTCAGGTATTATTTAGTGATCTTCGCAGAAATT  
TAAGATTATATAGATTTGCTGAGAGCTCTAAGATTCTTGAAGAGATTATTGAAATGCTTAATAATAAGAGATATTA  
G

TABLE 1. Nucleotide and Amino Acid Sequences

TGCTTTGTCAACGTC AATTTATTTTCTAAGGATATTTTCAAGTTTAAAGCTTGTAGATCAATTTTTTCCTTTTTTACT  
ACAAGAATAATAAAGGAGAAATATGAAGGACTTATTTTTTCTATTTTAGATAAAATGGGCAAAAGATAATAATGCTGA  
TATTATGGTTGAGCATATTGATAATTTAAATGAAAGTGAAATTGAAGACGAAGCAATATATTTAGGATTAACCTAT  
AATGTAAAATTAAATGATTTTTTTTATTTTAAAAGTGAGCTTGCTAGGAGTATTTCAATTTTATTTTTTAAAACT  
CTAATAAAAAATATAAAAAATACCCATTCAACATTTTTATCCAATTTTAATATAGGAGTTATTAATAATACAATATA  
TGAAGATATCTTAAGGTTAAAAAACGTTAACACCATTTTTTTGGCTGATAATTCTCAAGAGTTAGTATTGGCCTTA  
AAAAACGATAAAGTTGATTATATATATGGTGATTGCAAGACTTTACATTATATTGCAAAATACTTTTTAAGTGAAG  
ATCTTGTGATTTTTTACCGGGGATGTTTTTTATAGTATCAAAAATAGAGTGGCTATTAGTAGAAATGCCTCTGAGAT  
AGTAAAGAATTTGAATTTAGATTTGTTTTTCATATTTAATGAAAATGCCTGAGGAACCTGTTTTTCTTTTTTTAGAT  
AGCAATGCTAAGGGAAGTTTTGTTGATGTTGGTTTTATATAATGATTATCCTCCTTTAAGTTTTATTAAATTCACAGG  
GAAAATTGCTCGGCATTTAGTGGAATTTGTGGAATCTTCTCTCAAGACAACATATCTTTAAACCTATTTTTTAAGGG  
ATTTTCCAAAGAGGATATTAAAGAAATCATTTAGATGGAAAATCAGTAGGTATTTTTGGAGGAATTTATTAGCAATGAT  
AGTGTGTTGGAAAATGTTAATTATGTAGTAAGTAAGCCAATATATCCTCTTAATTTTTAAATTTTTATTCTAAAGACC  
TAAGCAATGATGCTGGTCCAATAAATTTCTCAGTTTTATTGATTTTTAATTTTTAATAATATTCAATTAATAAGAATAA  
AGATATTGTTAATAACTTTATAGATATTGTTAATAATTCATATGGGTTTATAGAAAATTCATAACAACAAAATAT  
TTGTTAAAATTAAATGGATATAACGGTAGATTAAAATCTTACGATTTCGATTTTTAATAAAAAATAGGTTTTTAGTAT  
TAGCCATTGATAATAGGATTTATAAGGTTATTAAATATATTTCTCAATTCTATATTTGATGATATTTTCATTTGAATC  
TTTGCTTCAAATAGATAAAAAATTGGTTGGATAAAGAAGAGATTAATAGTTCTAGAATAAAATAGTTATAAAATTATG  
AATAAGGTTAAATTTAATATAGAAGAAAAAATTTGGTTATCAAAAAATAATAAATTAAATCTTGCTGTTAAAAATT  
GGTATCCAATAGATTATGTTGAGGCAATAATTATAAAGGAATAAATCAATTTTTGCTTGATAAGATTAGAATGTT  
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TAGTAAAAATTTGGCTTCTAATATTAAATCAAAGCTTATTTCTGGTAAGCAGTTTTAATGAAGCGTTGCTTCTTCTT  
TATAAGGGAAGGTAGATGGGATTATTAGCGATGAGTATACAGCTGCTGCTGTTTTTGAGGAATTAATATTGATG  
ATGTTGAAAAAATTCCTACTTTTAGAGATTTGGCTTTTGATTTGAGTCTTGCTATTTATAATCAAGATTATATCTT  
GAAAGAAATTATTCAAAAAGTTGTTATGCGTTCAAATGTTGACAGTCAGATGTATTTAAATGATTGGAAATTTGAT  
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CTTTTTTTAGGATTTGATAATTATATTTATGTTTCAGATTATCATTTTGAGCAGAAAAGAAGATTTCTTTTGATGAA  
TGAAAAAAGATTGCGGAAGCCGCTAATGCTGCTAAAACCATTTTTATAGCCAATGTCAGTCATGATATTCGTACC  
CCTATTAACGGAATAATGGCGGCTACTGAGCTTTTGGATACAACATTTCTTACAGATGTTCAAAAAGATTATGTTA  
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TGAATTATATGTTGAGAGTCAAGAGATTGATTTAGAGAGTGAAATGGAAATGGTTTTAAAGCTTTTCAATCTCAA  
TGTGCAAAGAAAAATATTGATTTATTTCTCTTATTTCTAAATCTATTTTTAATAATTATATAAAGGGTGATATTGTAA  
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TGAAGAAGTATGTAGAACAAGAACTGATGGTAATAGGGTTTTGGTTACAGTTGAATTTAAGGTAATAGATACAGGC  
AAAGGGATTGAAAAAGAAAATTTTTCTAAGATATTTGAAATATTTAAACAAGAGGATGATTTCTTCTCAAGGGTTC  
ATGAAGGTGCAGGATTGGGATTGTCAATATCTAGAGAGCTTATAAGACTAATGGGTGGTCTTGGTATTGCTGTTGA  
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CGACTTGCCAATAATATTGAAAGACTAAATTTCTGATGTACAAATATTTTTTTTATTTTATTATTATTTAGATAATAAAG  
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AAGCCTTGTGTTTTGGTTGCTGTAAACAGCGCATGCTTTGCAAGAGTATAAAGACAAGTGCTTGTCAAGTGGTATGA  
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TATGCGTAGCGAATTGTATAAAGATTTTCAAAAATTTGAAACAAGTAAAGATTCAATTTCTGAGTTGAAAAAATG  
TATTCTTTTGTAAAAGATGATTTATTTCAACTAATAAGCGACATAAAGGAAAATATTTTGTTTGAGCTTGAGATTG  
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TABLE 1. Nucleotide and Amino Acid Sequences

GACTAGAAAGCCAAGAGAATACAAAGAAATTCCTTGAGAGCATTAATAAATATGTTTTAGACGATAATATTCAGGTA  
TTATTTAGTGATCTTCGCAGAAATTTAAGATTATATAGATTTGCTGAGAGCTCTAAGATTCCTGAAGAGATTATTG  
AAATGCTTAATAATAAGAGATATTAG

f527.aa

MNLLVKIAKFILILFLFTSCNQKQSEIQNLTHLLKSSNKNRLDKFLIIDRVVNIYIANKNYEDALEIVNNGIIDDE  
SREYYPLYLYLMGNIYDSMGEDFVAFNIYKRVDNFDDYVYENHSMKTRVAKKIVNLNIDSIDKINYKFIILNMG  
DNLNNEEKGNFYFNALSLQEDVQDYDESYFYKKFLSIPRAHLKIDSRDYFNVVTKINYFNNPEFVVYRNLDLIQ  
DVKNFVLSGNTSKLLNIRDKNFFIQSWDQKGGKSNISINTNSFLTMMIRLGRRKNGIQFAKHLEADSSDDISYLE  
SRGWDHIHEWYFVFKRIVYPKDPEINNGWTWIGVYLGGK

t527.m

CNQKQSEIQNLTHLLKSSNKNRLDKFLIIDRVVNIYIANKNYEDALEIVNNGIIDDESREYYPLYLYLMGNIYDSM  
GEDFVAFNIYKRVDNFDDYVYENHSMKTRVAKKIVNLNIDSIDKINYKFIILNMGIDNLNNEEKGNFYFNALSL  
EDVQDYDESYFYKKFLSIPRAHLKIDSRDYFNVVTKINYFNNPEFVVYRNLDLIQDVKNFVLSGNTSKLLNIRD  
KNNFFIQSWDQKGGKSNISINTNSFLTMMIRLGRRKNGIQFAKHLEADSSDDISYLESRGWDHIHEWYFVFKRIVY  
PKDPEINNGWTWIGVYLGGK

f527.nt

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AGATTCAAAATCTTACACATCTTTTAAATCTTCTAATAAAAAATAGATTAGATAAAATTTCTTATTATTGATAGAGT  
TGTTAACATATATATTGCAAATAAAAAATTATGAAGATGCTTTAGAAATTGTAAATAATGGAATTATTGATGATGAA  
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GATAATTTAAATAATGAGGAAAAGGGTAATTTATTTTATAATCTTGCGCTAAGTTTGAAGATGTTCAAGATTACG  
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TAATGTTGTTACAAAAATTAATTACTTTAATAATCCAGAGTTTGTTGTTTATAGAAATTTAGGAGATTTAATCCAG  
GATGTTAAAAATTTTGTTCTTTCTGGTAATACTTCTAAATTGCTTAATATAAGAGATAAGAATAATTTTTTTATTC  
AAAGCTGGGATCAAAAGGGTGGAAGAGTAATTCATTAATACTAATAGCTTTTAAACCATATGATTAGGCTTGG  
GGGAGAGAAGAAAAACGGAATACAATTTGCAAAGCATCTTGAGGCAGATTCTAGTGACGATATATCTTATCTTGAG  
TCAAGGGGCTGGGACCATATTTCATGAATGGTATTTTGTTTTTAAAAGAATTGTTTATCCTAAAGATCCAGAAATTA  
ATAATGGCTGGACTTGGATAGGCGTGATTTAGGTAAAAAATAA

t527.nt

TGCAACCAAAAGCAAAGCGAGATTCAAAATCTTACACATCTTTTAAATCTTCTAATAAAAAATAGATTAGATAAAAT  
TTCTTATTATTGATAGAGTTGTTAACATATATATTGCAAATAAAAAATTATGAAGATGCTTTAGAAATTGTAAATAA  
TGGAATTATTGATGATGAATCTAGAGAATATTATCCTTTGTATCTTTATTTAATGGGCAATATTTATGATTCCATG  
GGAGAAGATTTTGTAGCTTTTAAATATTTACAAGCGTGTTGTTGATAATTTTGATGATTATGTTTATGAAAACCAT  
CAATGAAAACAAGGGTTGCTAAAAAGATTGTCAATTTAAATATTGATTCAATCGATAAAATCAATTATTACAAAT  
TATATTAAATATGGGGATTGATAATTTAAATAATGAGGAAAAGGGTAATTATTTTATAATCTTGCGCTAAGTTTG  
GAAGATGTTCAAGATTACGATGAATCTTATTTTATTATAAAAAATTTCTTTCAATTCCAAGGGCACATTTAAAAA  
TAGATTCTAGAGACTATTTTAAATGTTGTTACAAAAATTAATTACTTTAATAATCCAGAGTTTGTTGTTTATAGAAA  
TTTAGGAGATTTAATCCAGGATGTTAAAAATTTTGTTCTTTCTGGTAATACTTCTAAATTGCTTAATATAAGAGAT  
AAGAATAATTTTTTTATTCAAGCTGGGATCAAAAGGGTGGAAGAGTAATTCATTAATACTAATAGCTTTTAA  
CCACTATGATTAGGCTTGGGGGAGAAGAAAAACGGAATACAATTTGCAAAGCATCTTGAGGCAGATTCTAGTGA  
CGATATATCTTATCTTGAGTCAAGGGCTGGGACCATATTTCATGAATGGTATTTTGTTTTTAAAAGAATTGTTTAT  
CCTAAAGATCCAGAAATTAATAATGGCTGGACTTGGATAGGCGTGATTTAGGTAAAAAATAA

f541.aa

MNKILLILLESIVFLSCSGKSLGSEIPKVSLIIDGTFDDKSFNESALNGVKVKEEFKIELVLKESSSNSYLS  
LEGLKDAGSDLIWLIGYRFSVAKVAALQNPDMKYAIIIDPIYSNDPIPANLVGMTFRAQEGAFLTGYIAAKLSKTG

150

TABLE 1. Nucleotide and Amino Acid Sequences

KIGFLGGIEGEIVDAFRYGYEAGAKYANKDIKISTQYIGSFADLEAGRSVATRMYSDEIDI IHHAAGLGGIGAIEV  
AKELGSGHYIIGVDEDQAYLAPDNVITSTTKDVGRALNIFTSNHLKTNTFEGGKLINYLKEGVVGFVRNPKMISF  
ELEKEIDNLSSKIINKEIIVPSNKESYEKFLKEFI

t541.aa

CSGKGS LGSEIPKVS LIIDGTFDDKSFNESALNGVKVKKEEFKIELVLKESSNSYLS DLEGLKDAGSDLIWLIGY  
RFS DVAKVAALQNPDMKYAIIDPIYSNDPI PANLVGMTFRAQEGAF LTGYIAAKLSKTGKIGFLGGIEGEIVDAFR  
YGYEAGAKYANKDIKISTQYIGSFADLEAGRSVATRMYSDEIDI IHHAAGLGGIGAIEVAKELGSGHYIIGVDEDQ  
AYLAPDNVITSTTKDVGRALNIFTSNHLKTNTFEGGKLINYLKEGVVGFVRNPKMISFELEKEIDNLSSKIINKE  
IIVPSNKESYEKFLKE  
FI

f541.nt

ATGAATAAAATATTGTTGTTGATTTTGCTTGAGAGTATTGTTTTTTTATCTTGTAGTGGTAAAGGTAGTCTTGGGA  
GCGAAATTCCTAAGGTATCTTTAATAATTGATGGAAC TTTTGATGATAAATCTTTAATGAGAGTGCTTTAAATGG  
CGTAAAAAAGTTAAAGAAGAATTTAAAATTGAGCTTGTTTTAAAAGAATCCTCATCAAATCTTATTTATCTGAT  
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CGGCTCTTCAAAATCCCGATATGAAATATGCAATTATTGATCCTATTTATTCTAACGATCCTATTCTGCAAATTT  
GGTGGGCATGACCTTTAGAGCTCAAGAGGGTGCA TTTTAAACGGGTATATATTGCTGCAAAACTTTCTAAACAGGT  
AAAATTGGATTTT TAGGGGGAATAGAAGGCGAGATAGTAGATGCTTTTAGGTATGGGTATGAAGCTGGTGCTAAGT  
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AACTAGGATGTATTCTGATGAGATAGACATTATTCATCATGCTGCAGGCC TTTGGAGGAATTGGGGCTATTGAGGTT  
GCAAAAGAACTTGGTTC TGGGCATTACATTATTGGAGTTGATGAAGATCAAGCATATCTTGCTCCTGACAATGTAA  
TAACATCTACAATAAAGATGTTGGTAGAGCTTTAAATATTTTACATCTAACCATTTAAAACTAATACTTTCTGA  
AGGTGGCAAATTAATAAATTATGGCCTTAAAGAAGGAGTTGTGGGGTTTGTAAGAAATCCTAAAATGATTTCCTTT  
GAACCTGAAAAAGAAATTGACAATCTTTCTAGCAAAATAATCAACAAAGAAATTATTGTTCCATCTAATAAAGAAA  
GTTATGAGAAGTTTCTTAAAGAATTTATTTAA

t541.nt

TGTAGTGGTAAAGGTAGTCTTGGGAGCGAAATTCCTAAGGTATCTTTAATAATTGATGGAAC TTTTGATGATAAAT  
CTTTTAATGAGAGTGCTTTAAATGGCGTAAAAAAGTTAAAGAAGAATTTAAAATTGAGCTTGTTTTAAAAGAATC  
CTCATCAAATCTTATTTATCTGATCTTGAAGGGCTTAAGGATGCGGGCTCAGATTTAATTTGGCTTATTGGGTAT  
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TGCTGCAAAACTTTCTAAACAGGTAAAATTGGATTTT TAGGGGGAATAGAAGGCGAGATAGTAGATGCTTTTAGG  
TATGGGTATGAAGCTGGTGCTAAGTATGCTAATAAAGATATAAAGATATCTACTCAGTATATTGGTAGTTTTGCTG  
ACCTTGAAGCTGGTAGAAGCGTTGCAACTAGGATGTATTCTGATGAGATAGACATTATTCATCATGCTGCAGGCC T  
TGGAGGAATTGGGGCTATTGAGGTTGCAAAAGAACTTGGTTC TGGGCATTACATTATTGGAGTTGATGAAGATCAA  
GCATATCTTGCTCCTGACAATGTAATAACATCTACAATAAAGATGTTGGTAGAGCTTTAAATATTTTACATCTA  
ACCATTTAAAACTAATACTTTCTGAAGGTGGCAAATTAATAAATTATGGCCTTAAAGAAGGAGTTGTGGGGTTTGT  
AAGAAATCCTAAAATGATTTCCTTTGAACCTGAAAAAGAAATTGACAATCTTTCTAGCAAAATAATCAACAAAGAA  
ATTATTGTTCCATCTAATAAAGAAAGTTATGAGAAGTTTCTTAAAGAATTTATTTAA

f561.aa

MYKNGFFKNYLSLFLI FLVIAC TSKDSSNEYVEEQEAENSSKPDDSKIDEHTIGHVFHAMGVVHSSKDRKSLGKNI  
KVIFYFSEEDGHFQ TIPS KENAKLIVFYDENVYAGEAPISISGKEAFIFVGITPDFKKIINSNLHGAKSDLIGTFKD  
LNINKSKLEITVDENNSDAKTFLESVNYIIDGVEKISPMLTN

t561.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CTSKDSSNEYVEEQEAENSSKPDDSKIDEHTIGHVFHAMGVVHSHKDRKSLGKNIKVFYFSEEDGHFQTI PSKENA  
KLIVFYFDNVYAGEAPISISGKEAFIFVGITPDFKKI INSNLHGAKSDLIGTFKDLNKNKLEITVDENNSDAKT  
FLESVNYIIDGVEKISPLMTN

f561.nt

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TACTATTGGGCACGTTTTTTCACGCTATGGGAGTAGTTCATTCAAAAAAGGATCGAAAAAGTTTGGGGAAAAATATA  
AAGGTTTTTTATTTTTCTGAAGAAGATGGACATTTTCAAACAATACCCTCAAAAGAGAATGCAAAGTTAATAGTTT  
ATTTTTATGACAATGTTTTATGCAGGAGAGGCTCCAATTAGTATCTCTGGAAAAGAAGCCTTTATTTTTGTTGGGAT  
TACCCTGACTTTAAAAAGATTATAAATAGCAATTTACATGGCGCTAAAAGTGATCTTATTGGTACTTTTAAAGAT  
CTTAATATTAAAAATTCAAAATTGGAAATTACAGTTGATGAGAATAAATTCAGATGCCAAGACCTTCCTTGAATCTG  
TTAATTACATTATCGACGGCGTTGAAAAAATTTACCTATGTTAACGAATTAA

t561.nt

TGTACTTCAAAAGATAGCTCAAATGAATATGTTGAGGAGCAAGAAGCGGAGAACTCTTCTAAGCCTGATGATTCTA  
AAATAGATGAACATACTATTGGGCACGTTTTTTCACGCTATGGGAGTAGTTCATTCAAAAAAGGATCGAAAAAGTTT  
GGGGAAAAATATAAAGGTTTTTTTATTTTTCTGAAGAAGATGGACATTTTCAAACAATACCCTCAAAAGAGAATGCA  
AAGTTAATAGTTTATTTTTATGACAATGTTTATGCAGGAGAGGCTCCAATTAGTATCTCTGGAAAAGAAGCCTTTA  
TTTTTGTGTTGGGATTACCCCTGACTTTAAAAAGATTATAAATAGCAATTTACATGGCGCTAAAAGTGATCTTATTGG  
TACTTTTAAAGATCTTAATATTAAAAATTCAAAATTGGAAATTACAGTTGATGAGAATAAATTCAGATGCCAAGACC  
TTCCTTGAATCTGTTAATTACATTATCGACGGCGTTGAAAAAATTTACCTATGTTAACGAATTAA

f604.aa

MSFNKTKKIGKKIKIVTLLMLAVSLIACNNNSEKEKLAFFKVYIGGAPSSLDPHLVDETIGARILEQIFSGLLTLNT  
KTGKLPGLAKNWEASKDKKTYQFYLRDNLFWSDGVEITAEGIRKSFLRILNKETGSTNVDMLKSIIKNGQEYFDG  
KVSDSELGIKAIDSKTLEITLTAPKPYFLELLLHYAFMPVPIHVIEKYKGNWTS PENMVTSGPFLKKRLPNEKII  
FEKNERYNAKEVELDELVYITSDNDLTVYNMYKNNEIDAIFNSIPPDIVNEIKLQKDYQHKSNAIYLYSFNTKI  
KPLDDARVREALTLAIDRETLYKVLNDGTVPTREITPDLKNYNYGKKLALFDPEKSKLLADAGYPNGKGF PMLT  
LKYN TNETHKKIAAFIQNQWKILNINMLTNENWPVLTNSRNTGNFEIIRVGRIGEYLDPHYFTIFTRENSQLA  
SYGYSNLEFDKLIRES DLEKDPIKRKQLLRKAESIIIEKDFPAAPIYIYSGHYLFRNDKWTGWNPNVSEVYYLSEL  
KPIKNAKHN

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CNNNSEKEKLAFFKVYIGGAPSSLDPHLVDETIGARILEQIFSGLLTLNTKTGKLPGLAKNWEASKDKKTYQFYLR  
DNLFWSDGVEITAEGIRKSFLRILNKETGSTNVDMLKSIIKNGQEYFDGKVSDSELGIKAIDSKTLEITLTAPKPY  
FLELLLHYAFMPVPIHVIEKYKGNWTS PENMVTSGPFLKKRLPNEKII FEKNERYNAKEVELDELVYITSDNDL  
TVYNMYKNNEIDAIFNSIPPDIVNEIKLQKDYQHKSNAIYLYSFNTKIKPLDDARVREALTLAIDRETLYKVLN  
DGTVP TREITPDLKNYNYGKKLALFDPEKSKLLADAGYPNGKGF PMLTLKYN TNETHKKIAAFIQNQWKILNIN  
LMLTNENWPVLTNSRNTGNFEIIRVGRIGEYLDPHYFTIFTRENSQLASYGYSNLEFDKLIRES DLEKDPIKRKQ  
LLRKAESIIIEKDFPAAPIYIYSGHYLFRNDKWTGWNPNVSEVYYLSELKPIKNAKHN

f604.nt

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CCCTCATTTGGTAGATGAGACAATAGGAGCAAGAATTTTAGAACAAATATTCTCAGGGCTTTTGACATTAAATACC  
AAAACAGGAAAGCTAAAGCCCGGACTTGCTAAAAATTGGGAAGCCTCAAAAGATAAAAAACATATCAATTTTATC  
TAAGGGACAACCTTTTTTGGAGCGATGGAGTTGAAATTACCGCTGAAGGGATAAGAAAATCTTTTTTAAAGATTTT  
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AAAGTATCCGATTCTGAACTTGGAATCAAGGCAATTGATAGTAAAAACGCTGGAAATAACACTTACGGCCCCAAAGC  
CATATTTTCTTGAACCTGCTTCTACATTACGCATTATGCCAGTACCTATTCATGTGATTGAAAAATATAAGGGAAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTGGACAAGCCCTGAAAACATGGTTACTAGCGGTCCTTTTAAATTAAAAAAAAGATTACCTAATGAAAAATTATC  
TTTGAAAAAACGAACGTTATTATAATGCAAAAGAAGTAGAACTTGATGAGCTTGTCTACATTACGTCTGACAATG  
ATCTTACTGTGTACAATATGTACAAAAACAACGAAATTGATGCTATTTTAAACAGCATCCCGCCGGACATTGTAAA  
TGAAATAAAACTACAAAAAGACTATTACCAACACAAAAGTAATGCAATTTATTTATATTTCATTTAATACAAAAATA  
AAACCCCTTGATGATGCTAGAGTTAGAGAAGCTTTAACCTTAGCTATTGACAGAGAACTTTAACTTACAAAGTGC  
TAAATGATGGCACAGTTCCCTACAAGAGAAATAACTCCTGATCTTAAAAATTACAATTACGGTAAAAAATTGGCTTT  
ATTTGATCCTGAAAAATCTAAAAAGCTTTTGGCAGATGCAGGGTATCCTAATGGGAAAGGATTCCCAATGCTAACA  
CTAAAAATATAATACAAACGAACTCATAAAAAAATTGCTGCATTTATTCAAACCAATGGAAAAAATTCTAAATA  
TCAATCTTATGCTTACCAACGAAAATTGGCCTGTTCTTACCAACAGCAGAAATACTGGCAATTTTGAAATAATAAG  
AGTTGGACGCATTGGGGAATATTTAGATCCACACACATACTTTACTATATTCCACAAGAGAAAATTCACAACCTGCA  
TCATACGGATATTCAAACCTAGAATTGACAAACTCATCAGAGAATCAGATCTTGAAAAAGATCCTATAAAAAAGAA  
AACAATTACTCAGAAAAGCAGAATCAATAATAATTGAAAAAGATTTTCTGCTGCACCAATATACATATATTCTGG  
GCATTATCTTTTAGAAACGATAAATGGACTGGATGGAATCCTAATGTATCAGAGGTTTATTATCTTTCTGAATTA  
AAACCAATTAAAAATGCAAAACATAATTAA

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TGCAATAATAATTCAGAAAAAGAAAAATTAGCATTTAAAGTATACATAGGGGGAGCGCCCTCATCGCTTGACCCTC  
ATTTGGTAGATGAGACAATAGGAGCAAGAATTTTAGAACAAATATTCTCAGGGCTTTTGACATTAAATACCAAAC  
AGGAAAGCTAAAGCCCGGACTTGCTAAAAATTGGGAAGCCTCAAAAGATAAAAAACATATCAATTTTATCTAAGG  
GACAACCTTTTTTGGAGCGATGGAGTTGAAATTACCGCTGAAGGGATAAGAAAATCTTTTTTAAGAATTTTAAATA  
AAGAAACAGGATCTACAAATGTTGACATGCTCAAATCAATAATAAAAAATGGACAAGAGTATTTTGACGGGAAAGT  
ATCCGATTCTGAACTTGGAATCAAGGCAATTGATAGTAAACGCTGGAAATAACACTTACGGCCCCAAAGCCATAT  
TTTCTTGAACTGCTTCTACATTACGCATTCATGCCAGTACCTATTCATGTGATTGAAAAATATAAGGGAAATTGGA  
CAAGCCCTGAAAACATGGTTACTAGCGGTCCTTTTAAATTAAAAAAAAGATTACCTAATGAAAAAATTATCTTTGA  
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CCTTGATGATGCTAGAGTTAGAGAAGCTTTAACCTTAGCTATTGACAGAGAACTTTAACTTACAAAGTGCTAAAT  
GATGGCACAGTTTCTACAAGAGAAATAACTCCTGATCTTAAAAATTACAATTACGGTAAAAAATTGGCTTTATTG  
ATCCTGAAAAATCTAAAAAGCTTTTGGCAGATGCAGGGTATCCTAATGGGAAAGGATTCCCAATGCTAACACTAAA  
ATATAATACAAACGAAACTCATAAAAAAATTGCTGCATTTATTCAAACCAATGGAAAAAATTCTAAATATCAAT  
CTTATGCTTACCAACGAAAATTGGCCTGTTCTTACCAACAGCAGAAATACTGGCAATTTTGAAATAATAAGAGTTG  
GACGCATTGGGGAATATTTAGATCCACACACATACTTTACTATATTCCACAAGAGAAAATTCACAACCTTGCATCATA  
CGGATATTCAAACCTAGAATTGACAAACTCATCAGAGAATCAGATCTTGAAAAAGATCCTATAAAAAAGAAAACAA  
TTACTCAGAAAAGCAGAATCAATAATAATTGAAAAAGATTTTCTGCTGCACCAATATACATATATTCTGGGCATT  
ATCTTTTTTAGAAACGATAAATGGACTGGATGGAATCCTAATGTATCAGAGGTTTATTATCTTTCTGAATTAAAACC  
AATTAAAAATGCAAAACATAATTAA

f736.aa

MKKVILIFMLSTSLYNCKNQDNEKIVSIGGSTTVSPILDEMILRYNKINNNTKVITYDAQSSVINGLNFNKIYK  
IAISSRDLTKEEIEQGAKETVFAYDALIFITSPEIKITNITEENLAKILNGEIQNWKQVGGPDAKINFNRDSSSG  
SYSSIKDLLLNKIFKTHEEAQFRQDGIVVKSNGEVIEKTSLTPHSIGYIGLYAKNSIEKGLNILSVNSTYPTKET  
INSNKYTIKRNLIIVTNNKYEDKSVTQFIDFMTSSTGQDIVEEQGFLGIKT

t736.aa

CKNQDNEKIVSIGGSTTVSPILDEMILRYNKINNNTKVITYDAQSSVINGLNFNKIYKIAISSRDLTKEEIEQGAK  
ETVFAYDALIFITSPEIKITNITEENLAKILNGEIQNWKQVGGPDAKINFNRDSSSGSYSSIKDLLLNKIFKTHE  
EAQFRQDGIVVKSNGEVIEKTSLTPHSIGYIGLYAKNSIEKGLNILSVNSTYPTKETINSNKYTIKRNLIIVTNN  
KYEDKSVTQFIDFMTSSTGQDIVEEQGFLGIKT

f736.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAAAAAGTTATTATCTTAATTTTTATGCTATCAACAAGTTTATTATACAACCTGTAAAAATCAAGACAATGAAA  
AAATTGTATCAATTGGAGGATCTACAACCTGTAAGCCCAATACTAGACGAAATGATTTTAAGATATAATAAAATAAA  
CAATAATACTAAAGTAACATACGATGCACAAGGAAGTAGTGTGGCATAAACGGGCTATTTAACAAAATATATAAA  
ATAGCAATATCATCAAGAGATTTAACAAAAGAAGAAATTGAACAAGGGGCAAAAGAACTGTATTTGCTTATGATG  
CTTTAATTTTTCATTACAAGCCCTGAAATAAAAATTACAAATATTACAGAAGAAAATCTAGCTAAAATACTAAATGG  
AGAAATTCAAAATTTGGAAACAAGTGGGAGGTCTGATGCTAAAATCAACTTTATCAATCGAGACTCTTCTTCTGGT  
TCTTATTCGCTCTATAAAAGACCTACTTCTTAATAAAAATATTCAAACTCACGAAGAAGCTCAATTTAGACAAGACG  
GAATAGTGGTAAATCTAATGGAGAGGTAATTGAAAAACAAGCCCTACTCCCCACTCAATAGGATATATAGGTCT  
TGGATACGCAAAAATTC AATAGAAAAGGGTTTGAATATTCTTCTGTTAACAGCACATATCCTACAAAAGAAACA  
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CTCAATTTATTGATTTTCATGACAAGCTCAACTGGACAAGATATTGTTGAAGAACAAGGCTTTTTAGGGATAAAAAC  
ATAA

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GTAAAAATCAAGACAATGAAAAAATTGTATCAATTGGAGGATCTACAACCTGTAAGCCCAATACTAGACGAAATGA  
TTTTAAGATATAATAAAATAAACAATAATACTAAAGTAACATACGATGCACAAGGAAGTAGTGTGGCATAAACGG  
GCTATTTAACAAAATATATAAAATAGCAATATCATCAAGAGATTTAACAAAAGAAGAAATTGAACAAGGGGCAAAA  
GAACTGTATTTGCTTATGATGCTTTAATTTTCATTACAAGCCCTGAAATAAAAATTACAAATATTACAGAAGAAA  
ATCTAGCTAAAATACTAAATGGAGAAATTCAAAATTGGAAACAAGTGGGAGGTCTGATGCTAAAATCAACTTTAT  
CAATCGAGACTCTTCTTCTGGTTCTTATTTCGCTCTATAAAAGACCTACTTCTTAATAAAAATATTCAAACTCACGAA  
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ACTCAATAGGATATATAGGTCTTGGATACGCAAAAATTC AATAGAAAAGGGTTTGAATATTCTTCTGTTAACAG  
CACATATCCTACAAAAGAAACAATAAATAGCAATAAATACACCATTAAGAAATTTAATAATAGTTACAAATAAC  
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f752.aa

MNKKLNEVLLKLDQDLIKCVKGS LDLEISGV TYSSKLVLPRFVFFALPGIHFDGHDFIEIAIQKGSNVVVC SRDVD  
FYSPNV TYIKVDDFNIRKFMSNFSNIFYDEPSKKLVIGVTGTDGKSSVCYIYLLFKKKGVKVGFI STVFFDDGS  
GSLIKNPYRQSTPESTEIHSFLSTMVKNEAQYAILESTSHGLDLETARLIDVNYFAVVFTNIGHEHLEFHGTIQNY  
LNVKLGLFRSVSDDAGFGVINLDDLYSSDFKNAVKKSFTYSLKSSKADFFVSFIDEKTDSTRFEFYHKGVKYLANV  
SLLGSFNVENVMAALILVSQILNIDIQDIVDKLNCIKSLDGRMDSINLGQNF SVIIDYAHTPGAFSKLFP IFKRFA  
TNRLISVFGSAGERDVEKRFLQGQIADIYSDLIILCDEDPRGENSMCI IKDIAKGIVNKVENKDLFFIADRKQAIE  
KAISLAKAGDLVVALGKGHESSI IYKNREVFVWNEQEVVKNAI LSLEKSEKEK

t752.aa

CVKGS LDLEISGV TYSSKLVLPRFVFFALPGIHFDGHDFIEIAIQKGSNVVVC SRDVD FYSPNV TYIKVDDFNIRK  
FMSNFSNIFYDEPSKKLVIGVTGTDGKSSVCYIYLLFKKKGVKVGFI STVFFDDGSGSLIKNPYRQSTPESTEI  
HSFLSTMVKNEAQYAILESTSHGLDLETARLIDVNYFAVVFTNIGHEHLEFHGTIQNYLNVKLGLFRSVSDDAGFG  
VINLDDLYSSDFKNAVKKSFTYSLKSSKADFFVSFIDEKTDSTRFEFYHKGVKYLANVSLLGSFNVENVMAALILV  
SQILNIDIQDIVDKLNCIKSLDGRMDSINLGQNF SVIIDYAHTPGAFSKLFP IFKRFA TNRLISVFGSAGERDVEK  
RFLQGQIADIYSDLIILCDEDPRGENSMCI IKDIAKGIVNKVENKDLFFIADRKQAIE KAISLAKAGDLVVALGKG  
HESSI IYKNREVFVWNEQEVVKNAI LSLEKSEKEK

f752.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

TTAAAAATGAAGCTCAATATGCAATTCTTGAATCTACTTCTCATGGGCTTGACCTTGAAACAGCAAGGCTTATTGA  
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TTGAATGTCAAGCTGGGTCTTTTTTCGGTCTGTTAGTGATGATGCTGGTTTTTGGGGTTATTAATCTTGATGACCTTT  
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AAAATAGAGAAGTTTTTTTGAATGAACAAGAGGTAGTTAAAAATGCTATTTTAAAGTTTAGAAAAATCAGAAAAGGA  
GAAGTGA

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TCATGGCACAATTCAAAATTATTGAAATGTCAAGCTGGGCTTTTTTCGGTCTGTTAGTGATGATGCTGGTTTTGGG  
GTTATTAATCTTGATGACCTTTATCTTCTGATTTTAAGAATGCTGTTAAGAAATCTTTTACTTATAGCTTAAAAA  
GCAGTAAAGCGGATTTTTTTTGTAGTTTTATTGATGAGAAAACCGATTCTACTAGATTTGAATTTTTATCACAAGGG  
GGTTAAATATCTTGCTAATGTTAGCCTACTGGGGAGTTTTAATGTTGAGAATGTAATGGCTGCTCTTATTTTAGTT  
TCTCAAATTTTAAATATCGATATTCAAGATATTGTTGATAAACTTAACTGCATTAAAAAGTCTTGATGGGCGTATGG  
ATAGTATTAATTTGGGGCAAAATTTTTCTGTAATAATTGATTATGCTCATACTCCTGGTGCTTTTTTCCAAGCTTTT  
TCCTATTTTTTAAAGATTTGCTACCAATAGATTGATTTCTGTTTTTGGCTCTGCAGGAGAAAGAGATGTTGAAAA  
AGATTTTTTGCAAGGGCAAATCGCAGATATTTATTCTGATTTAATAATACTTTGCGATGAAGATCCAAGAGGCGAGA  
ATAGTATGTGTATAATTAAAGACATTGCAAAAGGAATTGTAAATAAAGTTGAAAAATAAGGATTTATTTTTTATTGC  
TGATAGAAAGCAGGCTATTGAAAAAGCAATAAGTCTTGCAAAAGCAGGAGATTTGGTTGTTGCTTTGGGCAAGGT  
CATGAAAGTTCAATAATTTATAAAAAATAGAGAAGTTTTTTTGAATGAACAAGAGGTAGTTAAAAATGCTATTTTAA  
GTTTAGAAAAATCAGAAAAGGAGAAAGTGA

f798.aa

MVFRITYKHLELIMLPMLMLSCAFFKKPQSVHQDSNTGKPI SDEKLHLISGKISNKKLP IINSNHDVTWIKTKAMTI  
LGEDGKEIPEFKNKFGYSYIISPVKMDGKYSYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENS  
QEEGYVTAYPFGILMSDEIKNAFKLTYNKNGHWNMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILK  
DIAGDLFEDI

t798.aa

CAFFKKPQSVHQDSNTGKPI SDEKLHLISGKISNKKLP IINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYI  
ISPVKMDGKYSYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIK  
NAFKLTYNKNGHWNMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILKDIAGDLFEDI

f798.nt

ATGGTATTTAGAACATATAAACATTTGGAAC TAATAATGCTGCCCATGTTAATGCTGAGTTGCGCTTTTTTTAAGA  
AACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTACATTTAATATCAGGCAA  
AATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAACCTGGATAAAAAACAAAGGCAATGACAATC



TABLE 1. Nucleotide and Amino Acid Sequences

TTAGGCGAAGATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATAATATCTCCTGTAAAAA  
TGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACATAAAATGGAGATGATGAATATGA  
AATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCCTTTTTAGCTGTTGAAAATTCA  
CAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAAAATGCTTTTAAATTAA  
CATATAAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAAATAAACTTACTCAAGAAACTAAAA  
TTATAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTTAAAAAGAAGTGCTAAAAGAAAATTCATATATAAAA  
GACATAGCTGGAGATTTATTTGAAGATATATAA

t798.nt

TGCGCTTTTTTTTAAAGAAACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTAC  
ATTTAATATCAGGCAAAATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAACCTGGATAAAAAAC  
AAAGGCAATGACAACTTTAGGCGAAGATGGAAAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATA  
ATATCTCCTGTAAAAATGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAACATAAAAAATG  
GAGATGATGAATATGAAATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAATTCCTTTTT  
AGCTGTTGAAAATTCACAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAA  
AATGCTTTTAAATTAACATATAAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAAATAAACTTA  
CTCAAGAAACTAAAATTTATAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTTAAAAGAAGTGCTAAAAGA  
AAATTCATATATTAAGACATAGCTGGAGATTTATTTGAAGATATATAA

f805.aa

MLRKLKDISKIVLVTDLTPNCQTCGKLIANGDEVYIAEDGLFHSVKSNTIAGSTLTMIQGLKNLIEFGFSLSDAV  
QASSYNPTRILNIDKKGLICHGYDANLNVLDKDFNLKLTMIESKIIFNNL

t805.aa

CQTCGKLIANGDEVYIAEDGLFHSVKSNTIAGSTLTMIQGLKNLIEFGFSLSDAVQASSYNPTRILNIDKKGLICH  
GYDANLNVLDKDFNLKLTMIESKIIFNNL

f805.nt

ATGCTTAGAAAGCTTAAAGATATAAGTAAAATAGTCCTTGTAAGTACGCGACTTACTCCGAATTGTCAAACCTTGTG  
GAAAACATAATTGCAAACGGAGACGAAGTTTATATTGCAGAAGATGGATTATTCCATAGCGTGAAAAGCAACACAAT  
AGCTGGATCAACACTCACAATGATACAAGGTCTTAAAAATTTAATAGAATTTGGTTTCAGCTTAAGCGATGCTGTT  
CAAGCAAGCTCTTACAATCCAACAAGAATTCCTCAATATTGATAAAAAGGGCTTAATATGTCATGGATATGATGCAA  
ACCTCAATGTCCTAGATAAAGATTTTAATCTAAAGTTAACAATGATAGAATCTAAAATAATTTTAAACAATCTCTA  
A

t805.nt

TGTCAAACCTTGTGGAAAACATAATTGCAAACGGAGACGAAGTTTATATTGCAGAAGATGGATTATTCCATAGCGTGA  
AAAGCAACACAATAGCTGGATCAACACTCACAATGATACAAGGTCTTAAAAATTTAATAGAATTTGGTTTCAGCTT  
AAGCGATGCTGTTCAAGCAAGCTCTTACAATCCAACAAGAATTCCTCAATATTGATAAAAAGGGCTTAATATGTCAT  
GGATATGATGCAAACCTCAATGTCTTAGATAAAGATTTTAATCTAAAGTTAACAATGATAGAATCTAAAATAATTT  
TTAACAATCTCTAA

f635.aa

MKILWLIILVNLFLSCGNESKEKSNLGLRLRELEISGGSESKEIEVYKEFIEKEDKNILKIVNSIDKKARFFNLIG  
LEFFKLGQYGAIEYFAKNLEINPNNYLSHFYIGVASYNLAKNLRVKDEVEKYIILAENSFLKSLIRSDDFKDSL  
AISNMYVYDLKQLEAKNYLNKLGMGEDYFEFLMLRGANYYSGLDLGNAILFYDKASKKASTEEQKEGVSRIMSN  
LK

t635.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CGNESKEKSNLGLRLRELEISGGGSESKIEVYKEFIEKEDKNILKIVNSIDKKARFFNLIGLEFFKLGQYGP AIEY  
FAKNLEINPNNYLSHFYIGVASYNLAKNLRVKDEVEKYIILAENSFLKSL SIRDDFKDSLFAISNMVYDL DKQLE  
AKNYLNKLGD MGEDYFEFLMLRGANYYS LGDLGNAILFYDKASKKASTEEQKEGVSRIMSNLK

f635.nt

ATGAAAATTTTGTGGTTAATAATTCTTGTTAATTTATTTTTATCTTGTGGCAATGAATCTAAAGAAAAATCAAATC  
TTGGTCTTAGATTAAGAGAATTGGAAATTCAGGTGGTGGATCTGAATCTAAGATTGAAGTTTATAAAGAATTTAT  
TGAAAAAGAAGATAAGAATATTTTAAAGATAGTTAATTCATTGATAAGAAAGCCAGATTTTTTAATTTAATTGGT  
CTTGAATTTTTTAAGCTTGGTCAGTACGGACCTGCTATTGAATATTTTGTCTAAAAATTTAGAAATCAATCCCAATA  
ATTATTTATCTCATTTTTATATAGGTGTTGCTTCTTATAAATTTAGCTAAAAATTTAAGAGTAAAGATGAAGTTGA  
AAAAACATAAATCTTGTCTGAAAAATCTTTTTTAAAAATCACTTTCAATTAGAGATGATTTTAAAGATTCTCTTTTT  
GCCATTTCTAATATGTACGTATATGATCTTGATAAACAACCTGAAGCTAAAAATTATTTAAATAAACTTGGTGATA  
TGGGTGAGGACTATTTTGAGTTTTTAATGTTAAGAGGTGCAAATTATTATTCGCTGGGCGATCTTGGTAATGCTAT  
ATTGTTTTATGATAAAGCTAGTAAAAAGGCTTCAACTGAAGAGCAAAAAGAAGGTGTTTCTAGGATCATGAGTAAT  
TTGAAGTAA

t635.nt

TGTGGCAATGAATCTAAAGAAAAATCAAATCTTGGTCTTAGATTAAGAGAATTGGAAATTCAGGTGGTGGATCTG  
AATCTAAGATTGAAGTTTATAAAGAATTTATTGAAAAAGAAGATAAGAATATTTTAAAGATAGTTAATTCATTGA  
TAAGAAAGCCAGATTTTTTAATTTAATTGGTCTTGAATTTTTTAAGCTTGGTCAGTACGGACCTGCTATTGAATAT  
TTTGTCTAAAAATTTAGAAATCAATCCCAATAATTATTTATCTCATTTTTATATAGGTGTTGCTTCTTATAATTTAG  
CTAAAAATTTAAGAGTAAAGATGAAGTTGAAAAATACATAATTCTTGTCTGAAAAATCTTTTTTAAAAATCACTTTC  
AATTAGAGATGATTTTAAAGATTCTCTTTTTGCCATTTCTAATATGTACGTATATGATCTTGATAAACAACCTGAA  
GCTAAAAATTATTTAAATAAACTTGGTGATATGGGTGAGGACTATTTTGAGTTTTTAATGTTAAGAGGTGCAAATT  
ATTATTCGCTGGGCGATCTTGGTAATGCTATATTGTTTTATGATAAAGCTAGTAAAAAGGCTTCAACTGAAGAGCA  
AAAAGAAGGTGTTTCTAGGATCATGAGTAATTTGAAGTAA

f314.aa

MNNCLIKFFIFLLVFSNSYVAFSKNVNVLIVTAMDSEFDQINKLMSNKEEIVLKEYGLNKKILKGKLSNRNVMV I  
CGVGKVNAGVWTSYILSKYNI SHVINSVAGGVVS AKYKDIKVGDVVSSEVAYHDVDLTKFGYKVGQLTGGLPQK  
FNANKNLIKNAIEAIKSKVGGSNAYSGLIVSGDQFIDPTYINKIIGNFKDVI AVEMEGA AIGHVSHMFNIPFIVIR  
SISDIVNKEGNEVEYSKFSKIAAFNSAKVVQEILRKLZ

t314.aa

KNVNVLIVTAMDSEFDQINKLMSNKEEIVLKEYGLNKKILKGKLSNRNVMV IICVGKVNAGVWTSYILSKYNI SH  
VINSVAGGVVS AKYKDIKVGDVVSSEVAYHDVDLTKFGYKVGQLTGGLPQKFNANKNLIKNAIEAIKSKVGGSN  
AYSGLIVSGDQFIDPTYINKIIGNFKDVI AVEMEGA AIGHVSHMFNIPFIVIR SISDIVNKEGNEVEYSKFSKIAA  
FNSAKVVQEILRKLZ

f314.nt

ATGAATAATTGTTTAATAAAGTTTTTTATTTTTTTTATTAGTTTTTTCAAACAGTTATGTTGCTTTTTTCTAAAAATG  
TCAATGTTTTAATAGTAACTGCTATGGACTCTGAGTTTGATCAGATAAATAAGCTTATGTCTAATAAGGAAGAAAT  
AGTTCCTTAAGGAGTATGGTCTTAATAAAAAAGATTTTAAAGGGGAAGTTGTCTAATCGCAATGTTATGGTTATTATT  
TGTGGGGTTGTTAAGGTAAATGCTGGTGTGTGGACTAGCTACATTTTGTCAAATAACAACATAAGTCATGTCATTA  
ATTCTGGCGTTGCTGGTGGCGTTGTTAGTGCTAAATACAAAGATATTAAAGTGGGAGATGTGGTGGTGTCTTCAGA  
GGTTGCATATCATGATGTTGATTTGACTAAATTTGGATACAAGGTAGGACAGCTTACAGGAGGATTGCCTCAAAAA  
TTTAATGCCAATAAAAAATTTAATTAAGAATGCCATAGAGGCCATTAAATCAAAGGTTGGAGGTTCTAATGCATATT  
CAGGATTAATAGTTTTCAGGAGATCAGTTTATTGATCCAACCTTATATTAACAAAATTATAGGAACTTTAAAGATGT  
AATAGCTGTTGAGATGGAAGGTGCAGCAATAGGGCATGTTTCTCATATGTTTAAATATACCTTTTATAGTTATTAGG  
TCAATATCTGACATTGTAAATAAAGAAGGGAATGAGGTTGAATATAGTAAATTTTCTAAAAATAGCTGCTTTCAATT  
CAGCCAAAGTTGTACAAGAAATTTTAAGAAAACTTTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t314.nt

AAAAATGTCAATGTTTTAATAGTAACTGCTATGGACTCTGAGTTTGATCAGATAAAATAAGCTTATGTCTAATAAGG  
AAGAAATAGTTCTTAAGGAGTATGGTCTTAATAAAAAGATTTTAAAGGGGAAGTTGTCTAATCGCAATGTTATGGT  
TATTATTTGTGGGGTTGGTAAGGTTAATGCTGGTGTGTGGACTAGCTACATTTTGTCAAAAATACAACATAAGTCAT  
GTCATTAATTCTGGCGTTGCTGGTGGCGTTGTTAGTGTCTAAATACAAAGATATTAAAGTGAGGAGATGTGGTGGTGT  
CTTCAGAGGTTGCATATCATGATGTTGATTTGACTAAATTTGGATACAAGGTAGGACAGCTTACAGGAGGATTGCC  
TCAAAAATTTAATGCCAATAAAAATTTAATTAAGAATGCCATAGAGGCCATTAAATCAAAGGTTGGAGGTTCTAAT  
GCATATTCAGGATTAATAGTTTCAGGAGATCAGTTTATTGATCCAACCTATATTAACAAAATTATAGGAAACTTTA  
AAGATGTAATAGCTGTTGAGATGGAAGGTGCAGCAATAGGGCATGTTTCTCATATGTTTAATATACCTTTTATAGT  
TATTAGGTCAATATCTGACATTGTAAATAAAGAAGGGAATGAGGTTGAATATAGTAAATTTCTAAAATAGCTGCT  
TTCAATTCAGCCAAAGTTGTACAAGAAATTTTAAGAAACTTTAA

f32.aa

MNKTLYLISLILLACNKNKIPLIQKLDLPKSSILGFSNKMGIKDYAFLSKSTKKNSELDYDYAILLRKDEVV  
KIEKTLEKTERYGIEGNWILVNYKGTKRYIFSKDINIVNNLIIDHSKZ

t32.aa

CNKNKIPLIQKLDLPKSSILGFSNKMGIKDYAFLSKSTKKNSELDYDYAILLRKDEVVKIEKTLEKTERYGIE  
GNWILVNYKGTKRYIFSKDINIVNNLIIDHSKZ

f32.nt

ATGAATACAAAACATTATATTTAATATCCTTAATTCTTTTAGCTTGCAATAAAAATAACAAAATTCCTCTCATTC  
AAAAATTAGATTTGCCCCAAAAGCAGCATTCTTGGCTTTAGCAATAAAATGGGCATAATAATAAAAGATTATGCTTT  
TCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTACGCAATTCTACTCAGAAAAGACGAAGTCGTA  
AAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAAGGAAATTGGATCCTAGTCAATTACAAGGGAA  
CTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATTTAATAATTGATCATTCTAAATAG

t32.nt

TGCAATAAAAATAACAAAATTCCTCTCATTCAAAAATTAGATTTGCCCCAAAAGCAGCATTCTTGGCTTTAGCAATA  
AAATGGGCATAATAATAAAAGATTATGCTTTTCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTA  
CGCAATTCTACTCAGAAAAGACGAAGTCGTAAAAATTGAAAAAACACTAGAAAAAACAGAGCGCTATGGAATTGAA  
GGAAATTGGATCCTAGTCAATTACAAGGGAACAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATT  
TAATAATTGATCATTCTAAATAG

f320.aa

MKSIYALLFLFINLSLLANNISKDLEVLLKIAQAMNKECKNFIKNPIQFLKEIKPLVDAEKNLLTLINKKIPI  
PENYKIPDLVNIDDFEDLKNLGAKTIKVRKILIEDLIRLIKDAKKFGIEIKISAYRTQEYQKFLFDYNVKTYGRK  
VAETQSAIPGHSQHHMGTAIDFINIDNLLNTKEGKWLYENSLKYGFSVSYPKGYETDTGYKAEPWHYLYIGPKPC  
FIQKKYFNNLQHKLLLEFWNQKNTNLINLIEKYANZ

t320.aa

NNISKDLEVLLKIAQAMNKECKNFIKNPIQFLKEIKPLVDAEKNLLTLINKKIPIPENYKIPDLVNIDDFEDL  
KNLGAKTIKVRKILIEDLIRLIKDAKKFGIEIKISAYRTQEYQKFLFDYNVKTYGRKVAETQSAIPGHSQHHMG  
TAIDFINIDNLLNTKEGKWLYENSLKYGFSVSYPKGYETDTGYKAEPWHYLYIGPKPCFIQKKYFNNLQHKLLLEFW  
NQKNTNLINLIEKYANZ

f320.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAATCAATTTATGCTTTATTATTTCTATTTATTAATTTATCTTTGTTGGCTAACAACATTTCAAAAAAAGATT  
TAGAAGTACTGCTAAAGATTGCCCAAGCAATGAATAAGGAATGCAAAAATTTTATTGAAAAAATCCTATTCAGTT  
CTTAAAGAAATAAAACCCTTAGTAGATGCAGAAAAAATAACCTCTTAACCTCTAATAAAATAAAAAATACCAATT  
CCTGAAAAATTATAAAATACCTGATCTGGTAAATATTGATGATTTTGAAGATCTTAAAAATCTTGGAGCAAAGACTA  
TTAAAGTAAGAAAAATATTAATCGAAGATTTAATTCGACTAATAAAAGATGCAAAAAATTTGGGATTGAAATTAA  
AATCAAAATCTGCTTACAGAACGCAAGAATATCAAAAAATTTTATTTGATTACAATGTCAAACTTATGGCAGAAAA  
GTTGCAGAAACCCAATCAGCAATTCAGGCCATTCTCAACATCATATGGGAACAGCAATAGATTTTATAAATATAG  
ATGATAATTTACTAAACACAAAAGAAGGAAAATGGCTTTATGAAAACCTCTCTAAAATACGGATTTTCCGTTTCATA  
CCCAAAAGGATATGAAACGGACACTGGATATAAAGCAGAGCCTTGGCACTACTTATACATAGGACCTAAGCCATGC  
TTTATTCAGAAAAAATATTTTAATAATTTACAACATAAGCTTCTTTGAATTTTGGAACCAAGCAACAAAACAAATCTTA  
TTAACCTAATTGAAAAATATGCAAACTAA

t320.nt

AACAACATTTCAAAAAAAGATTTAGAAGTACTGCTAAAGATTGCCCAAGCAATGAATAAGGAATGCAAAAATTTTA  
TTGAAAAAATCCTATTCAGTTCTTAAAAGAAATAAAACCCTTAGTAGATGCAGAAAAAATAACCTCTTAACCTCT  
AATAAAATAAAAAATACCAATTCCTGAAAATTATAAAATACCTGATCTGGTAAATATTGATGATTTTGAAGATCTT  
AAAAATCTTGGAGCAAAGACTATTAAAGTAAGAAAAATATTAATCGAAGATTTAATTCGACTAATAAAAGATGCAA  
AAAAATTTGGGATTGAAATTAAATCAAATCTGCTTACAGAACGCAAGAATATCAAAAAATTTTATTTGATTACAA  
TGTCAAAACCTTATGGCAGAAAAGTTGCAGAAACCCAATCAGCAATTCAGGCCATTCTCAACATCATATGGGAACA  
GCAATAGATTTTATAAATATAGATGATAATTTACTAAACACAAAAGAAGGAAAATGGCTTTATGAAAACCTCTCTAA  
AATACGGATTTTCCGTTTCATACCCAAAAGGATATGAAACGGACACTGGATATAAAGCAGAGCCTTGGCACTACTT  
ATACATAGGACCTAAGCCATGCTTTATTCAGAAAAAATATTTTAATAATTTACAACATAAGCTTCTTTGAATTTTGG  
AACCAGAACAAAACAAATCTTATTAACCTAATTGAAAAATATGCAAACTAA

f342.aa

MLYLGDNKMAMRTKIIIMTIIILLAPISGFSNSKESARGKFGAGIILPLPIALQINIGNFDLDIGLYSGVNNLFSW  
KTLFIALDYIFYIYTFPGAANILDFSVGAGGYGTIWFSRFGGSKSGSGPMSIGARLPLALNIAVFRKKFDIFLRIA  
PGLGMNVWSNGVGFWEVFAAGLGLRFWFTZ

t342.aa

LAPISGFSNSKESARGKFGAGIILPLPIALQINIGNFDLDIGLYSGVNNLFSWKTTLFIALDYIFYIYTFPGAANI  
LDFSVGAGGYGTIWFSRFGGSKSGSGPMSIGARLPLALNIAVFRKKFDIFLRIAPGLGMNVWSNGVGFWEVFAAGL  
GLRFWFTZ

f342.nt

ATGCTATACTTAGGAGATAATAAAGCAATGAGAACAAAAATAATTATTATGACAATTATTATTTTATTAGCCCCAA  
TCTCAGGATTTTCTAATTCAAAAGAATCTGCAAGGGGTAAATTTGGAGCAGGAATTATACTTCCATTACCAATTGC  
TCTACAGATTAATATAGGAACTTTGATCTTGACATTGGTCTTTACAGCGGAGTAAATAATTTGTTTTCAGACTGG  
AAAACATTATTTATAGCATTAGACTATATTTTCTACATATACACATTCCCGGGAGCTGCTAATATTTTGGATTTT  
CAGTTGGCGCAGGGGGATATGGAACAATATGGTTTTCAAGATTTGGAGGCAGTAAGTCAGGCTCAGGACCAATGAG  
CATTGGAGCAAGATTGGCTTTTGGCCTTAAATATTGCAGTATTTAGGAAGAAATTCGACATATTTTACGAATAGCA  
CCCGGACTTGGAATGAATGTTTGGAGTAATGGCGTTGGATTTAGATGGGAAGTATTCGCAGGATTGGGACTAAGAT  
TCTGGTTTACTTAA

t342.nt

TTAGCCCCAATCTCAGGATTTTCTAATTCAAAAGAATCTGCAAGGGGTAAATTTGGAGCAGGAATTATACTTCCAT  
TACCAATTGCTCTACAGATTAATATAGGAACTTTGATCTTGACATTGGTCTTTACAGCGGAGTAAATAATTTGTT  
TTCAGACTGGAAAACATTATTTATAGCATTAGACTATATTTTCTACATATACACATTCCCGGGAGCTGCTAATATT  
TTGGATTTTTCAGTTGGCGCAGGGGGATATGGAACAATATGGTTTTCAAGATTTGGAGGCAGTAAGTCAGGCTCAG  
GACCAATGAGCATTTGGAGCAAGATTGCCTTTGGCCTTAAATATTGCAGTATTTAGGAAGAAATTCGACATATTTT

TABLE 1. Nucleotide and Amino Acid Sequences

ACGAATAGCACCCGGACTTGAATGAATGTTTGGAGTAATGGCGTTGGATTAGATGGGAAGTATTCGCAGGATTG  
GGACTAAGATTCTGGTTTACTTAA

f352.aa

MNKTKNRSLTYFIILSCISLFGANNNTISYSSIEIPLIEDLSEEFKSSGNKSDQINTSKHLNKNIVSYEDPKKGKDL  
KLPENIRDKKLPQKRMDENDLKSIVIENYENKIKNIEKLLKTKNQKTSSENENKKIESIEKKAKKYEILTNKLKNEIV  
EIKKLLNKKIKPKEDENYEKININIEEETDDDFEDNYEYNDEIEEQMRTITLLMKEZ

t352.aa

CISLFGANNNTISYSSIEIPLIEDLSEEFKSSGNKSDQINTSKHLNKNIVSYEDPKKGKDLKLPENIRDKKLPQKR  
MDENDLKSIVIENYENKIKNIEKLLKTKNQKTSSENENKKIESIEKKAKKYEILTNKLKNEIVEIKKLLNKKIKPKED  
ENYEKININIEEETDDDFEDNYEYNDEIEEQMRTITLLMKEZ

f352.nt

ATGAATAAAACAAAAAATCGAAGCCTTACGTATTTTATAATACTTTTCATGTATATCATTATTTGGGGCTAATAATA  
ATACAATAAGCTACTCTAGCATTGAAATTCCTCTAGAAGACTTAAGTGAAGAATTTAAAAGTTCTGGGAATAAAAG  
CGATCAAATAAATACCTCAAAACATTTAAACAAAAACATAGTTTCTTATGAAGACCCAAAAAAGGGTAAAGATCTA  
AAATTGCCAGAAAATATAAGAGACAAAAAACTACCCCAAAAAAGAATGGACGAAAATGATCTAAAATCTGTAATTG  
AAAATTATGAAAATAAAATTTAAAAACATAGAAAAGCTTTTAAAAACCAAAAAATCAAAAAACATCGGAAAATGAAAA  
TAAAAAATAGAATCAATCGAAAAAAAAGCAAAAAATATGAAATTTTAACCAATAAATTTAAAAACGAAATAGTA  
GAAATAAAAAAGCTCCTTAACAAAAAAATCAAGCCTAAAGAAGATGAAAATTACGAAAAAATAAATATTGAAAACA  
TTGAAGAAGAACTGATGATGATTTTGAAGACAATTATGAATATAATGATGAAATGAAGAACAAATGAGGACAAT  
TACCCTTCTAATGAAGGAATAA

t352.nt

TGTATATCATTATTTGGGGCTAATAATAATACAATAAGCTACTCTAGCATTGAAATTCCTCTAGAAGACTTAAGTG  
AAGAATTTAAAAGTTCTGGGAATAAAAGCGATCAAATAAATACCTCAAAACATTTAAACAAAAACATAGTTTCTTA  
TGAAGACCCAAAAAAGGGTAAAGATCTAAAATTGCCAGAAAATATAAGAGACAAAAAACTACCCCAAAAAAGAATG  
GACGAAAATGATCTAAAATCTGTAATTGAAAATTATGAAAATAAAATTTAAAAACATAGAAAAGCTTTTAAAAACCA  
AAAATCAAAAAACATCGGAAAATGAAAATAAAAAAATAGAATCAATCGAAAAAAAAGCAAAAAAATATGAAATTTT  
AACCAATAAATTTAAAAACGAAATAGTAGAAATAAAAAAGCTCCTTAACAAAAAATCAAGCCTAAAGAAGATGAA  
AATTACGAAAAAATAAATATTGAAAACATTGAAGAAGAACTGATGATGATTTTGAAGACAATTATGAATATAATG  
ATGAAATTGAAGAACAAATGAGGACAATTACCCTTCTAATGAAGGAATAA

f301.aa

MQIDGKIYSIIISFPVRDSVSTLGVIGILICFDESLDIIENQLYSSLKFGSKNYNFFMLDRNYMPIFSNLNNLQAKS  
FSTAYSENFLSKVIAAYAKKDSSSSQYTFNYERDFYSLNFVKTDFFLTQGLILNVNSIPIMFKSNWVIFVAFLLLSF  
AIIFYLCNTFVFLINDFNIRVDYQKSKSDPFSLESPLVKYSSSIISYISSKLDNLSSKSNESEFEKIKFYSEDNL  
EYLEQIETAISNTESIDSSILVYEQLRDTFSRFEKSIVDILKGFESIADPINDHNKYISEISSNFEESVSFFYSID  
KNLEIFNKVATINSTDIENIKSKVFDLNVFENVNKNFADLLSQTNLSQSVNKLVSISAQTNMLAMNAAIEAAGA  
GDAGKSAFVVAEEIRKLAINSGKYSKTIKDELKTVDSIIAVINSEIDTIYKNFIDIQDNVDNNFSRHEKVDLTLAK  
HFKEIGEFKERYLSHDTKIRDAKNMYKEIFNNHYFISGKFNNFSQDLKEFKVSKMNLDAVSSLQEYSSLVKSSKDK  
ILKTKELIQKINDEIKDILFZ

t301.aa

CFDESLDIIENQLYSSLKFGSKNYNFFMLDRNYMPIFSNLNNLQAKSFSTAYSENFLSKVIAAYAKKDSSSSQYTFN  
YERDFYSLNFVKTDFFLTQGLILNVNSIPIMFKSNWVIFVAFLLLSFAIIFYLCNTFVFLINDFNIRVDYQKSKS  
DPFSLESPLVKYSSSIISYISSKLDNLSSKSNESEFEKIKFYSEDNLNEYLEQIETAISNTESIDSSILVYEQLRDT  
FSRFEKSIVDILKGFESIADPINDHNKYISEISSNFEESVSFFYSIDKNLEIFNKVATINSTDIENIKSKVFDLNI  
VFENVNKNFADLLSQTNLSQSVNKLVSISAQTNMLAMNAAIEAAGAGDAGKSAFVVAEEIRKLAINSGKYSKTIK

TABLE 1. Nucleotide and Amino Acid Sequences

DELKTVDSIIIAVINSEIDTIYKNFIDIQDNVDNNSRHEKVDLTLAKHFKEIGEFKERYLSHDTKIRDAKNMYKEI  
FNNHYFISGKFNNFSQDLKEFKVSKMNLDAVSSLQEYSSLVKSSKDKILKTKELIQKINDEIKDILFZ

f301.nt

ATGCAAATAGATGGGAAAATTTATTCTATAATAAGTTTTCCAGTTAGAGATTCTGTTTCAACATTGGGTGTGATAG  
GGATTTTAATATGCTTTGATGAGTCGTTAGATATTATTGAAAATCAGTTGTATTCTTCTCTTAAATTTGGTAGTAA  
AAATTATAATTTTTTTATGCTTGACAGAAATTACATGCCCATTTTTTCAAACCTTAATAATCTTCAGGCCAAATCT  
TTTTCTACAGCTTATAGTGAGAAATTTTTGAGTAAAGTTATAGCTTATGCTAAAAAAGATTCTTCTAGCTCTCAGT  
ACACTTTTAATTATGAAAGAGATTTTTATTCTTTAAACTTTGTAAAAACCGATGATTTTTTTGACTCAGGGGCTTAT  
TTTAAATGTCAATTCCATTCTATTATGTTTAAATCAAATTGGGTATATTGTTGCATTTTTATTATTGTCTTTT  
GCAATTATTTTTTATTATGCAATACTTTTGTTTTTTTCATTAATTAATGATTTTAAACAGAATTGTTGACTATCAAA  
AATCAAAAAGCGATCCTTTTAGTCTTGAATCTCCCTTAGAGGTTAAGTATTCTTCATCTATTATTTCTTATATTAG  
TTCAAAGCTAGATAATCTGTCTTCTAAGAGTAATGAATCTTTTGAGAAGATAAAAATTTTATTCTGAAGATTTGAAT  
GAATATTTGGAACAAATAGAACTGCTATATCAAATACTGAGAGTATAGATTCTAGCATTTTAGTTTACGAACAAC  
TAAGAGATACTTTTTCTAGATTTGAAAAATCAATTGTTGATATTTTAAAGGCTTTGAATCTATTGCTGATCCGAT  
TAATGATCACAATAAATATATATCAGAAATCTCTCAAATTTTGAAGAGAGTGTTAGTTTTTTCTATAGTATAGAT  
AAAAATTTAGAAATTTTAAATAAGGTTGCTACTATAAATCTACTGATATTGAAAAATTTAAAGTAAGGTTTTTG  
ATTTAAATATTGTTTTTGAAGTGAATAAAAATTTTGCAGATCTTTTGTCTCAAACAAATAGTTTGCAGAGTGT  
AAATAAATCTTTTAGTTTCAATTTTCAGCTCAGACCAATATGCTTGCTATGAATGCAGCAATTGAAGCAGCAAAAGCA  
GGTGATGCAGGTAAAAGTTTTCAGTTGTTGCTGAGGAGATTAGAAAGCTTGCTATTAATTTCTGGAAAATATTCTA  
AAACCATTAAAGATGAACCTTAAACCGTTCGACAGCATTATTGCAGTAATTAATTCAGAGATTGATACAATTTATAA  
AAATTTTCATAGACATTCAAGATAATGTGGACAACAATTTTTCAAGACACGAGAAAGTAGATCTTACTCTTGCTAAG  
CATTTTAAAGAAATTGGCGAGTTTAAAGAAAGGTATTTGTCTCACGATACTAAGATCAGAGATGCTAAGAATATGT  
ATAAAGAAATATTTAATAATCATTTATTTATTAGTGGCAAGTTTAAACAATTTAGTCAAGATTTAAAGAGTTTAA  
AGTTTCTAAGATGAATTTAGATGCGGTAAGTTCTCTTCAAGAATATTCATCTTTAGTAAAGTCTTCTAAGGATAAG  
ATATTAAAGACAAAGGAATTGATTCAAAAGATTAATGATGAGATTAAAGATATTCTTTTTTTAG

t301.nt

TGCTTTGATGAGTCGTTAGATATTATTGAAAATCAGTTGTATTCTTCTCTTAAATTTGGTAGTAAAAATTATAATT  
TTTTTATGCTTGACAGAAATTACATGCCCATTTTTTCAAACCTTAATAATCTTCAGGCCAAATCTTTTTCTACAGC  
TTATAGTGAGAATTTTTTGAAGTAAAGTTATAGCTTATGCTAAAAAAGATTCTTCTAGCTCTCAGTACACTTTTAAT  
TATGAAAGAGATTTTTTATTCTTTAACTTTGTAAAAACCGATGATTTTTTGAAGTCAAGGGCTTATTTTAAATGTCA  
ATTCATTCTCTATTATGTTTAAATCAAATTGGGTTATATTGTTGCATTTTTATTATTGTCTTTTTGCAATTATTTT  
TTATTTATGCAATACTTTTGTTTTTTCATTAATTAATGATTTTAAACAGAATTGTTGACTATCAAAAATCAAAAAGC  
GATCCTTTTAGTCTTGAATCTCCCTTAGAGGTTAAGTATTCTTCATCTATTATTCTTATATTAGTTCAAAGCTAG  
ATAATCTGTCTTCTAAGAGTAATGAATCTTTTGAGAAGATAAAAATTTTATTCTGAAGATTTGAATGAATATTTGGA  
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ATAAATATATATCAGAAATCTCTCAAATTTTGAAGAGAGTGTTAGTTTTTTCTATAGTATAGATAAAAATTTAGA  
AATTTTAAATAAGGTTGCTACTATAAATCTACTGATATTGAAAATATTAAAGTAAGGTTTTTGATTTAAATATT  
GTTTTTGAAGTGTGAATAAAAATTTTGCAGATCTTTTGTCTCAAACAAATAGTTTGCAGAGTGTAATAAATCTT  
TAGTTTCAATTTTCAGCTCAGACCAATATGCTTGCTATGAATGCAGCAATTGAAGCAGCAAAAGCAGGTGATGCAGG  
TAAAGTTTTGCAGTTGTTGCTGAGGAGATTAGAAAGCTTGCTATTAATTTCTGGAAAATATTCTAAAACCATTTAA  
GATGAACCTTAAACCGTTCGACAGCATTATTGCAGTAATTAATTCAGAGATTGATACAATTTATAAAAATTTCTAG  
ACATTCAGATAATGTGGACAACAATTTTTCAAGACACGAGAAAGTAGATCTTACTCTTGCTAAGCATTTTAAAGA  
AATTGGCGAGTTTAAAGAAAGGTATTTGTCTCACGATACTAAGATCAGAGATGCTAAGAATATGTATAAAGAAATA  
TTTAATAATCATTTATTTTATTAGTGGCAAGTTTAAACAATTTAGTCAAGATTTAAAGAGTTTAAAGTTTCTAAGA  
TGAATTTAGATGCGGTAAGTTCTCTTCAAGAATATTCATCTTTAGTAAAGTCTTCTAAGGATAAGATATTAAAGAC  
AAAGGAATTGATTCAAAAGATTAATGATGAGATTAAAGATATTCTTTTTTTAG

f346.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MSIDKVPDEAFAEKIVGDGIAILPTSNEELLAPCDGKIGKIGKIFKTNHAFSLETKEGVEIFVHFGINTLNLNGKGFTRV  
AEEGINVKQGEVIIRLDLEYLKEHSESVITPVVIANSDEVSSIEYSFGRLENDSEYILSSSTVLTEEIRHKISQTK  
PVIAGKDLVLRVKKZ

t346.aa

CDGKIGKIFKTNHAFSLETKEGVEIFVHFGINTLNLNGKGFTRVAEEGINVKQGEVIIRLDLEYLKEHSESVITPV  
VIANSDEVSSIEYSFGRLENDSEYILSSSTVLTEEIRHKISQTKPVIAGKDLVLRVKKZ

f346.nt

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GCAATGAGTTGTTGGCGCCTTGTGATGGGAAAATAGGTAAAATTTTAAACCAATCATGCCTTTAGCCTTGAAAC  
TAAAGAGGGCGTTGAAATTTTGTCCATTTTGGAAATTAATACTCTTAATTTAAATGGTAAGGGTTTACAAGAGTT  
GCTGAAGAGGGCATTAAATGTTAAACAAGGTGAAGTTATTATTAGGCTTGATCTTGAATATTTAAAAGAGCATTGAG  
AATCCGTTATTACTCCGGTTGTTATTGCAAATCTGATGAAGTTTCAAGTATAGAATATTCTTTTGAAGGCTTGA  
AAATGATTCTGAATATATTTTATCATCTTCAACTGTCTTGACAGAAGAAATTAGGCATAAAATATCTCAAACAAAG  
CCTGTTATAGCGGGCAAAGATTGCTGTTGCGAGTTAAAAAGTAA

t346.nt

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TAAACAAGGTGAAGTTATTATTAGGCTTGATCTTGAATATTTAAAAGAGCATTGAGAATCCGTTATTACTCCGGTT  
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TTTGGTGTGCGAGTTAAAAAGTAA

f373.aa

MNYQRIKNYCKFTSVFLFFLFSCVSNELKLDQSLVKGKLVNGLRYYIYKNQTPKNAVNMGIVFNVGSLNEEDNERG  
IAHYLEHMAFNGTKDYPGNSIVDVLKKFGMQFGADINAATSFDFTYRDLSDGNNKDEIDESINILRNWASQISF  
MKEEIDLERNIIIEKKLGETYPGRIYEKMDKFLTSGSLYEFRSPIGLEEQILSFQPEDFKKFYRKWYRPELASVI  
VVGIDIDPIEIEEKIKKQFVSWKNPTDKIKEVKVSLDVELKDKFLLEDLEVGEPSLMFFKKEIINFVKTKDDLNA  
IKKSLAALFENRFSELKTAGVKQFKNVSNKDFFSFKSDNNTIVAKSISLNFNPDHLNEGIQDFFYELERIRKFGF  
TQGELEKVR SQFYKSLELRKKNINKTNSWAIFQDLIEIAINGSNKFD MNEYCDLSFQYLEKIDLKTINNLVGREFD  
VKNC AIFYSYHGRAHPVLTLEDIDNLQKIALKRELKPYENSLIEGKFFKKS LDDKDI IRENEFENEISSFVLENGV  
EVYFKYNDQKKGVIDFSATSWGGLINEDLKLIPVLSFAPGVVSGSGYGDYSALQIEKYLSDKAVSLRVGVGAQESY  
ISGSSDKKDL ETLFQLIYFTFKPKIDDVSLQNA INNIKALIKSNENSSDYHFHKAISKFLNNNDPRFEDTKDSDL  
QYFTKENILSFYKKRFTYANNFKFV LLETQIFRQZ

t373.aa

CVSNELKLDQSLVKGKLVNGLRYYIYKNQTPKNAVNMGIVFNVGSLNEEDNERGIAHYLEHMAFNGTKDYPGNSIV  
DVLKKFGMQFGADINAATSFDFTYRDLSDGNNKDEIDESINILRNWASQISFMKEEIDLERNIIIEKKLGETY  
PGRIYEKMDKFLTSGSLYEFRSPIGLEEQILSFQPEDFKKFYRKWYRPELASVIVVGIDIDPIEIEEKIKKQFVSWK  
NPTDKIKEVKVSLDVELKDKFLLEDLEVGEPSLMFFKKEIINFVKTKDDLNAIKKSLAALFENRFSELKTAGV  
KQFKNVSNKDFFSFKSDNNTIVAKSISLNFNPDHLNEGIQDFFYELERIRKFGFTQGELEKVR SQFYKSLELRKKN  
INKTNSWAIFQDLIEIAINGSNKFD MNEYCDLSFQYLEKIDLKTINNLVGREFDVKNCAIFYSYHGRAHPVLTLED  
IDNLQKIALKRELKPYENSLIEGKFFKKS LDDKDI IRENEFENEISSFVLENGVEVYFKYNDQKKGVIDFSATSWG  
GLINEDLKLIPVLSFAPGVVSGSGYGDYSALQIEKYLSDKAVSLRVGVGAQESYISGSSDKKDL ETLFQLIYFTFK  
EPKIDDVSLQNA INNIKALIKSNENSSDYHFHKAISKFLNNNDPRFEDTKDSDLQYFTKENILSFYKKRFTYANNF  
KFV LLETQIFRQZ

f373.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAATTATCAAAGAATTAAGAATTATTGTAAATTTACAAGCGTTTTTCTATTTTTTTTGTTCCTGTGTTTCTA  
ATGAGTTAAAGTTAGATCAAAGTTTGGTAAAAGGAAAACCTGTCAATGGGCTAAGGTATTATATTTATAAAAATCA  
AACCCCAAAGAAATGCCGTTAATATGGGAATTGTTTTTAATGTGGGCTCAC'TTAATGAAGAAGATAATGAGAGGGGA  
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AAAAATTTGGAATGCAATTTGGTGTCTGACATTAATGCTGCTACTAGTTTGTATTTCAC'TTATTATAGACTTGATTT  
GTCAGATGGTAATAATAAAGATGAAATTGATGAATCTATAAAATATTTTGAGAAACTGGGCTTCTCAAATCAGTTTC  
ATGAAAGAAGAAATAGATCTAGAGCGAAATATTATTATTGAGGAAAAAAGCTTGGTGAGACTTATCCTGGAAGAA  
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GTGGTAGGAGATATTGATCCTATAGAAATTGAAGAGAAGATAAAGAAGCAATTTGTTTCTTGGAAAAATCCAACCG  
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ACCCAAGGTGAGCTTGAAAAAGTTAGATCTCAATTTTACAAATCTTTAGAATTAAGGAAAAAGAATATAAATAAAA  
CAAATTCATGGGCTATTTTTTCAGGATTTAATAGAAATTGCTATTAATGGTCTAATAAATTTGATATGAATGAATA  
TTGCGATCTTTCTTTTCAATATTTGGAAGAGATTGATTTAAAAACAATAAACAATCTTGTAGGAAGAGAGTTTGAT  
GTAAAAAATGTGCAATTTTTTATTCTTACCATGGAAGAGCACATCCTGTTTTAACTCTTGAAGATATTGACAATC  
TTCAAAAGATAGCTTTAAAAAGAGAGTTAAAGCCTTATGAGAATCTTTAAATTGAAGGTAAATTTTTTAAGAAGTC  
TTTAGATGATAAAGATATTATTAGAGAAAATGAGTTTGAAAATGAAATTTCTGTCATTTGTTCTTGAAAATGGGGTT  
GAAGTTTATTTTAAATATAATGATCAAAAAAAGGTGTAATTGATTTTAGTGCAACTTCTTGGGGAGGTTTAATTA  
ATGAAGATTTAAACCTTATTCCTGTTTATCTTTTGCTCCCGGAGTAGTATCTGGTTCGGGTATGGTGATTATTC  
TGCATTACAGATTGAAAAATTTTATCAGATAAAGCTGTTTCTTTAAGAGTTGGGGTTGGAGCTCAAGAATCATAT  
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CAATATTTTACAAAAGAAAATATTTTGTCTTTTATAAGAAAAGGTTTACTTATGCAAATAATTTTAAGTTTGTCT  
TGCTGGAGACTCAGATATTCAGACAATAA

t373.nt

TGTGTTTCTAATGAGTTAAAGTTAGATCAAAGTTTGGTAAAAGGAAAACCTGTCAATGGGCTAAGGTATTATATTT  
ATAAAAATCAAACCCCAAAGAATGCCGTTAATATGGGAATTGTTTTTAATGTGGGCTCACTTAATGAAGAAGATAA  
TGAGAGGGGAATAGCGCATTATCTTGAACATATGGCTTTTAATGGTACAAAAGATTATCCAGGGAATTCTATAGTT  
GATGTTCTTAAAAAATTTGGAATGCAATTTGGTGTCTGACATTAATGCTGCTACTAGTTTTGATTTCACTTATTATA  
GACTTGATTTGTCAGATGGTAATAATAAAGATGAAATTGATGAATCTATAAAATATTTTGAGAACTGGGCTTCTCA  
AATCAGTTTCATGAAAGAAGAAATAGATCTAGAGCGAAATATTATTATTGAGGAAAAAAGCTTGGTGAGACTTAT  
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TGAATGAATATTGCGATCTTTCTTTTCAATATTTGGAAGAGATTGATTTAAAAACAATAAACAATCTTGTAGGAAG  
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ATTGACAATCTTCAAAGATAGCTTTAAAAAGAGAGTTAAAGCCTTATGAGAATCTTTAATTGAAGGTAAATTTT  
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GGTTTAATTAATGAAGATTTAAACCTTATTCCTGTTTATCTTTTGCTCCCGGAGTAGTATCTGGTTCGGGTATG  
GTGATTATTCTGCATTACAGATTGAAAAATTTTATCAGATAAAGCTGTTTCTTTAAGAGTTGGGGTTGGAGCTCA  
AGAATCATATATTTCTGGAAGTTCAGATAAAAAAGATCTTGAAACTCTTTTTTCAGCTTATATATTTTACTTTTAAG



TABLE 1. Nucleotide and Amino Acid Sequences

GAACCCAAAATTGATGATGTTTCTTTGCAAAATGCTATTAATAATATAAAAGCATTAATAAAGAGCAATGAAAATA  
GTTCTGATTATCATTTTTCATAAAGCCATTAGTAAATTTTTTAAACAATAATGATCCTAGATTTGAAGATACAAAAGA  
TAGTGATTTGCAATATTTTACAAAAGAAAATATTTTGTCTTTTTATAAGAAAAGGTTTACTTATGCAAATAATTTT  
AAGTTTGTCTTGCTGGAGACTCAGATATTCAGACAATAA

f384.aa

MDWDFEKIIFLLNESTRLLALSGCAKLILDFKSDGSIVTQVDKQIEQFLFKEIKKPGNFVLGEETISTYKEEYIKDA  
LISESTFIIDPIDGTSSFAAGLPSYGISLAYASGGKIEGAISLPLSGEFFITSKDNVIFYAKKNIGSYPLKKDFNK  
FIFDNSKCYNIHSL LAVRSII RLFNLDISSHIHINGSCVYSFAKLFTGSYKAYFSFVGLWDIAACLAIGNKLG MV  
GEFYCGNKMTLDILDSMYILEPNNHKRWSLK DFFIYSDNKSTIDI IRKDANKKINK

t384.aa

CAKLILDFKSDGSIVTQVDKQIEQFLFKEIKKPGNFVLGEETISTYKEEYIKDALISESTFIIDPIDGTSSFAAGL  
PSYGISLAYASGGKIEGAISLPLSGEFFITSKDNVIFYAKKNIGSYPLKKDFNK FIFDNSKCYNIHSL LAVRSII  
RLFNLDISSHIHINGSCVYSFAKLFTGSYKAYFSFVGLWDIAACLAIGNKLG MVGEFYCGNKMTLDILDSMYILEP  
NNHKRWSLK DFFIYSDNKSTIDI IRKDANKKINKZ

f384.nt

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GATCAAAAAGCCTGGAAATTTTGTCTTGAGAGAAGAGACAATATCTACTTATAAAGAAGAGTATATCAAAGATGCT  
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GAATATCGCTAGCGTATGCTAGTGGCGGCAAAATTATTGAAGGAGCCATTTCTCTTCCTTTAAGCGGAGAGTTTTT  
TATTACTTCTAAAGATAATGTATTTTATGCTAAAAAAACATTGGTAGCTATCCTTTAAAAAAGGATTTTAAATAAA  
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ATCTTGATATTTCTTCTCATATTCATATTAATGGTTCTTGTGTATATTCTTTTGCTAAACTTTTTACAGGTTCTTA  
TAAGGCCTACTTTTCTTTTGTAGGACTTTGGGATATTGCAGCGTGTTTAGCTATTGGTAATAAATTGGGCATGGTT  
GGCGAATTTTATTGTGGTAATAAAATGACATTAGATATCTTAGATTCAATGTATATTTTAGAGCCTAATAATCATA  
AAAGATGGTCCTTGAAAGATTTTTTTATTATTCTGATAATAAATCAACAATAGACATTATAAGAAAAGATGCAAA  
TAAAAAATCAATAAGTAA

t384.nt

AGTGGTTGTGCTAAATTAATTTTAGATTTTAAATCTGATGGGTCTATTGTAACCTCAGGTTGATAAGCAAATTGAGC  
AATCTTATTCAAAGAGATCAAAAAGCCTGGAAATTTTGTCTTGAGAGAAGAGACAATATCTACTTATAAAGAAGA  
GTATATCAAAGATGCTTTAATATCAGAGAGTACTTTTATTATTGATCCTATTGATGGAACCTCTTCTTTTGCAGCA  
GGCCTTCCTTCATATGGAATATCGCTAGCGTATGCTAGTGGCGGCAAAATTATTGAAGGAGCCATTTCTCTTCCTT  
TAAGCGGAGAGTTTTTTATTACTTCTAAAGATAATGTATTTTATGCTAAAAAAACATTGGTAGCTATCCTTTAA  
AAAGGATTTTAAATAAATTTATTTTGTGATAATTCTAAATGTTACAATATTCATAGTTTACTTGCAGTTTCAAGGTC  
ATTATAAGGTTATTTAATCTTGATATTTCTTCTCATATTCATATTAATGGTTCTTGTGTATATTCTTTTGCTAAAC  
TTTTTACAGGTTCTTATAAGGCCTACTTTTCTTTTGTAGGACTTTGGGATATTGCAGCGTGTTTAGCTATTGGTAA  
TAAATTGGGCATGGTTGGCGAATTTTATTGTGGTAATAAAATGACATTAGATATCTTAGATTCAATGTATATTTTA  
GAGCCTAATAATCATAAAAGATGGTCCTTGAAAGATTTTTTTATTATTCTGATAATAAATCAACAATAGACATTA  
TAAGAAAAGATGCAAAATAAAAAAATCAATAAGTAA

f860.aa

MAFYKLNDNIALAEDLLKYLLSSILNECSQDMDFLENYIEKGLIKKLENVINSNFEVITYTKAIEILENSKKNFEI  
KPYWGIDLQTDHERYLTEETFKKPVVVIDY PKNFKAFYMKANKDNKTVKGM DILVPKIGEI IGGSEREDDLQKLEN  
RIKELNLNIEHLNWYLDLRRFGSAPHSGFGLGLERLVQYSTGISNIRDSI PFPRTPKNLYFZ

t860.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CSQDMDFLENYIEKGLIKKLENVINSNFEVITYTKAIEILENSKKNFEIKPYWGIDLQTDHERYLTEETFKKPVVV  
IDYPKNFKAFYMKANKDNKTVKGMIDILVPKIGEIIIGSEREDDLQKLENRIKELNLNIEHLNWYLDLRRFGSAPHS  
GFGGLGLERLVQYSTGISNIRDSIPFPRTPKNLYFZ

f860.nt

ATGGCTTTTTTATAAGCTTAACGACAATATTGCCCTAGCAGAAGATCTCTTGAAATATCTTTTAAGTTCAATTTTAA  
ACGAATGCTCACAAGATATGGATTTTTTAGAAAATTACATTGAAAAAGGTTAATTAAAAAACTAGAAAATGTAAT  
AAATTCAAATTTTGAGGTATTACCTATACATAAGCAATTGAAATCTTGAAAACCTCAAAAAAAATTTTGAAATA  
AAACCTTACTGGGGAATAGATTTGCAAACAGATCACGAAAGATACCTAACAGAAGAGACTTTTAAAAAACCGGTAG  
TGGTCATTGATTATCCAAAAAATTTCAAAGCATTTTACATGAAAGCAAATAAAGACAATAAACTGTTAAAGGAAT  
GGACATACTTGTTCAAAAAATTTGGAGAGATTATAGGGGGAAGCGAAAGAGAAGATGACCTTCAAAAAATTAGAAAT  
AGAATAAAAGAATTAACTTAAACATTGAACATCTAACTGGTATCTTGATCTAAGAAGATTTGGCTCGGCTCCTC  
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ATTCCCAAGGACTCCTAAAAATCTTTATTTTTTAA

t860.nt

TGCTCACAAGATATGGATTTTTTAGAAAATTACATTGAAAAAGGTTAATTAAAAAACTAGAAAATGTAATAAATT  
CAAATTTTGAGGTATTACCTATACTAAAGCAATTGAAATCTTGAAAACCTCAAAAAAAATTTTGAAATAAAACC  
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CAAGGACTCCTAAAAATCTTTATTTTTTAA

f446.aa

MKILRLCLLFLFFACTFDYDEYSSRSDVAKKFPSIQILGIKYDVVYNKEQTVLNSLSFSYFNDYKIYKAENGRFL  
YHSLDNEISGKFNNLEGSYITKDLDMRDSVEFKIEDKNYYLLNSNRLWLKNDKKLQSPPNELVLIRFNDKING  
KGFSYFLKSNVIFYDSGVEGIMNZ

t446.aa

CTFDYDEYSSRSDVAKKFPSIQILGIKYDVVYNKEQTVLNSLSFSYFNDYKIYKAENGRFLYHSLDNEISGKFNN  
LEGSYITKDLDMRDSVEFKIEDKNYYLLNSNRLWLKNDKKLQSPPNELVLIRFNDKINGKGFSYFLKSNVIFY  
DSGVEGIMNZ

f446.nt

ATGAAAATACTTAGACTTTGTTTGTGTTTGTGTTTTGCTTGTTGACTTTTGATTATGATGAGTATTCTAGTAGAT  
CTGATGTGGCCAAAAAGTTTCTTCAATACAAATATTAGGAATCAAGTATTATGATGTTGTATACAATAAAGAGCA  
AACCGTTTTTAAATCTTTAAGCTTTAGTTATTTCAATGACTATAAAATTTATAAGGCAGAGAATGGAAGGTTTTTA  
TATCATTCCCTAGATAATGAAATTTACGGGAAGTTTAATAATTTGGAAGGTTCTTATATTACAAAGGATTTGGATA  
TGAGAGATTCTGTAGAATTTAAAATAGAAGATAAAAATAATTATTATTGCTTAATTCAAAATAGGCTTTTATGGAA  
GAATAAAGACAAGAAGTTGCAATCCCCCCCCAAATGAGCTAGTATTAATTAGATTTAATGATAGCAAATAAACGGA  
AAAGGATTTTCTTATTTTTTAAAGAGCAATGTTTTTTATTTTGATTCTGGAGTTGAAGGAATCATGAATTGA

t446.nt

TGTACTTTTGATTATGATGAGTATTCTAGTAGATCTGATGTGGCCAAAAAGTTTCTTCAATACAAATATTAGGAA  
TCAAGTATTATGATGTTGTATACAATAAAGAGCAAACCGTTTTTAAATCTTTAAGCTTTAGTTATTTCAATGACTA  
TAAAATTTATAAGGCAGAGAATGGAAGGTTTTTATATCATTCCTAGATAATGAAATTTACGGGAAGTTTAATAAT  
TTGGAAGGTTCTTATATTACAAAGGATTTGGATATGAGAGATTCTGTAGAATTTAAAATAGAAGATAAAAATAATT  
ATTATTTGCTTAATTCAAATAGGCTTTTATGGAAGAATAAAGACAAGAAGTTGCAATCCCCCCCCAAATGAGCTAGT

TABLE 1. Nucleotide and Amino Acid Sequences

ATTAATTAGATTTAATGATAGCAAAATAAACGGAAAAGGATTTTCTTATTTTTTAAAGAGCAATGTTTTTTATTTT  
GATTCTGGAGTTGAAGGAATCATGAATTGA

f457.aa

MKQKLSWILLFCFLSCRSESRLAENVLIEFFDSIKNFQSSPEIFFNYLNIPSDDDLKAKIRGLKSQAKDDFIFYPL  
FFNNLRYEIIIGRKNISKGFEEVVIKNINFQNGIEKFLAKLNKIEGRSLNIKNEKKERKKIFDNLINEVIGELDD  
FDYTEVHVHFRVVKSSSESYKIELLGVDLNIQSRNKLINDLFLVLSPGIZ

t457.aa

CFLSCRSESRLAENVLIEFFDSIKNFQSSPEIFFNYLNIPSDDDLKAKIRGLKSQAKDDFIFYPLFFNNLRYEIIIG  
RKNISKGFEEVVIKNINFQNGIEKFLAKLNKIEGRSLNIKNEKKERKKIFDNLINEVIGELDDFDYTEVHVHFR  
VVKSSSESYKIELLGVDLNIQSRNKLINDLFLVLSPGIZ

f457.nt

ATGAAGCAAAAATTAAGTTGGATTTTATTATTTTGTTTTTTGTCTTGTAGATCTGAATCTAGATTGGCTGAAAATG  
TTTTAATAGAGTTTTTTGATTCTATTAAAAATTTTCAAAGCAGTCCTGAAATATTTTTTAAATTATTAAATATTCC  
AAGTGATGATGATCTGAAGGCAAAAATTCGTGGGTGAAATCTCAGGCAAAGGATGATTTTCATTTTTTATCCTTTG  
TTTTTTAATAATCTAAGATATGAGATAATAGGTAGAAAAATATTTCTAAGGGCTTTGAATTTGAAGTTGTTATTA  
AAAATATTAACTTTCAAACGGTATAGAAAAATTTTGGCTAAATTAATAAAAATTGAAGGGAGATCTTTAAATAT  
TAAAAATTTAGAAAAAAAAGAGCGTAAAAAAATATTTGACAATTTAATAAATGAAGTTATTGGAGAGTTGGATGAT  
TTTGATTACACTGAAGTTGTTTCATTTTTTTAGAGTAGTTAAGAGTTCTTCTGAAAGTTATAAAATAGAGCTTTTAG  
GAGATGTTTTTAAATATACAGTCTAGAAATAAGCTTATTAATGATCTTTTTTTTGGTTTTATCGCCTGGAATTTAA

t457.nt

TGTTTTTTGTCTTGTAGATCTGAATCTAGATTGGCTGAAAATGTTTTAATAGAGTTTTTTGATTCTATTAAAAAT  
TTCAAAGCAGTCCTGAAATATTTTTTAAATTATTAAATATTCCAAGTGATGATGATCTGAAGGCAAAAATTCGTGG  
GTTGAAATCTCAGGCAAAGGATGATTTTCATTTTTTATCCTTTGTTTTTTAATAATCTAAGATATGAGATAATAGGT  
AGAAAAATATTTCTAAGGGCTTTGAATTTGAAGTTGTTATTAAAAATATTAACTTTCAAACGGTATAGAAAAAT  
TTTTGGCTAAATTAATAAAAATTGAAGGGAGATCTTTAAATATTAATAAATTTAGAAAAAAAAGAGCGTAAAAAAAT  
ATTTGACAATTTAATAAATGAAGTTATTGGAGAGTTGGATGATTTTGATTACACTGAAGTTGTTTCATTTTTTTTAGA  
GTAGTTAAGAGTTCTTCTGAAAGTTATAAAATAGAGCTTTTAGGAGATGTTTTTAAATATACAGTCTAGAAATAAGC  
TTATTAATGATCTTTTTTTTGGTTTTATCGCCTGGAATTTAA

f542.aa

MRIVIFIFGILLTSCFSRNGIESSSKKIKISMLVDGVLDDKSFNSSANEALLRLKKDFPENIEEVFSCAISGVYSS  
YVSDLDNLKRNGSDLIWLVGYMLTDASLLVSENPKISYGIIDPIYGDDVQIPENLIAVVFVRVEPRCFFGWLYCSQ  
KKLFWQNRFYRGNEGZ

t542.aa

CFSRNGIESSSKKIKISMLVDGVLDDKSFNSSANEALLRLKKDFPENIEEVFSCAISGVYSSYVSDLDNLKRNGSD  
LIWLVGYMLTDASLLVSENPKISYGIIDPIYGDDVQIPENLIAVVFVRVEPRCFFGWLYCSQKKLFWQNRFYRGNE  
GZ

f542.nt

ATGAGAATTGTAATTTTTATATTCGGTATTTTGTGACTTCTTGCTTTAGTAGAAATGGAATAGAATCTAGTTCAA  
AAAAAATTAAGATATCCATGTTGGTAGATGGTGTTCTTGACGACAAATCTTTTAATTCTAGTGCTAATGAGGCTTT  
ATTACGCTTGAAAAAAGATTTTCCAGAAAAATATTGAAGAAGTTTTTCTTGCTGCTATTTCTGGAGTTTATTCTAGT  
TATGTTTCAGATCTTGATAATTTAAAAAGGAATGGCTCAGACTTGATTTGGCTTGTAGGGTACATGCTTACGGACG  
CATCTTTATTGGTTTCATCGGAGAATCCAAAAATTAGCTATGGAATAATAGATCCCATTATGGTGATGATGTTCA

TABLE 1. Nucleotide and Amino Acid Sequences

GATTCTCTGAAAACCTTGATTGCTGTTGTTTTTCAGAGTAGAGCCAAGGTGCTTTTTTGGCTGGCTATATTGCAGCCAA  
AAAAAGCTTTTCTGGCAAAATAGGTTTATAGGGGGAATGAAGGGTAA

t542.nt

TGCTTTAGTAGAAATGGAATAGAATCTAGTTCAAAAAAATTAAGATATCCATGTTGGTAGATGGTGTCTTGACG  
ACAAATCTTTTAATTCTAGTGCTAATGAGGCTTTATTACGCTTGAAAAAAGATTTTCCAGAAAAATATTGAAGAAGT  
TTTTTCTTGTGCTATTTCTGGAGTTTATTCTAGTTATGTTTCAGATCTTGATAATTTAAAAAGGAATGGCTCAGAC  
TTGATTTGGCTTGTAGGGTACATGCTTACGGACGCATCTTTATTGGTTTCATCGGAGAATCCAAAAATTAGCTATG  
GAATAATAGATCCCATTTATGGTGATGATGTTTCAGATTCCTGAAAACCTTGATTGCTGTTGTTTTCAGAGTAGAGCC  
AAGGTGCTTTTTTGGCTGGCTATATTGCAGCCAAAAAAGCTTTTCTGGCAAAATAGGTTTATAGGGGGAATGAA  
GGGTAA

f93.aa

MKRILAMHDISSMGRSTLTICIPVISSFNMQVCPFVTAVLSASTAYKKFEIVDLTDHLEKFINIWKEQNEHFDILY  
TGFLGSEKQQITIEKIIKLIKFEKIVIDPVFADDGEIYPIFDNKIISGFRKIIKYANIITPNITELEMLSKSSKLN  
NKDDIIKAILNLDTKATVVVTSVKRGNLLGNICYNPKNKEYSEFFLEGLEQNFSGTGDLFTSLLIGYLEKFETEQALEKTTKAIHLIIKESIKENVSKKEGVRIENFLKNTFZ

t93.aa

CIPVISSFNMQVCPFVTAVLSASTAYKKFEIVDLTDHLEKFINIWKEQNEHFDILYTGFLGSEKQQITIEKIIKLI  
KFEKIVIDPVFADDGEIYPIFDNKIISGFRKIIKYANIITPNITELEMLSKSSKLNKDDIIKAILNLDTKATVVV  
TSVKRGNLLGNICYNPKNKEYSEFFLEGLEQNFSGTGDLFTSLLIGYLEKFETEQALEKTTKAIHLIIKESIKENV  
SKKEGVRIENFLKNTFZ

f93.nt

ATGAAAAGAATTTTAGCAATGCATGATATTTCAAGCATGGGAAGAACATCTCTTACAATATGCATACCAGTAATAT  
CTTCGTTTAATATGCAAGTTTGTCTTTTGTGACAGCTGTCCTTTCTGCTTCCACAGCTTATAAAAAATTTGAAAT  
AGTGGATTTAACCGATCATTTAGAAAAATTTATCAATATATGGAAGAACAATAAGAGCACTTTGACATACTCTAT  
ACCGGATTTCTGGGAAGCGAAAAACAACAATAACAATAGAGAAAATAATTAAATTAATAAAATTTGAAAAAATTG  
TAATTGATCCTGTGTTTGTGCTGACGATGGAGAAATTTACCCTATATTTGATAATAAAATAATTAGTGGATTTAGAAA  
AATCATAAAGTACGCAACATAATAACACCCAATATCACAGAACTTGAAATGCTAAGCAAAAGCTCAAAACTTAAC  
AACAAAGATGATATCATAAAGCAATATTAATCTTGATACAAAAGCGACGGTAGTTGTTACAAGCGTTAAAAGGG  
GAAATCTCTTGGGAACATTTGCTACAATCCTAAAAACAAAGAATACTCGGAGTTTTTTTTTAGAAGGATTAGAACA  
AAATTTAGTGAACAGGAGATTTATTTACCAGCTTACTTATAGGATATTTGGAAAAATTTGAAACAGAGCAAGCC  
TTAGAAAAACAACAAGGCTATTCACCTAATAATAAAGAGTCAATTAAGAAAATGTTTCAAAAAAGAAGGGG  
TCCGAATTGAAAATTTCTTAAAAAATACATTTTGA

t93.nt

TGCATACCAGTAATATCTTCGTTTAATATGCAAGTTTGTCTTTTGTGACAGCTGTCCTTTCTGCTTCCACAGCTT  
ATAAAAAATTTGAAATAGTGGATTTAACCGATCATTTAGAAAAATTTATCAATATATGGAAGAACAATAAGAGCA  
CTTTGACATACTCTATACCGGATTTCTGGGAAGCGAAAAACAACAATAACAATAGAGAAAATAATTAAATTAATA  
AAATTTGAAAAAATTGTAATTGATCCTGTGTTTGTGCTGACGATGGAGAAATTTACCCTATATTTGATAATAAAATA  
TTAGTGGATTTAGAAAAATCATAAAGTACGCAACATAATAACACCCAATATCACAGAACTTGAAATGCTAAGCAA  
AAGCTCAAAACTTAACAACAAGATGATATCATAAAGCAATATTAATCTTGATACAAAAGCGACGGTAGTTGTT  
ACAAGCGTTAAAAGGGGAAATCTCTTGGGAACATTTGCTACAATCCTAAAAACAAAGAATACTCGGAGTTTTTTTT  
TAGAAGGATTAGAACAATAATTTAGTGAACAGGAGATTTATTTACCAGCTTACTTATAGGATATTTGGAAAAATT  
TGAAACAGAGCAAGCCTTAGAAAAACAACAAGGCTATTCACCTAATAATAAAGAGTCAATTAAGAAAATGTT  
TCAAAAAAGAAGGGGTCCGAATTGAAAATTTCTTAAAAAATACATTTTGA

f105.aa

TABLE 1. Nucleotide and Amino Acid Sequences

MGLYLKLLRQSINLKSLFPLSVLFFSCNVVDTDVSVLEFKVANFNLNDDFSQGLLDSAYNILNRSFDLIIKLNKLN  
KNVLDLINNRVLFRAFKNAYFIDQGSGLSVSILSKRKINIKVLSVMQDSCDLKLGLLVDFKFENNHYGIVINYLSK  
DFIKSIANLQISEQILYLKAQMDKLMFILDESEFVIFDLLIKNGFFSLINDSNYTSMLANKIDFRVFSNFFARVSL  
YSFMFVIADYLHSNYVVENFPQKIVINZ

t105.aa

CNVVDTDVSVLEFKVANFNLNDDFSQGLLDSAYNILNRSFDLIIKLNKKNVLDLINNRVLFRAFKNAYFIDQGS  
GLSVSILSKRKINIKVLSVMQDSCDLKLGLLVDFKFENNHYGIVINYLSKDFIKSIANLQISEQILYLKAQMDKLM  
FILDESEFVIFDLLIKNGFFSLINDSNYTSMLANKIDFRVFSNFFARVSLYSFMFVIADYLHSNYVVENFPQKIVI  
NZ

f105.nt

ATGGGCTTGTATTTGAAGTTGTTGAGACAAAGTATCAACTTGAAGAGTTTATTTCCGCTTAGTGTTTTATTTTTTT  
CCTGTAATGTTGTAGATACAGATTTTAGTGTTTTGGAGTTTAAGGTTGCAAATTTTAATTTAAATGATGATTTTTC  
TCAAGGGTACTTGATTCTGCCTTATAATATTCTAAATCGAAGTTTTGATTTAATAATTATTAAGAATCTTAAGAAT  
AAAAATGTTCTTGATTTAATTAATAATAGAGTTTTATTAGAGCTTTTAAGAATGCTTATTTTATTGATCAAGGTA  
GTGGCCTTCTGTAGCATTCCTTCTAAGCGCAAAATAAATATTAAGTTTTAAGTGTAATGCAAGATTCTTGCGA  
TTTAAATTAGGATTGCTTGTGGATTTTAAATTTGAGAATAATCACTATGGTATTGTTATTTATAATTTAAGCAAG  
GATTTTATTTAAAGTATTGCCAATTTGCAAATTAGTGAACAAATTTTATATTTAAAGCCCCAAATGGATAAATTGA  
TGTTTATTTAGATGAATCTGAATTTGTTATTTTGGATTTATTAATCAAAAATGGATTTTTTAGCTTAATAAATGA  
TTCAAACACACTCAATGTTAGCAAATAAATGATTTTAGAGTTTTTCTAATTTTTTGTCTAGGGTTTCTTTA  
TATTCATTTATGTTTGTAAATGCAGATTATTTGCATAGCAATTATGTTGTTGAGAATTTTCCTCAAAAAATAGTTA  
TCAATTGA

t105.nt

TGTAATGTTGTAGATACAGATTTTAGTGTTTTGGAGTTTAAGGTTGCAAATTTTAATTTAAATGATGATTTTCTC  
AAGGGTACTTGATTCTGCCTTATAATATTCTAAATCGAAGTTTTGATTTAATAATTATTAAGAATCTTAAGAATAA  
AAATGTTCTTGATTTAATTAATAATAGAGTTTTATTAGAGCTTTTAAGAATGCTTATTTTATTGATCAAGGTAGT  
GGCCTTCTGTAGCATTCCTTCTAAGCGCAAAATAAATATTAAGTTTTAAGTGTAATGCAAGATTCTTGCGATT  
TAAATTAGGATTGCTTGTGGATTTTAAATTTGAGAATAATCACTATGGTATTGTTATTTATAATTTAAGCAAGGA  
TTTTATTTAAAGTATTGCCAATTTGCAAATTAGTGAACAAATTTTATATTTAAAGCCCCAAATGGATAAATTGATG  
TTTATTTTAGATGAATCTGAATTTGTTATTTTGGATTTATTAATCAAAAATGGATTTTTTAGCTTAATAAATGATT  
CAAACACACTCAATGTTAGCAAATAAATGATTTTAGAGTTTTTCTAATTTTTTGTCTAGGGTTTCTTTATA  
TTCATTTATGTTTGTAAATGCAGATTATTTGCATAGCAATTATGTTGTTGAGAATTTTCCTCAAAAAATAGTTATC  
AATTGA

f150.aa

MKTFVIIIGLSNLGIHLLLEDLSRLDCQIIIIIDTSKELIEEYDVISTESFVVEQFTKNALKRIIPVDTDAVVIDFDD  
LGKSALVTHYCNLLGLKEICVKTENRDDAEILKTLGATKIIFPSKDAARRLTPLLVSPNLSTYNIIGYDIIVAETV  
IPKEYVGKTLFEADLRRECGITVIAVRNLSNSRYEFVDGDYFFLKDDKIVICGKPDSIENFTNNKDLIKDLISGSK  
EDENLNKDAEKKSRFLGIFNFMKIFQKDRKDNZ

t150.aa

CQIIIIIDTSKELIEEYDVISTESFVVEQFTKNALKRIIPVDTDAVVIDFDDDLGKSALVTHYCNLLGLKEICVKTE  
NRDDAEILKTLGATKIIFPSKDAARRLTPLLVSPNLSTYNIIGYDIIVAETVIPKEYVGKTLFEADLRRECGITVI  
AVRNLSNSRYEFVDGDYFFLKDDKIVICGKPDSIENFTNNKDLIKDLISGSKEDENLNKDAEKKSRFLGIFNFMKI  
FQKDRKDNZ

f150.nt

TABLE 1. Nucleotide and Amino Acid Sequences

ATGAAAACATTTGTTATTATTGGACTTAGTAATTTAGGCATTCACTTACTTGAAGATTTAAGCAGGCTTGATTGTC  
AAATTATTATTATAGATACATCTAAAGAGCTTATTGAAGAATATGATGTGATATCTACAGAAAGCTTTGTTGTTGA  
GCAATTCATAAAAAATGCTTTGAAAAAGAATAATTCCAGTAGATACAGACGCTGTTGTTATTGATTTTGATGATGAT  
CTTGGCAAAAGTGCTCTTGTACTCACTATTGTAATCTTTTAGGTTTGAAAGAAATATGCGTTAAGACAGAAAATA  
GAGATGATGCTGAAATCTTAAAACTCTTGGGGCAACAAAAATTATATTTCCAAGTAAAGATGCTGCAAGAAGATT  
AACTCCATTATTAGTATCTCCAAATCTTCAACTTATAATATTATTGGGTATGATATTATTGTTGCTGAACTGTT  
ATTCCCAAAGAATATGTTGGTAAACTCTTTTGAAGCCGATCTTAGAAGAGAATGTGGGATTACAGTTATTGCTG  
TTAGAAATTTAAGTAATCTAGGTATGAATTTGTTGATGGCGATTATTTTTTTTTTAAAGATGATAAAATTGTAAT  
TTGTGGTAAACCAGATAGCATTGAAAAATTTACAAATAATAAAGATTTAATTAAAGATTTAATTTTCAGGCTCTAAA  
GAGGATGAAAAATTTAAATAAAGATGCTGAGAAAAATCTAGATTTTTAGGGATTTTCAATTTTATGAAAATTTTTTC  
AAAAAGATCGTAAGGATAATTAG

t150.nt

TGTCAAATTATTATTATAGATACATCTAAAGAGCTTATTGAAGAATATGATGTGATATCTACAGAAAGCTTTGTTG  
TTGAGCAATTCATAAAAAATGCTTTGAAAAAGAATAATTCCAGTAGATACAGACGCTGTTGTTATTGATTTTGATGA  
TGATCTTGGCAAAAGTGCTCTTGTACTCACTATTGTAATCTTTTAGGTTTGAAAGAAATATGCGTTAAGACAGAA  
AATAGAGATGATGCTGAAATCTTAAAACTCTTGGGGCAACAAAAATTATATTTCCAAGTAAAGATGCTGCAAGAA  
GATTAACCTCATTATTAGTATCTCCAAATCTTCAACTTATAATATTATTGGGTATGATATTATTGTTGCTGAAAC  
TGTTATTCCCAAAGAATATGTTGGTAAACTCTTTTGAAGCCGATCTTAGAAGAGAATGTGGGATTACAGTTATT  
GCTGTTAGAAATTTAAGTAATCTAGGTATGAATTTGTTGATGGCGATTATTTTTTTTTTAAAGATGATAAAATTG  
TAATTTGTGGTAAACCAGATAGCATTGAAAAATTTACAAATAATAAAGATTTAATTAAAGATTTAATTTTCAGGCTC  
TAAAGAGGATGAAAAATTTAAATAAAGATGCTGAGAAAAATCTAGATTTTTAGGGATTTTCAATTTTATGAAAATT  
TTTCAAAAAGATCGTAAGGATAATTAG

f219.aa

MLIARIMNINTLFYGMIIIFALISCNHKNIQYDKRIKKFLDNKIEYKIDSENDFIAFKDINNNEKEEVIIRSRL  
NSYKNSKIREIFGIVKVFNDINTPKIKEISDSLMSDSYNNRVFGSWEIIHNAERGINSLVYIVKAEFANDTFLDLA  
IDEIASTISIFKKIITNNENIDNNEENNTNESNEQPTLKQEKTNSTKESNNELKEDQIEEELQEIKAQZ

t219.aa

CNHKNIQYDKRIKKFLDNKIEYKIDSENDFIAFKDINNNEKEEVIIRSRLNSYKNSKIREIFGIVKVFNDINTPKI  
KEISDSLMSDSYNNRVFGSWEIIHNAERGINSLVYIVKAEFANDTFLDLAIDEIASTISIFKKIITNNENIDNN  
EENNTNESNEQPTLKQEKTNSTKESNNELKEDQIEEELQEIKAQZ

f219.nt

ATGCTAATTGCAAGAATAATGAATATTAATACATTATTCTACGGCATGATCATTATCATTTTTGCACTCATTTCTT  
GCAATCATAAGAATATACAGTACGACAAGAGAATTAATAAATTTTAGATAAAAAACAAAATTGAATATAAAATAGA  
CTCAGAAAATGACTTTATAGCATTTAAAGATATAAACAATAACGAAAAAGAAGTAATCATCAGATCAAGACTA  
AACTCATATAAAAAATTCAAAGATAAGAGAAAATATTTGGAATTGTTAAAGTATTTGATATAAACACACCAAAAAATA  
AAGAAATATCTGACTCGCTTATGAGCGATAGTTATAATAACAGAGTATTTGGATCGTGGGAGATTATTCATAATGC  
AGAAAGAGGAATCAACTCTTTGGTATATATTGTAAAAGCAGAAGAATTTGCAAATGATACATTTTTGCTTGATGCA  
ATTGATGAGATTGCCTCAACAATAAGTATTTTCAAAAAATAATAACAACCAACAACGAAAAACATTGATAATAATG  
AAGAAAATAACAATACAAATGAATCAAAATGAACAGCCACCTTAAAGCAAGAAAAACAAATTCACAAAAGAATC  
TAATAACGAACCTTAAAGAAGATCAAAATAGAAGAAGAACTTCAAGAAATCAAAGCCCAATAA

t219.nt

TGCAATCATAAGAATATACAGTACGACAAGAGAATTAATAAATTTTAGATAAAAAACAAAATTGAATATAAAATAG  
ACTCAGAAAATGACTTTATAGCATTTAAAGATATAAACAATAACGAAAAAGAAGTAATCATCAGATCAAGACT  
AACTCATATAAAAAATTCAAAGATAAGAGAAAATATTTGGAATTGTTAAAGTATTTGATATAAACACACCAAAAAATA  
AAAGAAATATCTGACTCGCTTATGAGCGATAGTTATAATAACAGAGTATTTGGATCGTGGGAGATTATTCATAATG  
CAGAAAGAGGAATCAACTCTTTGGTATATATTGTAAAAGCAGAAGAATTTGCAAATGATACATTTTTGCTTGATGC

TABLE 1. Nucleotide and Amino Acid Sequences

AATTGATGAGATTGCCTCAACAATAAGTATTTTCAAAAAATAATAACAACCAACAACGAAAACATTGATAATAAT  
GAAGAAAATAACAATACAAATGAATCAAATGAACAGCCACCTTAAAGCAAGAAAAACAAATTCAACAAAAGAAT  
CTAATAACGAACCTTAAAGAAGATCAAATAGAAGAAGAACTTCAAGAAATCAAAGCCCAATAA

f229.aa

MRVDLLPLVELSLYINLSFCKDFSIFNRILEELKCHLILLGHPIIKTLYIKHVDFCLSRQDNLKFIFTSLSKYIN  
LELLEEFTLEIIPGYVDFEKFLLDEFICITRINLNVQSFSLFRKIVGIPEISYKKNILINNIRKFPFDLNIDMT  
VNMPLQKKSHLKRDLQRIAFIYAZ

t229.aa

CKDFSIFNRILEELKCHLILLGHPIIKTLYIKHVDFCLSRQDNLKFIFTSLSKYINLELLEEFTLEIIPGYVDFE  
KLLDEFICITRINLNVQSFSLFRKIVGIPEISYKKNILINNIRKFPFDLNIDMTVNMPLQKKSHLKRDLQRIAF  
IYAZ

f229.nt

ATGAGAGTAGATCTTTTACCTCTTGTCGAGTTAAGTCTTTATATTAATTTGTCATTTTGTGTAAAGATTTTAGCA  
TTTTTAATAGAATTTTAGAGGAATTAAATGTCATTTAATCTTGCTGGGTCATCCAATTATAAAAAACACTTTACAT  
TAAGCACGTAGATTTTGTGTTATCTAGGCAAGATAATTTAAAATTTATTTTCACTTCTTTGTCCAAGTATATTAAT  
TTGGAGTTATTAGAAGAATTTACTTTAGAAATTATTCGGGTTATGTTGATTTTGAAAAATTCAAACCTTTGGATG  
AATTTTGTATTACTAGAATTAATCTTAATGTTCAAAGTTTTCTTTAGAGTTTAGAAAGATTGTGGGGATACCCGA  
AATTTCTTATAAAAAATTGAATATTTTGATTAACAATATTAGAAAGTTTCCTTTTGATTTGAATATTGACATGACT  
GTCAATATGCCTTTGCAAAAAAATCTCATCTCAAGCGAGATTTGCAAAGAATTGCTTTCATATATGCCTGA

t229.nt

TGTAAAGATTTTAGCATTTTAAATAGAATTTTAGAGGAATTAAATGTCATTTAATCTTGCTGGGTCATCCAATTA  
TAAAAACACTTTACATTAAGCACGTAGATTTTGTGTTATCTAGGCAAGATAATTTAAAATTTATTTTCACTTCTTT  
GTCCAAGTATATTAATTTGGAGTTATTAGAAGAATTTACTTTAGAAATTATTCGGGTTATGTTGATTTTGAAAA  
TTCAAACCTTTGGATGAATTTGTATTACTAGAATTAATCTTAATGTTCAAAGTTTTCTTTAGAGTTTAGAAAGA  
TTGTGGGGATACCCGAAATTTCTTATAAAAAATTGAATATTTTGATTAACAATATTAGAAAGTTTCCTTTTGATTT  
GAATATTGACATGACTGTCAATATGCCTTTGCAAAAAAATCTCATCTCAAGCGAGATTTGCAAAGAATTGCTTTC  
ATATATGCCTGA

f22.aa

MLKTLTKIITISCLIVGCASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNLSLPKYKSVLGLISNLYFSY  
KKENNDIFALLIMGNFPKIDIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTT  
KYIGEIEKNEMFFWIQDPTLLLPNQIVSSKNLIPFSSGTLINSNLNQEYIFKSLIKTNNPPILKILSKKLIPTVL  
TNMTNLTISSHIKTTIKDQNTVEIEFNIQKSSVESLIEKLASNIQT

t22.aa

CASLPYTPPKQNLNYLMELLPGANLYAHVNLIKNRSIYNLSLPKYKSVLGLISNLYFSYKKENNDIFALLIMGNFPK  
DIFWGIHKNRNTESIGNIFTNPKWKLKNSNIYIIPNKARTSIAITQKDITAKDNNMLTTKYIGEIEKNEMFFWIQD  
PTLLLPNQIVSSKNLIPFSSGTLINSNLNQEYIFKSLIKTNNPPILKILSKKLIPTVLTNMTNLTISSHIKTTIK  
DQNTVEIEFNIQKSSVESLIEKLASNIQT

f22.nt

ATGTTAAAAACATTAACAAAAATAATTACCATTTTCATGCCTCATAGTGGGATGCGCAAGCCTGCCTTACACTCCTC  
CAAAACAAAATCTAAATTACTTAATGGAACCTTTTACCTGGCGCAAATTTATACGCCCATGTAAATTTAATTA  
CAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCTTATAAGCAATTTTACTTTTAGCTAT  
AAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAATTTCCCAAAAGATATTTCTGGGGAATTCATAAAA

TABLE 1. Nucleotide and Amino Acid Sequences

ATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAACTTAAAAATTCAAATATATACATTAT  
TCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGCAAAAGACAATAATATGCTAACAACA  
AAATATATTGGGGAAATAGAAAAAAATGAAATGTTTTTTTGGATTCAAGATCCAACATTATTGCTCCCAAACCAAA  
TAGTAAGCAGCAAAAATTTAATTCCCTTTAGCAGTGGAACTTTGTCTATAAACAGCTTAAATCAAGAAGAATATAT  
TTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTCAAAAAAGTTAATTCCAACCGTCTTG  
ACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAAGACCAAAAATACGGTTGAAATAGAAT  
TTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAACTAGCTTCAAATATTCAAACCTAA

t22.nt

TGCGCAAGCCTGCCTTACACTCCTCCAAAACAAAATCTAAATTACTTAATGGAACTTTTACCTGGCGCAAATTTAT  
ACGCCCATGTAAATTTAATTAAAAAACAGGTCTATTTATAACTCTTTAAGCCCTAAATATAAATCAGTTCTTGGGCT  
TATAAGCAATTTATACTTTAGCTATAAAAAAGAAAATAACGATTTTGCTCTACTAATAATGGGTAAATTTCCCAAAA  
GATATTTTCTGGGGAATTCATAAAAAATAGAAATACAGAATCAATAGGCAATATATTTACAAATCCAAAATGGAAAC  
TTAAAAATTCAAATATATACATTATTCCAAACAAAGCTAGAACTAGCATTGCAATAACCCAAAAAGATATAACCGC  
AAAAGACAATAATATGCTAACAACAAAATATATTGGGGAAATAGAAAAAAATGAAATGTTTTTTTGGATTCAAGAT  
CCAACATTATTGCTCCCAAACCAATAGTAAGCAGCAAAAATTTAATTCCCTTTAGCAGTGGAACTTTGTCTATAA  
ACAGCTTAAATCAAGAAGAATATATTTTAAATCCTTAATCAAAACAAATAATCCACCAATACTAAAAATATTGTC  
AAAAAAGTTAATTCCAACCGTCTTGACAAACATGACAAACCTCACAATATCAAGCCACATAAAGACCACAATAAAA  
GACCAAAATACGGTTGAAATAGAATTTAATATTCAAAAATCTAGTGTTGAAAGCCTTATAGAAAACTAGCTTCAA  
ATATTCAAACCTAA

f32.aa

MNTKTLYLISLILLACNKNKIPLIQKLDLPKSSILGFSNKMGIKDYAFLSKSTKKNSELDYDYAILLRKDEVV  
KIEKTLEKTERYGIEGNWILVNYKGTKRYIFSKDINIVNNLIIDHSK

t32.aa

CNKNKIPLIQKLDLPKSSILGFSNKMGIKDYAFLSKSTKKNSELDYDYAILLRKDEVVKIEKTLEKTERYGIE  
GNWILVNYKGTKRYIFSKDINIVNNLIIDHSK

f32.nt

ATGAATACAAAACATTATATTTAATATCCTTAATTCTTTTAGCTTGCAATAAAAAATAACAAAATTCCTCTCATTC  
AAAAATTAGATTTGCCCAAAGCAGCATTCTTGGCTTTAGCAATAAAATGGGCATAATAATAAAAGATTATGCTTT  
TCTTAGTAAAAGCACTAAGAAAAATAGCGAATTGGATTATGATTACGCAATTCTACTCAGAAAAGACGAAGTCGTA  
AAAATTGAAAAAACACTAGAAAAACAGAGCGCTATGGAAATTGAAGGAAATTGGATCCTAGTCAATTACAAGGGAA  
CTAAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATTTAATAATTGATCATTCTAAATAG

t32.nt

TGCAATAAAAAATAACAAAATTCCTCTCATTCAAAAATTAGATTTGCCCAAAGCAGCATTCTTGGCTTTAGCAATA  
AAATGGGCATAATAATAAAAGATTATGCTTTTCTTAGTAAAAGCACATAAGAAAAATAGCGAATTGGATTATGATTA  
CGCAATTCTACTCAGAAAAGACGAAGTCGTA AAAAATTGAAAAAACACTAGAAAAACAGAGCGCTATGGAAATTGAA  
GGAAATTGGATCCTAGTCAATTACAAGGGAACATAAAGATACATCTTTAGCAAAGACATCAATATAGTCAACAATT  
TAATAATTGATCATTCTAAATAG

f186.aa

MKKLIIIFTLFLSQACNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENTITHTL  
FGTTPMQRIHKYDQSFNLTREILASGIELNRVVNWLNSPSHKEALINTDIDKIGGYRLKTTDNIDIFVVLFGKRK  
YKN

t186.aa



TABLE 1. Nucleotide and Amino Acid Sequences

CNLSTMHKIDTKEDMKILYSEIAELRKKLNLNHLEIDDTLEKVAKEYAIKLGENTRTITHTLFGTT  
PMQRIHKYDQSFNLTREILASGIELNRVNVNWLNSPSHKEALINTDTDKIGGYRLKTTDNIDIFVVLFGKRKYKN

f186.nt

ATGAAAAAATTGATTATAATTTTTTACACTGTTTTTATCTCAAGCATGCAATTTAAGTACAATGCATAAAATAGATA  
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AGATGATACCCCTTGAAAAAGTTGCAAAAGAATATGCCATTAAACTGGGAGAAAAATAGAACAATAACTCACACCCTT  
TTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCCTTTAATTTAACAAGAGAAATACTGGCATCAG  
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TATAAGAATTGA

t186.nt

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GGGAGAAAAATAGAACAATAACTCACACCCTTTTTTGGCACAACCCCAATGCAAAGAATACATAAATACGATCAATCC  
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f216.aa

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LKEQS

t216.aa

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YYVNLNLSREFYDSFNNGDYNESNESFDVKVNLFAMSLIKTMRFNYPGKIKKIVILVEGCILKEQS

f216.nt

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ACAAAATTTGAAAGATAATTTAGATCTTTTAGTAAAGATTTTCTTTTAGGAAGCAATGAAGGGTTTTCTTTTGGG  
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t216.nt

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f328.aa

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IENPAKLFLGLIKACI

TABLE 1. Nucleotide and Amino Acid Sequences

t328.aa

CLGLQLAVIEFARNVCGILDADTEENLARDKPLKSPVIHLLPEQKGIKDKGATMRLGGYPVILKKNTIAFKLYGQD  
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LGLIKACI

f328.nt

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t328.nt

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CGGATAATTGAAAGATTTAGACATAGGTATGAAGTCAATAATGATTATATAGATTTATTTGCAAAAAATGGGCTTA  
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TGA

f352.aa

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EIKLLNKKIKPKEDENYEKINIEENIEEETDDDFEDNYEYNDEIEXTNEDNYPNENGIINNLENLNENEKYIYAIN  
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KHLKELEDKIKENEEITLKLQKELNNFKKKEIYQKPLNEETFTPSITSKNDDLEENKKLKKEYLKPKEKESRDL  
EENTKSTPKTTMIKTADFQIYPIYLNYYKFKEKGDQFAFKKENTYYIEIDPTNNLNEALKNHEIISKYKFEKYFI  
NPILKNKEEFFRNLIIEVKNIHELIMYKNLKPEFKQIKIIE

t352.aa

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NYEKINIEENIEEETDDDFEDNYEYNDEIEXTNEDNYPNENGIINNLENLNENEKYIYAINENEKKIDELEDRIENEN  
TILDQLRELNRNFKKDNNDKLEEEIENLSSIGRIINDLKRKISANEAINKENQKKIRTDKHLKELEDKIKENEE  
TILKLQKELNNFKKKEIYQKPLNEETFTPSITSKNDDLEENKKLKKEYLKPKEKESRDL EENTKSTPKTTMIKT  
ADFQIYPIYLNYYKFKEKGDQFAFKKENTYYIEIDPTNNLNEALKNHEIISKYKFEKYFINPILKNKEEFFRNLI  
E VKNIEHELIMYKNLKPEFKQIKIIE

f352.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

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t352.nt

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A

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PFYKRDSYKIVEIVSDGDYSIDEQIAVIEDDSGMRHNITMSFHWPVKVPITNYKERLIPSEPMLTQTRI IDTFFPV  
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PVAAREASVYTAITIGEYYRQMGLDILLADSTSRWAQAMREMSGRLEEIPGEEAFPAYLESVIASFYERAGIVVL  
NNGDIGSVTVGGSVSPAGGNFEEPTQATLKVVGAFLTRERSDARKFPAISPLESWSKYKVIDQKKTEYARSF  
LVKGNEINQMMKVVGEEGISNDDFLIYLKSEL DSCYLQNSFDSIDAAVSSERQNYMFDIVYNILKTNFEFSDKL  
QARDFINELRQNLLDMNLSSF KDHKFNKLEHALGELINFKKVI

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LRPLNKDKKWNFKKTSKVGDIVIAGDFLG FVIEGTVHHQIMIPFYKRDSYKIVEIVSDGDYSIDEQIAVIEDDSGM  
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AACGERAGEVVETLKEFPELMDPKTGKSLMDRTC I ICNTSSMPVAAREASVYTAITIGEYYRQMGLDILLADSTS  
RWAQAMREMSGRLEEIPGEEAFPAYLESVIASFYERAGIVVLNNGDIGSVTVGGSVSPAGGNFEEPTQATLKVVG  
AFHGLTRERSDARKFPAISPLESWSKYKVIDQKKTEYARSF LVKGNEINQMMKVVGEEGISNDDFLIYLKSEL D

TABLE 1. Nucleotide and Amino Acid Sequences

SCYLQNSFDSIDAAVSSERQNYMFDIVYNILKTNFEFSDKLQARDFINELRQNLLDMNLSSEFKDHFKNKLEHALG  
ELINFKKVI

f867.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

f868.aa

MKRVYSKIESIAGNVITVTAQGIKYGELAIVKAKDTSSLAEVIKLDREKVS LQVYGGTRGVSTSD EIKFLGHSMQV  
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DNTGYITEGQYYLKGGRIEFPGLSRLKQMVNSRTRDDHRTIMDSMIKLYASSKESVEKKAMGFNMTKWDEKLLKY  
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t868.aa

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GMGLKHDDYLT FKDSLEKGGALSRAIFFVHTANDSVVESLTVPDISLSVAEKFALKGKKVLVLLTDMTNFADAMKE  
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FGLSRLKQMVNSRTRDDHRTIMDSMIKLYASSKESVEKKAMGFNMTKWDEKLLKYSNMFESKMDLSVNIPL EEA  
LDLGWSILASCFSPKETGIKTDLIEKYWPKKET Y

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AGAGACTTATTGA

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CAAGGTATTAAGTATGGTGAGCTTGCTATTGTAAAAGCAAAAGATACAAGTTCTCTAGCCGAAGTAATTAACCTTG  
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TABLE 1. Nucleotide and Amino Acid Sequences

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f872.aa

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ENSMNNELNASFYLT SYLKQVRGAFGIDFTFNLYRKFKNYNVIDTHQLLSKVYLHLKAYELSITHGLIAAVGILTR  
MYDYVCYEPVYQFKNLRSFVQKINKYKAIKNAFESTDFWEIVYNVAAATYAYSNGNYKFRAIDTWKLVVDLAPRF  
SPYIAKRSRSQIKNSVYLKKN

t872.aa

SNKNFPYWILLEKGRQFLYSKSEFSKSNLTHAINYLQEALLRKGVYPEASYLSVAYMSGNAILEKLNLYKSFED  
RYLLDESFEKKILFSLAKMAELENNYVDITIDYLNILNKFSTKKDYYSYHDYSQGENSMNNELNASFYLT SYLK  
QVRGAFGIDFTFNLYRKFKNYNVIDTHQLLSKVYLHLKAYELSITHGLIAAVGILTRMYDYVCYEPVYQFKNLRSF  
VQKINKYKAIKNAFESTDFWEIVYNVAAATYAYSNGNYKFRAIDTWKLVVDLAPRFSPYIAKRSRSQIKNSVYLKKN

f872.nt

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GAAAACAGTATGTCAAATAATGAACCTTAATGCTTCATTTTATTAACTTCTTATTTAAAAACAAGTAAGAGGAGCTT  
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AGTATAAGGCAATAAAAAATGCTTTTGAATCTACAGATTTTGGGAAATAGTTTATAATGTTGCTGCTGCTACTTA  
TGCATATTCTAATGGCAATTATAAATTTAGAGCAATAGATACTTGGAAATTAGTAGTAGATCTTGCGCCAAGGTTT  
TCTCCTTATATTGCTAAATCAAGAAGTCAAATTA AAAATCTGTATATTTAAAAAAAATTA

t872.nt

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TAA

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MLKSNKVVLIGAGGVGSSFAYAL TIDNSLVHELVIIDV NENKAKGEVMDLNHGQMFLKKNINVLFGTYKDCANADI  
VVITAGLNQKPGETRLDLVDKNSKIFKDIITNVVSSGFDGIFVVASNPVDIMTYVTM KYSKFPPIHKVIGTG TILD T  
SRLRYFLSDHFNVTQNIHSYIMGEHXDSSSFATWDETKIAMKPLSEYLAEGKITELELDEIHKKVVNAA YEVIK LK

TABLE 1. Nucleotide and Amino Acid Sequences

GATYYAIGLGKINIVNAIIGDQNVILPISSYINGQYGGGLIKDIYIGAPAIVCKEGVKEVLNFKISPKELDKFNSSA  
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t874.aa

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NSKIFKDIITNVSSGFDGIFVVASNPVDIMTYVTMKSYPPIHKVIGTGTILDTSRLRYFLSDHFNVTQNIHSY  
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TATGACTTATGTTACAATGAAATATTCCAAATTTCTATTTCATAAGGTTATTGGTACTGGGACTATTCTTGATACT  
TCAAGACTTAGATATTTTTTAAAGTGATCATTTTTAATGTGAACACTCAAAATATACATTCATATATTATGGGTGAGC  
ACGTGACAGTTCTTTTGCTACGTGGGATGAAACAAAAATAGCAATGAAGCCTTTGTCAGAATATCTTGCTGAAGGC  
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GCCAATATCTTCTTATATTAATGGCCAGTATGGGGGATTGATTAAAGATATTTATATTGGAGCGCCTGCTATAGTT  
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GCCTGCTATAGTTTGTAAGGAAGGAGTCAAAGAAGTTTTAACTTTAAGATAAGCCCTAAAGAGCTTGATAAGTTT  
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f886.aa

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KITCYDTKDKTKRKEEIDNLLNNKIQEIEYDSKGTLETANYVYENENLISKNLKTINQPKLIYYSKDDNGKLLKI  
TGSNFQIWNYGINGDIKSTYFDIKKATTKVIKYDDKKRNSNSTIIVNNKIKSKEKNQYLDEEKIVNTFEEENTKII  
STYKANNLIKEETYKNNELIKVNDFQYNESDMIIFQNTKEKDKDQYTNTKIEYEYNKDNQLKSKKIYENDIIYLLKT  
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t886.aa

SYFASDVFFNKYQKLNEKPKTGFIYIEYYSVDDTEKLYLYKENNLIKTYKIQIIENTKKITCYDTKDKTKRKEEIDN  
LNNKIQEIEYDSKGTLETANYVYENENLISKNLKTINQPKLIYYSKDDNGKLLKITGSNFQIWNYGINGDIKST  
YFDIKKATTKVIKYDDKKRNSNSTIIVNNKIKSKEKNQYLDEEKIVNTFEEENTKIIISTYKANNLIKEETYKNNEL  
IKVNDFQYNESDMIIFQNTKEKDKDQYTNTKIEYEYNKDNQLKSKKIYENDIIYLLKTEYHNDNEYEEEEIYNNKKPA  
LRVKHKNGKVTEEKPIGTN

TABLE 1. Nucleotide and Amino Acid Sequences

f886.nt

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TGAATACGAATATAACAAAGACAATCAATTAAAAAGCAAAAAAATTTATGAGAACGATATAATTTATCTAAAACT  
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TATAATTTATCTAAAACTGAATACCACAATGACAATGAATATGAAGAAGAAATATACTACAATAAAAAACCTGCT  
CTTAGGGTAAAACACAAGAACGGAAAAGTCACCGAAGAAAAACCAATAGGAACAAATTAA

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MEKLKLLAIPLLVFTICKIHSQSNIENFSYIINTKKENIDLKKGIEKQLDKIYDKITEHIVNDDKSIIEDIYI  
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TNISNLNKEFFIREELFFINYIDLKKIENYILLEISNITPEKIETKKAVFKTSSSVNEIADHITKYSLEILGREF  
LKININVKNNSDAKIYINEKFVSKGIYHDNIFDISKLPNKEIEIQITSANFENYSIKRTVKNADSIILDLKRTI  
SKKVSISNVQSKVFKKGIFMGETPIEIEKPENQDIILLKSKGYKDKFKLINKEEDQVEIEMIKTNKNRLIDTRDK  
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HLVEYIKEANMGE

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QNIITAKEKHNTKTKIDELKKNIQNINNKQKKFAEYFNNLKKLVKVKKIEEQTNISNLNKEFFIREELFFINYID  
LKKIENYILLEISNITPEKIETKKAVFKTSSSVNEIADHITKYSLEILGREFLKININVKNNSDAKIYINEKFVS  
KGIYHDNIFDISKLPNKEIEIQITSANFENYSIKRTVKNADSIILDLKRTISKKVSISNVQSKVFKKGIFMGE  
TPIEIEKPENQDIILLKSKGYKDKFKLINKEEDQVEIEMIKTNKNRLIDTRDKFYVNLAVFTLSTIGAI FAGTLLN  
NEVLYKITGNHFINKRLTAEDVYMAKAEQMTATFLFGVGITLTIGSFISLITHLVEYIKEANMGE

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TABLE 1. Nucleotide and Amino Acid Sequences

ATGGAAAAGCTTAACTAAAGCTAGCAATACCATTTGCTAGTATTTACAATATGCAAAATACATTCTCAAAGTAATA  
TTGAATACAATTTTTTCTATATCATTAATACAAAAAAGAAAATATTGACCTAAAAAAGGGTATTGAAAAACAATT  
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AATCAAGATATAATAAAAAACAGAACTTGAAATTAGCAAATTAaaaaaaAGAAATGGATAAAAAAACTTCAAACA  
TAATAACCGCAAAAGAAAAGCATAACACCAAAACCAAATTTGATGAGCTTAAAAAAATATTCAAAATATTAACAA  
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CAAAAGCGGAACAAATGACTGCAACATTTCTATTTGGAGTAGGAATCACTTTAACTATTGGAAGCTTTATCTCAT  
ATAACTCATTTAGTAGAATATATTAAAGAAGCAAATATGGGAGAATAG

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MVRFLGFLYLITTIPLIKSCDAAQFGDYKPLYFENENDLKTANEYINSLGYKTISEYTTKIDILDFPENKEITINE  
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LLIFLDPTNSIFTLIFLLISSLAFMISKEIMYFYPFTVLSYLLFLIISFNKNYNKIYLKEINFLTLMTKIKHLLF  
LFTFTALYFITITFTFTNIDPTFI AFVAIPTLCIFLIFSWIKTESNFKDTFLFPIEIKEKKIEGKKALKSKIAIH  
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FSLPFFVLLFLFKAIRFTILLNIN  
EKTYKKYIQG

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CDAAQFGDYKPLYFENENDLKTANEYINSLGYKTISEYTTKIDILDFPENKEITINEINKLNNLDLRKSIFLKKLS  
NLFNIEHKKLLYVENRFSINFKNLKKELNINADIHSLDYKTKINFISSIIFLI  
LLIFLDPTNSIFTLIFLLI

TABLE 1. Nucleotide and Amino Acid Sequences

SSLAFMISKEIMYFYPFTVLSYLLFLIISNFNKNYNKIYLKEINFLTLMTKIKHLLFLFTFTALYFITITTTFFTTN  
IDPTFIAFVAIPTLCIFLIFSWIKTESNFKDFTLFPFIEIKEKKIEGKKALKSKIAIHLHLLFTLSLIPFAYSSMYLN  
SYENINYLKSKKLNLYFDYLNPNNIYIMLGYNKMDPNIIIGYLSHILYQNELKYNITAKYGI PKDIKENYFEIKNDK  
IEIHPKTVYEVDKSFIDEILKDLASFLKNKNPILYKENKNNINTDKKNYKILFFFSLPFFVLLFLFKAIRFTI  
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AAACCTATAAAAAATATATTCAAGGATAA

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TGTGATGCAGCTCAATTTGGAGACTACAAACCTTTTATACCTTTGAAAATGAAAATGATCTAAAAACTGCCAATGAAT  
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GTCTGTTTTTAAAAAATAAAATCCAATCCTAATATATAAAGAAAAACAAGAATAATATCAACACAGATAAAAAA  
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MIRALLTNDLFLSCLVSGISAQVIKYGIQTVKTRKLKLPVHLLKKIFLETGGMPSSHSSTVTALSTSIALTEGID  
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F

TABLE 1. Nucleotide and Amino Acid Sequences

t895.aa

AQVIKYGIQTVKTRKLKLPVHLLKKIFLETGGMPSSHSSTVTALSTSIALTEGIDTNFIIALAFALITIRDSFGV  
RYMSGVQAEYLNALSEKLKKEIKIDTTKIKVVKGHKKKEVLTGIIIGIVSAYIVCYF

f895.nt

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TTCAAGCAGAATATTTAAATGCATTATCAGAAAAATTAAAAAAGAAATAAAATTTGACACAACAAAAATAAAAGT  
GGTCAAGGGGCACAAAAGAAAGAGGTTCTAACGGGCATAATAATAGGAATAGTCTCTGCGTATATTGTGTGCTAT  
TTTTAG

t895.nt

GCTCAAGTGATTAAATATGGTATCCAACTGTAAAAACAAGAAAGTTAAACTAACTCCAGTACATCTTTTAAAAA  
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AGATATATGTCTGGAGTTCAAGCAGAATATTTAAATGCATTATCAGAAAAATTAAAAAAGAAATAAAATTTGACA  
CAACAAAAATAAAAGTGGTCAAGGGGCACAAAAGAAAGAGGTTCTAACGGGCATAATAATAGGAATAGTCTCTGC  
GTATATTGTGTGCTATTTTTAG

f605.aa

MYIGAAGKSFSIIIDSAFLSNCFLEFIGSFSRSDSLMSLSNSRFEYPYDASCEFSLVNIVKYVCGSKYSPMRPTLII  
SKLPVFLLLVRTGQFSLVSIRLIFRIFFHWFZ

t605.aa

CFLFIGSFSRSDSLMSLSNSRFEYPYDASCEFSLVNIVKYVCGSKYSPMRPTLIISKLPVFLLLVRTGQFSLVSIR  
LIFRIFFHWFZ

f605.nt

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t605.nt

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TTGATATTTAGAATTTTTTTCCATTGGTTTTGA

f606.aa

MKLQRSFLIIFFLTFLCCNNKERKEGVSKISLGAEPSSSLDPQLAEDNVASKMIDTMFRGIVTGPNTGGNKPGL  
AKGWDISSDGTVYTFNLREKITWSDGVAITAEGIRKSYLRILNKETGSKYVEMVKSIVKNGQKYFDGQVTDSELGI  
RAIDEKTLTLESPPKPYFIDMLVHQSFIPVPVHVTEKYQONWTSPEMVTSGPFKLKERIPNEKYVFEKNNKYD  
SNEVELEEITFYTTNDSSTAYKMYENEELDAIFGSIPPDLIKLNKLRSDYYSSAVNAIFYAFNTHIKPLDNVKIR  
KALTLAIDRETLTYKVLNNGTTPTRRATPNFSSYSYAKSLELFNPEIAKTLLEAGYPNGNGFPILKLKYNTNEAN

TABLE 1. Nucleotide and Amino Acid Sequences

KKICEFIQNQWKKNLNIDVELENEEWTTYLNTKANGNYEIARAGWIGDYADPLTFLSIFTQGYTQFSSHNYSNPEY  
NELIKKSDLELDPIKRQDILRQAEIIIEKDFPIAPIYIYGNSYLFRNDKWTGWNTNILERFDLSQLKLKNKZ

t606.aa

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YFIDMLVHQSFI PVPVHVTEKYGQNWTS PENMVTSGFPKLKERIPNEKYVFEKNKYYDSNEVELEEITFYTTNDS  
STAYKMYENEELDAIFGSI PPDLIKNLKLRSDYYSSAVNAIFYAFNTHIKPLDNVKIRKALT LAIDRET LTYKVL  
DNGTTPTRRATPNFSSYSYAKSLELFNPEIAKTLLEAGYPNGNFPILKLKYNTNEANKKICEFIQNQWKKNLNI  
DVELENEEWTTYLNTKANGNYEIARAGWIGDYADPLTFLSIFTQGYTQFSSHNYSNPEYNELIKKSDLELDPIKRQ  
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f606.nt

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GGACAACATACTTAACACTAAGGCAATGGAAATTATGAAATAGCAAGAGCAGGATGGATAGGCGATTATGCTGA  
TCCTTTGACATTTTAAAGCATATTCACACAAGGATACACACAATTCTCATCTCATAATTACTCAAACCCAGAATAC  
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TAATTATTGAAAAAGATTTTCCAATAGCACCAATATACATATATGGGAACAGTTACCTTTTCAGAAATGACAAATG  
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t606.nt

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TACAGGGGGAAATAAACCGGGACTTGCAAAAGGGTGGGATATTTCTTCTGATGGAACAGTTTACACATTTAACCTA  
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GACAACGGGACTACCCCTACAAGAAGAGCAACTCCCAACTTTAGTTCATATCTTATGCAAAAAGTTTAGAATTAT  
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CAGGATGGATAGGCGATTATGCTGATCCTTTGACATTTTAAAGCATATTCACACAAGGATACACACAATTCTCATC

TABLE 1. Nucleotide and Amino Acid Sequences

TCATAATTACTCAAACCCAGAATACAACGAAC TTATAAAGAAATCCGACCTTGAGCTTGATCCAATAAAAAGACAA  
GACATTTTAAAGACAAGCAGAAGAGATAATTATTGAAAAAGATTTTCCAATAGCACCAATATACATATATGGGAACA  
GTTACCTTTTTCAGAAATGACAAATGGACAGGGTGGAAACACCAATATTTTAGAAAAGATTTGATTTATCTCAGCTAAA  
ATTAAAAAATAAATAA

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MFNRSSCVLQNFLFLFLFLSLVSCFAKKEISGNFIKAHSKEFDLNNLNWLWNFDYTKKNFDKHFNIDPSSYIYVA  
YLFKKIGFEEKFVEYMKKAIANGDSIASQFAGIKLIEYFNSAKEYFASELIGEKLKYYENNKFIILGYFKSLYWQ  
KKNDKALSLNKLDMKFSQYQENENILLKAVLYLNLNSVSESKIYFNELFENLPANYLHVRAVDYFIENKSRF  
GANFLNLVRFKYEVANGNFNGAINILNKNGLNDYYDNNIVLSDVYKAFISSGKVSNAITFFSKIISKYKNYYLGIL  
NLREKNNLGLLLLKEYLEGLDLNNEINRLDLLNTAFSNLIFTKSARDYFAESLPKFYTEGDKKNSTFIKILEEYIL  
ESIQLEDYGNLYKLYSNAQKVISNSVLSKLAFINARLIYHKLIKPNVSGEYKSLLSHAVNYDKWSYSSFMSRYLLD  
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KELKYFNLDLKI PKDNIIIGTYYLKKRISTTGSLYKALASYNGGIGNVRKWEKSYGHL SKELFIEAIPFSQTRNYI  
KKILVYSVFDALYEKKGIDSVIVKIMGEFPKNZ

t679.aa

CFAKKEISGNFIKAHSKEFDLNNLNWLWNFDYTKKNFDKHFNIDPSSYIYVAYLFKKIGFEEKFVEYMKKAIANG  
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NILNKNGLNDYYDNNIVLSDVYKAFISSGKVSNAITFFSKIISKYKNYYLGILNLREKNNLGLLLLKEYLEGLDLN  
NEINRLDLLNTAFSNLIFTKSARDYFAESLPKFYTEGDKKNSTFIKILEEYILESIQLEDYGNLYKLYSNAQKVIS  
NSVLSKLAFINARLIYHKLIKPNVSGEYKSLLSHAVNYDKWSYSSFMSRYLLDQNIDEFFTGGSDIKYEQSDYEIF  
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GSLIEYWAKRRGLEASVVFSLIKAESSFEKNAVSKPGAVGLMQVMPSTANDISKELKYFNLDLKI PKDNIIIGTY  
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VKIMGEFPKNZ

f679.nt

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TABLE 1. Nucleotide and Amino Acid Sequences

TGAAAAAATGCTGTCTCAAAACCGGGTGCTGTTGGCCTTATGCAGGTATGCCATCAACAGCAAATGATATTTCT  
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t679.nt

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f11-12.nt

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TCTAAATTTT	CTGAATTAAT	TAGAGAAGTA	CGTGTAATTA	AAGATGAATA	TGCTTTAATA
AAAGCTGATT	TGTATGATGT	AATTGGAAAG	ATTAACAATA	AAAAACATC	ATTAATGGAG
AATCCTAAGA	ACAATAGAGA	TAAGATAAAT	AAATTAACAC	AATTGTTGCA	AAATAATTTA
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AGCTCTGCGG	CTTTCTTTT	TGACAACGCT	CAGAAAAGGT	TAAAAGAAAG	CATTATTAAA
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GACGCAAGAA	GTGCTTTAAG	TAATTTAGAA	TCTTTTGCCT	CTAAAAGAAT	TGAACCAATG
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AATAAAAAAT	AA				

TABLE 1. Nucleotide and Amino Acid Sequences

t11-12.nt

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 ATTGAACCAATGGTGAGAAAGGAAGAAATAAAAGAGCTTATTAAACATGCAAAAACCTGTTTTAGAAAGTCTCAATA  
 AAAAA

f11-12.aa

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 EEKEADAAIK YLEENILKNS KFSELIREVR VIKDEYALIK ADLYDVIGKI NNKKTSLMEN  
 PKNNRDKINK LTQLLQNNLK IDSELEQLIN MIDMAENEIS SAAFFFDNAQ KRLKESIIKR  
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 KK

t11-12.aa

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 NISIAHTEKKETKKENLIPSTNEEKEADAAIKYLEENILKNSKFSELIREVRVIKDEYALIKADLYDVIGKINNKK  
 TSLMENPKNNRDKINKLTQLLQNNLKIDSELEQLINMIDMAENEISSAFFFDNAQKRLKESIIKRLESKNNRSYA  
 LKLSRQALSDARSALSNLFSFASKRIEPMVRKEEIKELIKHAKTVLESNLKK

f11-4.nt

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 ACATCTATTG ATCAAGTATT AGATGAGATA AGTGAAGCCA CAGGCCTAAG TTCGGAAAAA  
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 GCTGAAAATT CGGTAAGCGT TTCTTTTAAA GAACATTCAA ACAGTAAAAAT TGAAACTAAA  
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 CTTAAAAACA AAAATGATGG TGAGTACGAA AAAACATTGA CAACTTTAAG CTAA

t11-4.nt

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 TTTCAAACACTAATTAATATAGGTTATAATGCTACCTATGCAGCCAAAAAGTAATTTGAAGAATGGACTAAAGATGG  
 TGAAATTACTGGATGAGTTGCTAAAAATATCGGTAAGTAGCAATGGTGATAAAAGTACCCAAAAATACAATGAACT  
 TAAACCGTTGTAAATAAGTTTAATGCTGAAAATTTCGGTAAGCGTTTCTTTTAAAGAACATTCAAACAGTAAATTT

TABLE 1. Nucleotide and Amino Acid Sequences

GAAACTAAAAATGTATTCAAACCTCTTATGAAAAATGTAGAAACATACTTTGAAGGTGTATGCAGCGAACTTAAAA  
ACAAAAATGATGGTGAGTACGAAAAA

f11-4.aa

RSLQMSKLIL AISILLIISC KQYVDNTIDE ATVESKSALT SIDQVLDEIS EATGLSSEKI  
TKLTPEELEN LAKEAQDDSE KSKKEIEDQK NTKESKNIEV KDTPLRIKLI KNSSEKIDSV  
FQTLINIGYN ATYAAKSNLK NGLKMKVLLD ELLKISVSSN GDKSTQKYNE LKTVVNKFNA  
ENSVSVSFKE HSNSKIETKK CIQTLMKNVE TYFEGVCSEL KNKNDGEYK TLTTLS

t11-4.aa

CKWYVDNTIDEATVESKSALTSIDQVLDEISEATGLSSEKITKLTPEELENLAKEAQDDSEKSKKEIEDQKNTKES  
KNIEVKDTPRLIKLIKNSSEKIDSVFQTLINIGYNATYAAKSNLKNGLKMKVLLDELLKISVSSNNGDKSTQKYNEL  
KTVVNKFNAENSVSVSFKEHSNSKIETKKCIQTLMKNVETTYFEGVCSELKNKNDGEYK

f112-1.nt

TGAATCTCTA AAGATTTTAG CAGGGGAGAA AATATGAAAA AAAGTTTTTT ATCAATATAC  
ATGTTAATTT CAATAAGTTT ATTATCATGT GATGTTAGTA GATTAAATCA GAGAAATATT  
AATGAGCTTA AAATTTTGTG TGAAAAGGCC AAGTATTATT CTATAAAATT AGACGCTATT  
TATAACGAAT GTACAGGAGC ATATAATGAT ATTATGACTT ATTCGGAAGG TACATTTTCT  
GATCAAAGTA AGGTTAATCA AGCTATATCT ATATTTAAAA AAGACAATAA AATTGTTAAT  
AAGTTTAAGG AGCTTGAAAA GATTATAGAA GAATACAAAC CTATGTTTTT AAGTAAATTA  
ATTGATGATT TTGCGGGATC CGTT

t112-1.nt

ATGTGATGTTAGTAGATTAAATCAGAGAAATATTAATGAGCTTAAAAATTTTGTGTTGAAAAGGCCAAGTATTATTCT  
ATAAAATTAGACGCTATTTATAACGAATGTACAGGAGCATATAATGATATTATGACTTATTCGGAAGGTACATTTT  
CTGATCAAAGTAAGGTTAATCAAGCTATATCTATATTTAAAAAAGACAATAAAATTGTTAATAAGTTTAAGGAGCT  
TGAAAAGATTATAGAAGAATACAAACCTATGTTTTTAAGTAAATTAATTGATGATTTT

f112-1.aa

ISKDFSRGEN MKKSFLSIYM LISISLLSCD VSRLNQRNIN ELKIFVEKAK YYSIKLDAIY  
NECTGAYNDI MTYSEGTFSQ QSKVNQAISI FKKDNKIVNK FKELEKIEE YKPMFLSKLI  
DDFAGSV

t112-1.aa

CDVSRNLQRNINELKIFVEKAKYYSIKLDAIYNECTGAYNDIMTYSEGTFSQSKVNQAISIFKKDNKIVNKFEL  
EKIIEEYKPMFLSKLIDDF

f14-8.nt

TAAATACAGA GCCATTCAAG GAGAGTATTT ATGAAATACT ATATATGTGT GTGTGTTTTT  
TTGCTTTTGA ATGCTTGCAA TTCAGATTTT AGCACTAATC AAGAAGATAT TAAATATCCA  
TCTGATAAAG AGAAATCAAA ATCCAACATG GAAGCAAGCT CTAAAGAAGA AGATCCAAAT  
AAAAAATAA AAAATACACT GCTTAATGAT TTAATAAATT TGATAGAAAT AGCTAATGAG  
CATAAAGAAA AATATGAAAA AAGAATGCAA GAAGAACCCT CAGATCAATA CGGAATATTG  
GCTTTCAGG AATTAGACTT GTCCGTTGGA AAAATATCTG AAGACACCCC GCAATCTAAA  
AAATTTAGAA AAAACACCTA TTCTCCCTTA AGCGCTATTG ATGTCAATAA ATTAAAAGAT  
CTTTCAGAGA TTATAAGAAA TTCGGGCCAA ATACAAGGTT TATTTAATAT TTTCAACAGA  
TTCGGAGGCA TTTTGTGACG CTCACTTAAT CACGTATATT CTAAAAAGA TATCCTAGGG  
GGACTAGAAA TTTTGGATTT AGATAAACTA AAAAATTCGT TTGAAAAATT ACTATCTATA



TABLE 1. Nucleotide and Amino Acid Sequences

AAAGAACTT TCTCAAAAAT GCTAAATCAA CTTTTATTAG ATTATAAAAA TGATAAAGAT  
 CATATACGAA CAGAGACAAA TAAACTTAAA TCTCATACAA CTGCACTTTT CGAACAACTT  
 GATAAAAAAG AAGACGAAGC ATATGAACCT AAAAATCAGA TATTTTCAAT AAGTAACCTT  
 TAA

t14-8.nt

TTGCAATTCAGATTTTAGCACTAATCAAGAAGATATTAAATATCCATCTGATAAAGAGAAATCAAAATCCAACATG  
 GAAGCAAGCTCTAAAGAAGAAGATCCAAATAAAAAATAAAAAATACACTGCTTAATGATTTAATAAATTTGATAG  
 AAATAGCTAATGAGCATAAAGAAAAATATGAAAAAGAATGCAAGAAGAACCTTCAGATCAATACGGAATATTGGC  
 TTTCCAGGAATTAGACTTGTCCGTTGGAAAAATATCTGAAGACACCCCGCAATCTAAAAAATTTAGAAAAACACC  
 TATTCTCCCTTAAGCGCTATTGATGTCAATAAATTAAAAGATCTTTTCAGAGATTATAAGAAATTCGGGCCAAATAC  
 AAGGTTTATTTAATATTTTCAACAGATTCGGAGGCATTTTTGACGACTCACTTAATCACGTATATTCTAAAAAGA  
 TATCCTAGGGGGACTAGAAATTTTGGATTTAGATAAACTAAAAAATTCGTTTGAAAAATTACTATCTATAAAGAA  
 ACTTTCTCAAAAATGCTAAATCAACTTTTATTAGATTATAAAAAATGATAAAGATCATATACGAACAGAGACAAATA  
 AACTTAAATCTCATACAACCTGCACCTTTTCGAACAACCTTGATAAAAAAGAAGACGAAGCATATGAACCTAAAAATCA  
 G

f14-8.aa

IQSHSRRVFM KYIICVCFVL LLNACNSDFS TNQEDIKYPs DKEKSKSNME ASSKEEDPNK  
 KIKNTLLNDL INLIEIANEH KEKYEKRMQE EPSDQYGILA FQELDLSVGK ISEDTPQSKK  
 FRKNTYSPLS AIDVNKLKDL SEIIRNSGQI QGLFNIFNRF GGIFDDSLNH VYSKKDILGG  
 LEILDLDLKL NSFELLSIK ETFSKMLNQL LLDYKNDKDH IRTETNKLKS HTTALFEQLD  
 KKEDEAYEPK NQIFSISNL

t14-8.aa

CNSDFSTNQEDIKYPsDKEKSKSNMEASSKEEDPNKKIKNTLLNDLINLIEIANEHKEKYEKRMQE EPSDQYGILA  
 FQELDLSVGK ISEDTPQSKKFRKNTYSPLSAIDVNKLKDLSEIIRNSGQIQGLFNIFNRF GGIFDDSLNHVYSKKD  
 ILGGLEILDLDLKLNSFEKLLSIKETFSKMLNQLLLDYKNDKDHIRTETNKLKSHTTALFEQLDKKEDEAYEPKNQ

f17-6.nt

TAAAGGAGGG TATTTATGAA ATACCACATA ATTACAACATA TATTTGTTTT TCTGTTTTTA  
 GCTTGCAGGC CGGATTTTAA TATCGATCAA AAAGACATTA AATACCCGCC TACTGAAAAA  
 TCAAGGCCCA AACTGAAAG CTCTAAGCAA AAAGAATCAA AGCCTAAAAC AGAAGAAGAG  
 CTTAAGAAAA AACAACAAGA AGAAGAGCTT AAGAAAAAAC AACAAGAAGA AGAGCTTAAG  
 AAAAAACAAC AAGAAGAAGA GCTTAAGAAA AAACAACAAG AAGAAGAGAA GGAAGAACTA  
 AGAAAAACAAC AACTAAAAAA TACGCTATCT AATGATTTAA AAAAGCAAAT AGAATCGGCC  
 TACAATTTTA AAGAAAAATA TGTA AAAAGT ATGGAAAAAG AACCTGAAGA CCATTACGGG  
 ATGACGTCTT TTAGGGGATT GAATTGGGGG CCAGGGACTG AAGATATATC TGACAATACC  
 GAAAGATCTA TAAGATATAG AAGACACACT TATACTGTTT TAAGCCCCCT GGATCCTCAT  
 GAATTAAAGG AATTCGCAAA TATTATTCAA GATATAAATA AACTAGCATC AGTAGCAAGT  
 ATATTTAATT CTTTTAGCGC TATTGGAGGA GCTCTTGACA TAGTAAGTGA TCACCTATAT  
 TTCAAAAAAG ACAATCTAGA CAACTAGAT ATTGCAGATT TAGAAATACT TAAAAATTCA  
 TTTGAACAAA TATTATATAT AAAAGGAAGT GTTGCAGGAA AAGCAAAAAA ACTTTTATTA  
 GATTATAAAA ATCTAAAAAC AGATATTAAT AAGCTTAAAT CTTATTCAA TGAAGTGGTT  
 AATGGAATTA AGCAACAAGC TCTAGAAGCA GAAATCTAG AAGAGCTTAT AGTGTCAAAA  
 TATAAACTTT AA

t17-6.nt

TTGCAGGCCGGATTTTAAATATCGATCAAAAAGACATTAAATACCCGCCTACTGAAAAATCAAGGCCCAAACTGAA  
 AGCTCTAAGCAAAAAGAATCAAAGCCTAAAACAGAAGAAGAGCTTAAGAAAAACAACAAGAAGAGCTTAAGA

TABLE 1. Nucleotide and Amino Acid Sequences

AAAAACAACAAGAAGAAGAGCTTAAGAAAAACAACAAGAAGAAGAGCTTAAGAAAAACAACAAGAAGAAGAGAA  
 GGAAGAACTAAGAAAACAACAATAAAAAATACGCTATCTAATGATTTAAAAAAGCAAATAGAAATCGGCCCTACAAT  
 TTTAAAGAAAAATATGTAAAAAGTATGGAAAAAGAACCTGAAGACCATTACGGGATGACGCTCTTTTAGGGGATGA  
 ATTGGGGGGCCAGGGACTGAAGATATATCTGACAATACCGAAAGATCTATAAGATATAGAAGACACACTTATACTGT  
 TTTAAGCCCCCTGGATCCTCATGAATTAAAGGAATTCGCAAATATTATTCAAGATATAAATAAACTAGCATCAGTA  
 GCAAGTATATTTAATTCCTTTTAGCGCTATTGGAGGAGCTCTTGACATAGTAAGTGATCACCTATATTTCAAAAAAG  
 ACAATCTAGACAACTAGATATTGCAGATTTAGAAATACTTAAAAATTCATTTGAACAAATATTATATATAAAAGG  
 AAGTGTTGCAGGAAAAGCAAAAAAATTTTATTAGATTATAAAAAATCTAAAAACAGATATTAATAAGCTTAAATCT  
 TATTCAAATGAAGCTGGTTAATGGAATTAAGCAACAAGCTCTAGAAGCAGAAAATCTAGAAGAGCTTATAGTGTCAA  
 AATATAAACTT

f17-6.aa

RRVFMKYHII TTIFVFLFLA CRPDFNIDQK DIKYPPTSEKS RPKTESSKQK ESKPKTEEEL  
 KKKQQUEELK KKKQQUEELK KKKQQUEELK KKKQQUEELK KKKQQUEELK KKKQQUEELK KKKQQUEELK  
 NFKEYVKSM EKEPEDHYGM TSFRGLNWGP GTEDISDNTE RSIRYRRHTY TVLSPLDPHE  
 LKEFANIIQD INKLASVASI FNSFSAIGGA LDIVSDHLYF KKDNLKLDI ADLEILKNSF  
 EQILYIKGSV AGKAKLLLD YKNLKT DINK LKSYSNELVN GIKQQALEAE NLEELIVSKY  
 KL

t17-6.aa

CRPDFNIDQKDIKYPPTSEKSRPKTESSKQKESKPKTEEELKKKKQQUEELKKKKQQUEELKKKKQQUEELKKKKQQUEEL  
 EELRKQQLKNTLSNDLKKQIESAYNFKEYVKSM EKEPEDHYGMTSFRGLNWGP GTEDISDNTERSIRYRRHTYTV  
 LSPLDPHELKEFANIIQDINKLASVASIFNSFSAIGGALDIVSDHLYFKKDNLKLDIADLEILKNSFEQILYIKG  
 SVAGKAKLLLDYKNLKT DINK LKSYSNELVNGIKQQALEAENLEELIVSKYKL

f19-2.nt

TAAAGAAAGA TTAAATCATA TTCAAGGAGA GTATTTATGA AACACTATAT AATTGTGCAT  
 ATATTTGTTT TTCTATTTTT AAATGCTTGT TATCCAGTTG CATCTAATAA AATAGAATTA  
 AAACCTAAAA CAGAAACAAG CTAAATCAA GAAGAAGTCC CAAATCAAGA AGCAAACTAC  
 AAAGAAGAAA AAGAAGCAAA AGAAGAAGGC ATTAATAAAA AAACAGAAAA CACGCTGCTT  
 AATGATTTAA GAAATTTAAT AGAAACAGCT AAAAAAGATA ATGATAAATA TACACAAAAG  
 TTTAAAGAAG AATCCTCAAG CCAATACGGA ATACTGGCTT TCAAAGATTT GTTCTGGCTA  
 GATGGAACAA ATGAACAATT GTCCGCAAAT ACCGAAAGAT CTAAAGCCTA TAGAAAACGA  
 GCTTATAGCA TC'TTAAATAC TATTAATGAC GCTTCCTTAA AGAATTTTTC AGAAATTGTA  
 ATGGCATCAG GACAAACACA GGGCATATTT AATACCCCTA ACTCACTTGG GGGTAATTTT  
 GAAAAGATAG TTAATTGTTT GTATCCCAA AAAGACAATT TGGAAAAATT AGAGACTTCA  
 GTTTTAAAAA AGCTTAAAGA TTCTTTGGAA AATTTTTTAG AGATAAAAAA AATCGCCTCA  
 GAAATGATGC ACAAGCTCTT ATTAGACTAT CAAAATAATA CAAATCGTAT ACAAACAGAT  
 AAAAATGAAC TTAAGTCTTA TGCAGACACA CTTTCAATC AAATGACAAA AAAACCCGAA  
 GAAGCACTAA AGCTAAAAAA TACCATATGC TCAATAGAGG ACCTTTAA

t19-2.nt

TTGTTATCCAGTTGCATCTAATAAAATAGAATTAAACCTAAAACAGAAACAAGCTTAAATCAAGAAGAAGTCCCA  
 AATCAAGAAGCAAACCTACAAAGAAGAAAAAGAAGCAAAAGAAGAAGGCATTAATAAAAAAACAGAAAACACGCTGC  
 TTAATGATTTAAGAAATTTAATAGAAACAGCTAAAAAAGATAATGATAAATATACACAAAAGTTAAAAGAAGAATC  
 CTAAGCCAATACGGAATACTGGCTTTCAAAGATTTGTTCTGGCTAGATGGAACAAATGAACAATTGTCCGCAAAT  
 ACCGAAAGATCTAAAGCCTATAGAAAACGAGCTTATAGCATCTTAAATACTATTAATGACGCTTCCTTAAAGAATT  
 TTTTCAGAAATTGTAATGGCATCAGGACAAACACAGGGCATATTTAATACCTTAACTCACTTGGGGGTAAATTTTGA  
 AAAGATAGTTAATTGTTTGTATCCCAAAAAAGACAATTTGGAAAAATTAGAGACTTCAGTTTAAAAAAGCTTAAA  
 GATTC'TTTGGAAAAATTTTTTAGAGATAAAAAAATCGCCTCAGAAATGATGCACAAGCTCTTATTAGACTATCAAA  
 ATAATACAAATCGTATACAAACAGATAAAAAATGAAC'TTAAGTCTTATGCAGACACACTTTTCAATCAAATGACAAA  
 AAAACCCGAAGAAGCACTAAAG

TABLE 1. Nucleotide and Amino Acid Sequences

f19-2.aa

RKIKSYSRRV FMKHYIIVHI FVFLFLNACY PVASNKIELK PKTETSLNQE EVPNQEANYK  
 EEKEAKEEGI NKKTENTLLN DLRNLIETAK KDNDKYTQKL KEESSQYGI LAFKDLFWLD  
 GTNEQLSANT ERSKAYRKRA YSILNTINDA SLKNFSEIVM ASGQTQGIFN TLNSLGGNFE  
 KIVNCLYPKK DNLEKLETSV LKKLKDSLEN FLEIKKIASE MMHKLLLDYQ NNTNRIQTDK  
 NELKSYADTL FNQMTKKPEE ALKLNKTICS IEDL

t19-2.aa

CYPVASNKIELKPKTETSLNQE EVPNQEANYK EEKEAKEEGINKKTENTLLN DLRNLIETAK KDNDKYTQKL KEES  
 SSQYGILAFKDLFWLDGTNEQLSANTERSKAYRKRA YSILNTINDASLKNFSEIVMASGQTQGIFNTLNSLGGNFE  
 KIVNCLYPKKDNLEKLETSVLKKLKDSLENFLEIKKIASEMMHKLLLDYQNNTNRIQTDKNELKSYADTLFNQMTK  
 KPPEALK

f19-4.nt

TAATCTATAC TAATTGAGGA GAATATTTTT ATGAAAAACA ACATAATTTT ATGCATGTGT  
 GTTTTTTTTAC TTTTAAATAG CTGCACCGCT AACCATGAAG CTGAAGCGAA AATAAAAAAA  
 CATGTTGATA AAACAAAAAA CGAATATATT AATGAAATAA AAAATTTAAT AGCAACAACC  
 AAAGAAATCA TCGAAAAACG AAAATTGCTA CAAGCTAAAC CAGTAGATCA AAACCCCGTA  
 GATGATACAA ACAATAAGAA AGTTTTTCGAG ATAGATAAAA GAGCTTTTCGA TTTTATAAAT  
 AGTTTTTTAA CAGATGATGA ATTTAATAAA TTTGTAACAA TATTTTCATAA ACCAACACTA  
 AAATCACCCG GAAAAGTATT AAATAGCATA GCAATTCTAG AGCTAAACAT AGAGCAGGTA  
 ATTAATCACC TAGACTCAAA AAATGAGACC TTAAATAAAG CAAGCTCTTT AGATTTGGAA  
 AAGATCAAAA ATTCCTTTGA ACAGCTGTTT TCTATAAGGA ATTTTTTTTC AACAAATCATA  
 AAAAGGGTCT TATTAGATCA TCAAAACAAT GAAAATTCTA TAAACCAGA TGATTCTAAA  
 TCAGGAACCT ATTTGATAC GATATACGAT CAGTTTAATG AAAAAATAA AGAGGTTAGA  
 AATCTGAAAA AAACCATATT ATCACTGCCG AATTAA

t19-4.nt

CTGCACCGCTAACCATGAAGCTGAAGCGAAAAATAAAAAACATGTTGATAAAACAAAAACGAATATATTAATGAA  
 AAAAAAATTTAATAGCAACAACCAAGAAATCATCGAAAAACGAAATTTGCTACAAGCTAAACCAGTAGATCAAA  
 ACCCCGTAGATGATACAAACAATAAGAAAGTTTTTCGAGATAGATAAAAGAGCTTTTCGATTTTATAAATAGTTTTTT  
 AACAGATGATGAATTTAATAAATTTGTAACAATATTTTCATAAACCAACACTAAAATCACCCGAAAAGTATTAAAT  
 AGCATAGCAATTTCTAGAGCTAAACATAGAGCAGGTAATTAATCACCTAGACTCAAAAAATGAGACCTTAAATAAAG  
 CAAGCTCTTTAGATTTGGAAAAGATCAAAAATTCCTTGAACAGCTGTTCTCTATAAGGAATTTTTTTTCAACAAT  
 CATAAAAAGGGTCTTATTAGATCATCAAAACAATGAAAATTTCTATAAAACCAGATGATTCTAAATCAGGAACCTAT  
 TTCGATACGATATACGATCAGTTTAATGAAAAAATAAAGAGGTTAGAAATCTGAAAAA

f19-4.aa

SILIEENIFM KNNIILCMCV FLLNSCTAN HEAEAKIKKH VDKTKNEYIN EIKNLIATTK  
 EIEKRKLLQ AKPVDQNPVD DTNNKKVFEI DKRAFDINS FLTDDEFNKF VTIFHKPTLK  
 SPGKVLNSIA ILELNIEQVI NHLDSKNETL NKASSLDLEK IKNSLEQLFS IRNFFSTIIK  
 RVLLDHQNE NSIKPDDSKS GTYFDTIYDQ FNEKNKEVRN LKKTILSLPN

t19-4.aa

CTANHEAEAKIKKHVDKTKNEYINEIKNLIATTK EIEKRKLLQ AKPVDQNPVDDTNNKKVFEIDKRAFDINSFL  
 TDDEFNKFVTIFHKPTLKSPGKVLNSIA ILELNIEQVINHLDSKNETLNKASSLDLEKIKNSLEQLFSIRNFFSTI  
 IKRVLLDHQNNENSIKPDSSKSGTYFDTIYDQFNEKNKEVRNLKK

f19-6.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TAAAGGAGAG TATTAATGAA ATGCCATATA ATTGCAACTA TATTTGTTTT TCTATTTTTTA  
 GCTTGCAGTA CAGATTTTAA TACTGATCAA AAAGGCATTA AATACCCGCC TACCGAAAAA  
 TCAAAGCCCA AAAGTGAAGA CTCTAAGCAA AAAGAATTAA AGCCTAAAAAC AGAAAAAGAA  
 CTAAAGAAAA AACAACTAACT AAAAAATAAA CTACTTAATG ATTTAAAAAA TTCAATAGAA  
 ACAGCTAATA AGCATAAAGA AAAGTATAAA AAAAGAATGA AAGAAGAACC CGAAGATCAA  
 TACGGGGTAC AGGCTTTCAA AGGATCGAAT TGGGGGCCGG GGAAGTGAAGA TGTATCTGCC  
 AACACCGAAA GATCTATAAG ATTTAGAAGA CATACTTATA CTATTTTAAG CACGCTGAGT  
 CTTTCATGAAT TAAAGGAATT CTCAAATATT GTTACAAATG AAAATAAACT GGTGCCAGTA  
 GTAGATATGT TTAATTTCTT TAGCTCTATT GGGACAGCTC TTGATATAAC AACCGATAGC  
 TTATATCCCA AAAAGACAAT CTGGACAAAC CAGATCTGTC GGATTTAG

t19-6.nt

TTGCGTACAGATTTTAATACTGATCAAAAAGGCATTAAATACCCGCCTACCGAAAAATCAAAGCCCCAAAACCTGAA  
 GACTCTAAGCAAAAAGAATTAAAGCCTAAAACAGAAAAAGAACTAAAGAAAAACAACAATAAAAAATAAACTAC  
 TTAATGATTTAAAAAATTCAATAGAAACAGCTAATAAGCATAAAGAAAAAGTATAAAAAAGAATGAAAGAAGAACC  
 CGAAGATCAATACGGGGTACAGGCTTTCAAAGGATCGAATTGGGGGCCGGGACTGAAGATGTATCTGCCAACACC  
 GAAAGATCTATAAGATTTAGAAGACATACCTTATACTATTTTAAGCACGCTGAGTCTTCATGAATTAAAGGAATTCT  
 CAAATATTGTTACAAATGAAAAATAAACTGGTGCCAGTAGTAGATATGTTTAATTTCTTTAGCTCTATTGGGACAGC  
 TCTTGATATAACAACCGATAGCTTATATCCCAAAAAGACAATCTGGACAAACCAGATCTGTCCG

f19-6.aa

RRVLMKCHII ATIFVFLFLA CSTDFNTDQK GIKYPTEKS KPKTEDSKQK ELKPKTEKEL  
 KKKQQLKNKL LNDLKNSIET ANKHKEKYKK RMKEEPEDQY GVQAFKGSNW GPGTEDVSAN  
 TERSIRFRRH TYTILSTLSL HELKEFSNIV TNENKLVVPM DMFNFFSSIG TALDITTDLSL  
 YPKKTIWTNQ ICRI

t19-6.aa

CSTDFNTDQKGIKYPTEKSKPKTEDSKQKELKPKTEKELKKKQQLKNKLLNDLKNSIETANKHKEKYKKRMKEEP  
 EDQYGVQAFKGSNWGPGTEDVSANTERSIRFRRHTYTILSTLSLHELKEFSNIVTNENKLVVPMDMFNFFSSIGTA  
 LDITTDLSLYPKKTIWTNQICR

f21-4.nt

TAGGAGACAA TCTTTATGAA TAAAAAATA AAAATGTTTA TTATTTGTGC TATTTTATG  
 CTGATAAGTT CTTGTAAGAA TGATGTAAC AGTAAAGATT TAGAAGGGGC GGTGAAAGAT  
 TTAGAAAGTT CAGAACAAA TGTAAAAAA ACAGAACAAG AGATAAAAA ACAAGTTGAA  
 GGATTTTATG AAATTTTAGA GACAAAAGAT TTAAACACAT TAGATACAAA AGAAATTGAA  
 AAACAAATTC AAGAATTAAA GAATAAGATA GAAAAATTAG ACTCTAAAA AACTTCTATT  
 GAAACATATT CTGGGTATGA AGAAAAATA AACAAAATAA AAGAAAAAT AAACGGAAAA  
 GGACTTGAAG ATAAATTAAA TGAACTTTCA GAGAGCTTAA AAAAGAAAA AGAGGAGAGA  
 AAAAAAGCTT TACAAGAGGC TAAAAAGAAA TTTGAAGAGT ATAAAAACCA AGCTGAATCT  
 GCAACTGGAG TAACGCATGG TTCTCAAGTC CAAAGACAAG GTGGTGTTGG ATTACAAGCT  
 TGGCAGTGTG CTAATAGTTT GGGGTTTAAA AATATGACTA GTGGTAATAA TACTAGCGAT  
 ATGACCAATG AAGTTATAAC TAATTCGCTT AAAAGATTG AAGAAGAAT TAAAAATAT  
 GGAGAACTG TAGAAGGTAA AAAAGAATAA

t21-4.nt

TTGTAAGAATGATGTAAGTAGTAAAGATTTAGAAGGGGCGGTGAAAGATTTAGAAAGTTCAGAACAAAATGTAAAA  
 AAAACAGAACAAGAGATAAAAAACAAGTTGAAGGATTTTGTAGAAATTTTAGAGACAAAAGATTTAAACACATTAG  
 ATACAAAAGAAATTGAAAAACAAATTCAGAATTAAAGAATAAGATAGAAAAATTAGACTCTAAAAAACTTCTAT  
 TGAAACATATTCTGGGTATGAAGAAAAATAACAAAATAAAAGAAAAATTAACGGAAAAGGACTTGAAGATAAA

TABLE 1. Nucleotide and Amino Acid Sequences

TTAAATGAACTTTCAGAGAGCTTAAAAAAGAAAAAGAGGAGAGAGAAAAAAGCTTTACAAGAGGCTAAAAAGAAAT  
 TTGAAGAGTATAAAAACCAAGCTGAATCTGCAACTGGAGTAACGCATGGTTCTCAAGTCCAAAGACAAGGTGGTGT  
 TGGATTACAAGCTTGGCAGTGTGCTAATAGTTTGGGGTTTAAAAATATGACTAGTGGTAATAACTAGCGATATG  
 ACCAATGAAGTTATAACTAATTCGCTTAAAAAGATTGAAGAAGAACTTAAAAATATTGGAGAACTGTAGAAGGTA  
 AAAAAGAA

f21-4.aa

ETIFMNNKKIK MFIICAIFML ISSCKNDVTS KDLEGAVKDL ESSEQNVKKT EQEIKKQVEG  
 FLEILETKDL NTLDTKEIEK QIQELKNKIE KLDSKKTSE TYSGYEKIN KIKEKLNGKG  
 LEDKLNELSE SLKKKKEERK KALQEAKKFF EYKQNAESA TGVTHGSQVQ RQGGVGLQAW  
 QCANSLGFKN MTSGNNTSDM TNEVITNSLK KIEEELKNIG ETVEGKKE

t21-4.aa

CKNDVTSKDLEGAVKDLESSEQNVKKTQEIEKKQVEGFLEILETKDLNTLDTKEIEKQIQELKNKIEKLDSKKTSE  
 ETYSGYEEKINKIKEKLNGKGLDKLNELSESLKKKKEERKKALQEAKKFF EYKQNAESATGVTHGSQVQRQGGV  
 GLQAWQCANSLGFKNMTSGNNTSDMTNEVITNSLKKIEEELKNIGETVEGKKE

f24-1.nt

TAAGCTGGTA ACACTGTAAA GACAGCTGAG GGGGCTTCAA GTGGTACTGA TGCAATTGGA  
 GAAGTTGTGG ATAATGATGC TAAGGTTGCT GATAAGGCGA GTGTGACGGG GATTGCTAAG  
 GGGATAAAGG AGATTGTTGA AGCTGCTAGG GGGAGTGAAA AGCTGAAAGT TGCTGCTGCT  
 AAAGAGGGCA ATGAAAAGGC AGGGAAGTTG TTTGGGAAGG CTGGTGCTAA TGCTCATGGG  
 GACAGTGAGG CTGCTAGCAA GCGGCTGGT GCTGTTAGTG CTGTTAGTGG GGAGCAGATA  
 TTAAGTCCGA TTGTTAAGGC TCGGATGCG GCTGAGCAGG ATGGAAAGAA GCCTGCAGAT  
 GCTACAAATC CGATTGCTGC TGCTATTGGG AATAAAGATG AGGATGCGGA TTTTGGTGAT  
 GGGATGAAGA AGGATGATCA GATTGCTGCT GCTATTGCTT TGAGGGGGAT GGCTAAGGAT  
 GGAAAGTTTG CTGTGAAGAA TGATGAGAAA GGGAAGGCTG AGGGGGCTAT TAAGGGAGCT  
 GCTGCAATTG GAGAAGTTGT GGATAATGCT GGTGCTGCGA AGGCTGCTGA TAAGGATAGT  
 GTGAAGGGGA TTGCTAAGGG GATAAAGGAG ATTGTTGAAG CTGCTGGGGG GAGTGAAAAG  
 CTGAAAGCTG CTGCTGCTGA AGGGGAGAAT AATAAAAAGG CAGGGAAGTT GTTTGGGAAA  
 GTTGATGGTG CTGCTGGGGA CAGTGAGGCT GCTAGCAAGG CCGCTGGTGC TGTTAGTGCT  
 GTTAGTGGGG AGCAGATATT AAGTGCGATT GTTAAGGCTG CTGGTGAGGC TGAGCAGGAT  
 GGAGAGAAGC CTGAGGATGC TAAAAATCCG ATTGCTGCTG CTATTGGGAA GGGTAATGGG  
 GATGGTGCGG AGTTTGATCA GGATGAGATG AAGAAGGATG ATCAGATTGC TGCTGCTATT  
 GCTTTGAGGG GGATGGCTAA GGATGGAAG TTTGCTGTGA AGGGTAATAA TGAGAAAGAG  
 AAGGCTGAGG GGGCTATTAA AGAAGTTAGC GAGTTGTTGG ATAAGCTGGT AACAGCTGTA  
 AAGACAGCTG AGGGGGCTTC AAGTGGTACT GATGCAATTG GAGAAGTTGT GGATAATGNT  
 GCNAAGGNTG CTGATAAGGC GAGTGTGACG GGGATTGCTA AGGGGATAAA GGAGATTGTT  
 GAAGCTGCTN GGGGGAGTGA AAAGCTGAAA GTTGCTGCTG CTANAGNGGN NAATAATAAA  
 GAGGCAGGGA AGTTGTTTGG GAAGGCTGGT GCTGATGCTA ATGGGGACAG TGAGGCTGCT  
 AGCAAGGCGG CTGGTGCTGT TAGTGCTGTT AGTGGGGAGC AGATATTAAG TGCGATTGTT  
 AAGGCTGCGG CTGCTGGTGC GGCTGATCAG GATGGAGAGA AGCCTGGGGA TGCTAAAAAT  
 CCGATTGCTG CTGCTATTGG GAAGGGTAAT GCGGATGATG GTGCGGATTT TGGTGATGGG  
 ATGAAGAAGG ATGATCAGAT TGCTGCTGCT ATTGCTTTGA GGGGGATGGC TAAGGATGGA  
 AAGTTTGCTG TGAAGAAGGA TGAGAAAGGG AAGGCTGAGG GGGCTATTAA GGGAGCTAGC  
 GAGTTGTTGG ATAAGCTGGT AAAAGCTGTA AAGACAGCTG AGGGGGCTTC AAGTGGTACT  
 GCTGCAATTG GAGAAGTTGT GGATAATGCT GCGAAGGCTG CTGATAAGGA TAGTGTGACG  
 GGGATTGCTA AGGGGATAAA GGAGATTGTT GAAGCTGCAG GGGGGAGTGA AAAGCTGAAA  
 GTTGCTGCTG CTAAAGGGGA GAATAATAAA GGGGCAGGGA AGTTGTTTGG GAAGGCTGGT  
 GCTAATGCTC ATGGGGACAG TGAGGCTGCT AGCAAGGCGG CTGGTGCTGT TAGTGCTGTT  
 AGTGGGGAAC AGATATTAAG TGCGATTGTT AAGGCTGCTG GTGAGGCTGC TGGTGATCAG  
 GAGGGAAAGA AGCCTGAGGA GGCTAAAAAT CCGATTGCTG CTGCTATTGG GGATAAAGAT  
 GGGGATGCGG AGTTTAATCA GGATGGGATG AAGAAGGATG ATCAGATTGC TGCTGCTATT

TABLE 1. Nucleotide and Amino Acid Sequences

GCTTTGAGGG	GGATGGCTAA	GGATGGAAAG	TTTGCTGTGA	AGGATGGTGG	TGAGAAAGAG
AAGGCTGAGG	GGGCTATTAA	AGGAGTTAGC	GAGTTGTTGG	ATAAGCTGGT	AAAAGCTGTA
AAGACAGCTG	AGGGGGCTTC	AAGTGGTACT	GCTGCAATTG	GAGAAGTTGT	GGCTGATGCT
GCTAAGGTTG	CTGATAAGGC	GACTGTGACG	GGGATTGCTA	AGGGGATAAA	GGAGATTGTT
GAAGCTGCTG	GGGACAGTGA	GGCTGCTAGC	AAGGCAGCTG	GTGCTGTTAG	TGCTGTTAGT
GGGGAGCAGA	TATTAAGTGC	GATTGTTAAG	GCTGCGGCTG	CTGGTGCGGC	TGAGCAGGAT
GGAGAGAAGC	CTGCAGAGGC	TAAAAATCCG	ATTGCTGCTG	CTATTGGGAA	GGGTGATGGG
GATGCGGATT	TTGGTGAGGA	TGGGATGAAG	AAGGATGATC	AGATTGCTGC	TGCTATTGCT
TTGAGGGGGA	TGGCTAAGGA	TGGAAGTTT	GCTGTGAAGA	ATGATGAGAA	AGGGAAGGCT
GAGGGGGCTA	TTAAGGGAGC	TGCTGCAATT	GGAGAAGTTG	TGGATAATGC	TGGTGCTGCG
AAGGCTGCTG	ATAAGGATAG	TGTGAAGGGG	ATTGCTAAGG	GGATAAAGGA	GATTGTTGAA
GCTGCTGGGG	GGAGTGAAAA	GCTGAAAGCT	GCTGCTGCTG	AAGGGGAGAA	TAATAAAAAAG
GCAGGGAAGT	TGTTTGGGAA	AGTTGATGGT	GCTGCTGGGG	ACAGTGAGGC	TGCTAGCAAG
GCGGCTGGTG	CTGTTAGTGC	TGTTAGTGGG	GAGCAGATAT	TAAGTGCGAT	TGTTAAGGCT
GCGGATGCGG	CTGAGCAGGA	TGGAAGAAG	CCTGCAGATG	CTACAAATCC	GATTGCTGCT
GCTATTGGGA	ATAAAGATGA	GGATGCGGAT	TTTGGTGATG	GGATGAAGAA	GGATGATCAG
ATTGCTGCTG	CTATTGCTTT	GAGGGGGATG	GCTAAGGATG	GAAAGTTTGC	TGTGAAGGGT
AATAATGAGA	AAGGGAAGGC	TGAGGGGGCT	TCAAGTGGTA	CTGATGCAAT	TGGAGAAGTT
GTGGATAATG	ATGCGAAGGC	TGCTGATAAG	GCGAGTGTGA	CGGGGATTGC	TAAGGGGATA
AAGGAGATTG	TTGAAGCTGC	TGGGGGGAGT	GAAAAGCTGA	AAGCTGTTGC	TGCTGCTACA
AGGGAGAATA	ATAAAGAGGC	AGCGAAGTTG	TTTGGGAAAG	TTGATGATGC	TCATGCTGGG
GACAGTGAGG	CTGCTAGCAA	GGCGGCTGGT	GCTGTTAGTG	CTGTTAGTGG	GGAGCAGATA
TTAAGTGCGA	TTGTTACGGC	TGCGGCTGCT	GGTGAGCAGG	ATGGAGAGAA	GCCTGCAGAG
GCTACAAATC	CGATTGCTGC	TGCTATTGGG	AAGGGTAATG	AGGATGGTGC	GGATTTTGGT
AAGGATGAGA	TGAAGAAGGA	TGATCAGATT	GCTGCTGCTA	TTGCTTTGAG	GGGGATGGCT
AAGGATGGAA	AGTTTGCTGT	GAAGAGTAAT	GATGGTGAGA	AAGGGAAGGC	TGAGGGGGCT
ATTAAGGAAG	TTAGCGAGTT	GTTGGATAAG	CTGGTAAAAG	CTGTAAAGAC	AGCTGAGGGG
GCTTCAAGCG	GTA CTGATGC	AATTGGAGAA	GTTGTGGCTA	ATGCTGGTGC	TGCCAAGGCT
GCTGATAAGG	CGAGTGTGAC	GGGGATTGCT	AAGGGGATAA	AGGAGATTGT	TGAAGCTGCT
GGGGGGAGTA	AAAAGCTGAA	AGCTGCTGCT	GCTGAAGGGG	AGAATAATAA	AAAGGCAGGG
AAGTTGTTTG	GGAAGGCTGG	TGCTGGTGGT	GGTGCTAATG	GGGACAGTGA	GGCTGCTAGC
AAGGCGGCTG	GTGCTGTTAG	TGCTGGTTAG			

t24-1.nt

TGGTGAGGCTGAGCAGGATGGAGAGAAGCCTGAGGATGCTAAAAATCCGATTGCTGCTGCTATTGCGGAAGGGTAAT  
 GGGGATGGTGCGGAGTTTGATCAGGATGAGATGAAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGGA  
 TGGCTAAGGATGGAAAGTTTGCTGTGAAGGGTAATAATGAGAAAGAGAAGGCTGAGGGGGCTATTAAAGAAGTTAG  
 CGAGTTGTTGGATAAGCTGGTAACAGCTGTAAAGACAGCTGAGGGGGCTTCAAGTGGTACTGATGCAATTGGAGAA  
 GTTGTGGATAATGNTGCNAAGGNTGCTGATAAGGCGAGTGTGACGGGGATTGCTAAGGGGATAAAGGAGATTGTTG  
 AAGCTGCTNCGGGGAGTGAAAAGCTGAAAGTTGCTGCTGCTANAGNGGNAATAATAAAGAGGCAGGGAAGTTGTT  
 TGGGAAGGCTGGTGTGATGCTAATGGGGACAGTGAGGCTGCTAGCAAG

f24-1.aa

AGNTVKTAEG	ASSGTD AIGE	VVDND AKVAD	KASVTGIAKG	IKEIVEAARG	SEKLKVA AAK
EGNEKAGKLF	GKAGANAHGD	SEAASKAAGA	VSAVSGEQIL	SAIVKAADAA	EQDGKKPADA
TNP IAAAIGN	KDEDADFGDG	MKKDDQIAAA	IALRGMADKG	KFAVKNDEKG	KAEGA IKGAA
AIGEVVDNAG	AKAADKDSV	KGI AKGIKEI	VEAAGGSEKL	KAAAAEGENN	KKAGK LFGKV
DGAAGDSEAA	SKAAGAVSAV	SGEQILSAIV	KAAGEAEQDG	EKPEDAKNPI	AAAIGKGNND
GA EFDQDEM	KDDQIAAAIA	LRGMADKGK	AVKGNNEKEK	AEGAIKEVSE	LLDKLV TAVK
TAEGASSGTD	AIGEVVDNAX	KXADKASVTG	IAKGIKEIVE	AAXGSEKLKV	AAAXXNNKE
AGK LFGKAGA	DANGDSEAAS	KAAGAVSAVS	GEQILSAIVK	AAAAGAADQD	GEKPGDAKNP
I AAAIGK GNA	DDGADFGDGM	KKDDQIAAAI	ALRGMADKGK	FAVKKDEK GK	AEGA IKGASE
LLDKLVKAVK	TAEGASSGTA	AIGEVVDNAA	KAADKDSVTG	IAKGIKEIVE	AAGGSEKLKV
AAAKGENNKG	AGK LFGKAGA	NAHGDSEAAS	KAAGAVSAVS	GEQILSAIVK	AAGEAAGDQE

TABLE 1. Nucleotide and Amino Acid Sequences

GKKPEEAKNP IAAAIGDKDG DAEFNQDGMK KDDQIAAAIA LRGMADGKGF AVKDGGEKEK  
 AEGAIGKVSE LLDKLVKAVK TAEGASSGTA AIGEVVADAA KVADKASVTG IAKGIKEIVE  
 AAGDSEAASK AAGAVSAVSG EQILSAIVKA AAAGAAEQDG EKPAEAKNPI AAAIGKGDGD  
 ADFGEDGMKK DDQIAAAIAL RGMADGKFA VKNDEKGKAE GAIKGAAAIG EVVDNAGAAK  
 AADKDSVKGI AKGIKEIVEA AGGSEKLKAA AAEGENNKKA GKLFQKVDGA AGDSEAASKA  
 AGAVSAVSGE QILSAIVKAA DAAEQDGKKP ADATNPPIAAA IGNKDEDADF GDGMKKDDQI  
 AAAIALRGMA KDGKFAVKN NEKGKAEGAS SGTDAIGEVV DNDAAADKA SVTGIKGIK  
 EIVEAAGGSE KLKAVAAATR ENNKEAGKLF GKVDDAHAGD SEAASKAAGA VSAVSGEQIL  
 SAIYVAAAAG EQDGEKPAAE TNPIAAAIGK GNEDGADFGK DEMKKDDQIA AAIALRGMK  
 DGKFAVKSND GEKGKAEGAI KEVSELLDKL VKAVKTAEGA SSGTDAIGEV VANAGAAKAA  
 DKASVTGIAK GIKEIVEAAG GSKKLKAAAA EGNNKKAGK LFGKAGAGAG ANGDEAASK  
 AAGAVSAG

t24-1.aa

GEAEQDGEKPEDAKNPAAAAIGKNGDGAEFDDQDEMKKDDQIAAAIALRGMADGKFAVKGNNEKEKAEGAIKEVS  
 ELLDKLVTAVKTAEGASSGTDAGIEVVNDXAKXADKASVTGIAKGIKEIVEAAXGSEKLKVAAXXXNNKEAGKLF  
 GKAGADANGDSEAASK

f28-2.nt

TAAAAAGGAA ATATAAATAT TATGCGATTA TGTTTAATAA AAATTTTAT TATACCTAAT  
 TTAGTATTTA GTTCTCTTTT TTTATTTGAA AGTTGTTCTG GTTTTCTATC TAAAAATCT  
 ATAGAACAGT TTGCATTAGC ATTAAAAGAT CATCAAGAAA ATAAAAATAC TACTAATACT  
 TCAGTAGATA AAAATAGTAA GGAAATTGAA TCTCCTAAAG ACGTTACATC ATCAAATAAA  
 AAAACTTATG ATCCAATCTT ACAAGTAGGT TCTAATCAAC ATATGTCAGA TGATCCTGGT  
 GCTAATAATA AAGAATCCCT ACCAAATTCA AGTCCAGCAA TAATACAAAA TGATCCGCAT  
 GCTCAAAATA ATGTAAAGAT GGAAGAAAAT AAATCAGCTA CTCCACAACA TGATCCAATT  
 GAACAAAGTA ATTTTAAAA TAGCCTTACT ACAACAAGTA AAATCCTGC TATTCCTTCA  
 GAAGAAGAAA TTAAAGCTAA CTTAGATGAA TTTGCACAAG AAGAGTATGA GCAAACATCT  
 CTTTCAGAAA TTAAAAATGC CACGCAAAAT GTTAATCATG CTAATCCTGA AAACAAATTA  
 AACAAATACAC TCCTTGAGTT TGAAAAAGAT TATGAACTT TATCAAATCT GTTATTCTCT  
 AATTTAGACG CATCTCCTTT GAATAGAAAA ATAAAGACTA TTATGCCTAA ATTACAAGAA  
 ATGCGTTCTT TTATGGAGCA AGCAACTAAT TCTTGGGTAT CTGCTAAAGG CATGCTAGAT  
 GAGGCTAAGG ATAACTAGC AGAATCTATT TATAAAAGAC TATACAATGG CAATTCATAC  
 CGGTTCGGTG GCAGTTTTTA CGGACGTGAT ATGCAACATG CAAAAAATT AGCATACAGA  
 GCTATAGACT TTGCTTCTGC ATGCATTGAA TATACACAAA AAGCTATTGA TTATCTTCAA  
 CAGGGAAATT CTTGCAAAAA AGAAATAGAA AATATATTCA AGCTTTAA

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AAAAGATCATCAAGAAAAATAAAATACTACTAATACTTCAGTAGATAAAAAATAGTAAGGAAATTGAATCTCCTAAA  
 GACGTTACATCATCAAATAAAAAAATCTTATGATCCAATCTTACAAGTAGGTTCTAATCAACATATGTCAGATGATC  
 CTGGTGCTAATAATAAAGAATCCCTACCAAATTCAGTCCAGCAATAATACAAAATGACTCGCATGCTCAAAATAA  
 TGTAAGATGGAAGAAAAATAATCAGCTACTCCACAACATGATCCAATTGAACAAAGTAATTTTAAAAATAGCCTT  
 ACTACAACAAGTAAATCCTGCTATTCTTTCAGAAAGAAATTAAGCTAACTTAGATGAATTTGCACAAGAAG  
 AGTATGAGCAAACATCTCTTTCAGAAATTAATAATGCCACGCAATTTGTTAATCATGCTAATCCTGAAAACAAAT  
 AAACAATACACTCCTTGAGTTTGAAGAAATTATGAACTTTATCAAATTTGTTATTCTCTAATTTAGACGCATCT  
 CCTTTGAATAGAAAAATAAGACTATTATGCCTAAATTAAGAAGATGCGTTCTTTTATGGAGCAAGCAACTAATT  
 CTTGGGTATCTGCTAAAGGCATGCTAGATGAGGCTAAGGATAAACTAGCAGAATCTATTTATAAAAGACTATACAA  
 TGGCAATTCATACCGGTTCCGGTGGCAGTTTTAACGGACGTGATATGCAACATGCAAAAAATTTAGCATACAGAGCT  
 ATAGACTTTGCTTCTGCATGCATTGAATATACACAAAAAGCTATTGATTATCTTCAACAGGGAAATCTTGCAAAA  
 AAGAAATAGAAAAATATATTCAAG

f28-2.aa

TABLE 1. Nucleotide and Amino Acid Sequences

KGNINIMRLC LIKIFIIPNL VFSSFLFES CSGFLSKKSI EQFALALKDH QENKNTTNTS  
 VDKNSKEIES PKDVTSSNKK TYDPILQVGS NQHMSDDPGA NNKESLPNSS PAIIQNDSHA  
 QNNVKMEENK SATPQHDPPIE QSNFKNSLT TSKTPAIPSE EEIKANLDEF AQEYEQTSLS  
 SEIKNATQIV NHANPENKLN NTLLEFEKDY ETLSNLLFSN LDASPLNRKI KTIMPKLQEM  
 RSFMEQATNS WWSAKGMLDE AKDKLAESY KRLYNGNSYR FGGSFNGRDM QHAKNLAYRA  
 IDFASACIEY TQKAIDYLQ GNSCKKEIEN IFKL

t28-2.aa

KDHQENKNTTNTSVDKNSKEIESPKDVTSSNKKTYDPILQVGSNQHMSDDPGANNKESLPNSSPAIIQNDSHAQNN  
 VKMEENKSATPQHDPPIEQSNFKNSLT TSKTPAIPSEEEIKANLDEF AQEYEQTSLSSEIKNATQIVNHANPENKL  
 NNTLLEFEKDYETLSNLLFSNLDASPLNRKIKTIMPKLQEMRSFMEQATNSWWSAKGMLDEAKDKLAESYKRLYN  
 GNSYRFGGSFNGRDMQHAKNLAYRAIDFASACIEYTQKAIDYLQ GNSCKKEIENIFK

f28-3.nt

TAGATGAATT TAATTGCTAA ATTATTTATT TTATCCACTT TAGTTTCAAT TCCAAATATC  
 CTCTCTTGTA ACCTATATGA TAATCTTGCA GACAACGCTG AGCAGGTAC AGACATACTA  
 GACAACAACA AGTCTTTTAA TACTTTAGGA AGCAGCAATG AGAGTAGAAG TCGCAGGCCT  
 AGAAGTACAA ATAATGCTTA TATGAAACAA AACATAGACA AAAATCATTT AGTTGTTGCA  
 GATATGCAAA ATGATAATAG TAGCAGCAGT CTTCCCAAC AAGTTAATAG TGAATCCAGT  
 AAAGCTAATG AAGATAGTAA TATTATGAAG GAAATTGAAT CTTCTACAGA AGAGTGCCT  
 AGACTAAGAA AAGATTTAGA AACTATAAAA CAAATACTTG ATAATATAGA AAGCTTGCTT  
 AATACAGCTA ATTCTTATTT AGAGAACGCT AGAAAAGCAC CTAAATCTAA TCAAGATAAT  
 CAAACCTTAT TGCTTAGCCT GCACCAAGCT ATTGCTAAGG TTAAGAGTAG TCATACTTCT  
 TTTATCATTT GTTATAATGA TGCATTTAAT TCCCTGGGAA TAGCTGATAC TGCCTTTAAA  
 GATGCAAAGA GAAAGGCAGT TGAGGCATAA

t28-3.nt

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 ACTTTAGGAAGCAGCAATGAGAGTAGAAGTCGAGGCCTAGAAGTACAAATAATGCTTATATGAAACAAAACATAG  
 AAAAAATCATTTAGTTGTTGCAGATATGCAAAATGATAATAGTAGCAGCAGTCTTCCCAACAAGTTAATAGTGA  
 ATCCAGTAAAGCTAATGAAGATAGTAATATTATGAAGGAAATTGAATCTTCTACAGAAGAGTGCCTAGACTAAGA  
 AAAGATTTAGAACTATAAAACAAATACCTTGATAATATAGAAAGCTTGCTTAATACAGCTAATTCTTATTTAGAGA  
 ACGCTAGAAAAGCACCTAAATCTAATCAAGATAATCAAACCTTATTGCTTAGCCTGCACCAAGCTATTGCTAAGGT  
 TAAGAGTAGTCATACTTCTTTTATCATTTGTTATAATGATGCATTTAATTCCTGGGAATAGCTGATACTGCCTTT  
 AAAGATGCAAAGAGAAAGGCAGTTGAGGCA

f28-3.aa

MNLIAKLFIL STLVSIPI NIL SCNLVDNLAD NAEQVTDILD NNKSFNTLGS SNESRSRRPR  
 STNNAYMKQN IDKNHLVVAD MQNDNSSSSL PQQVNSESSK ANEDSNIMKE IESSTEECAR  
 LRKDLETIKQ ILDNIESLLN TANSYLENAR KAPKSNQDNQ TLLLSLHQAI AKVKSSHTSF  
 IICYNDAFNS LGIADTAFKD AKRKAVEA

t28-3.aa

CNLYDNLADNAEQVTDILDNNKSFNTLGSSNESRSRRPRSTNNAYMKQNIDKNHLVVADMQNDNSSSSLPQQVNSE  
 SSKANEDSNIMKEIESSTEECARLRKDLETIKQILDNIESLLNTANSYLENARKAPKSNQDNQTLLLSLHQAIKVK  
 KSSHTSFIICYNDAFNSLGIADTAFKDAKRKAVEA

f31-2.nt

TAAAAAATA AGGAGGTATT AATGAAAAGG AAAAGCAATA TATGTATTTT ACTTCTAGTC  
 ACAATATTAT TTGTGTCTTG CAAGTTTTTT GGAAATAAAA GCGCAAGTAA AGAAAAAGAA



TABLE 1. Nucleotide and Amino Acid Sequences

GAAACTTCTT	TTTCTGATAC	TGCTAGCAAG	ATTAGTAAGT	CGGGAACAGC	TGCTTCTTCA
GACAAACAAG	AAAAAAATAC	AAGTGATGTT	ACAGGTGACG	CCAAAAAGCA	TACTAGTAGC
CCTTACATGC	TTGCTGATGC	CCTTATTGTT	AGTGATACTA	CTAATAGAGA	TAGAGATAAG
CAAGAAAATA	AAGATAAATT	AAATGAAGAA	GATAAAAAAA	AGCTTAATGC	TTTTTTTAGC
ACAATAAAA	CATATCAATC	TAGCCTAGAT	TCCATTTATA	ACAAATATAC	AGGCTATTAT
AATACCATTG	ATACCTATGG	CAGCTGTGAT	ACGTATCGCA	TTGAGTGTTC	TAGTGTAGGA
CCTTCTGAAA	AACGTAAACA	AGCTCTTGCT	GATCTAGAGA	AGTTAAAACT	AGACGAAAAG
TACATCAGC	TTAGCACAAAT	GTAAAGAGT	GCTGTGCCTA	GTTATTACAA	AAAAAATTTA
GATGATTCTA	TTGCACAGTA	TAAGGAAGCC	ATAAAGCAGG	CTATTGAAGC	TGAAAGTAAA
ATAGAGACAG	TAAAAGACTA	TGCAACAGCT	CAAAGTGCTG	CCGATGACGA	AAAGAAAAGA
AATATAGATA	ATTTAAAAAT	AGTTAGAGAT	GTTCTTCTTA	TTATTAAAAA	AACATTGAG
AAAGCCAGCC	GATCTTATGC	TGATGCTTTT	GCTATTGCAA	CATCTAGCTT	ATCTTGTAGC
GAATTTAAGC	AAGCTGTTAA	AGAGTTTAAT	GATGCTGCTA	AACAATATGC	TAATGGAAAT
AAAGGAGACA	ATGCTGTCAA	TGTTATTGTA	GGCACTATTT	CTAGTATGCC	TTATGTCAAA
TTTAAAGATG	AGTTTGCAAG	AGCAAAAATG	TTTGCTCGTA	ATTATAGAGG	AGACGAGGTA
GACAAGATGA	TAAGAGCTAT	CGACAAGCTG	TGTGATGTTT	ATAAAAAAGT	TGCGCTTTAG

t31-2.nt

TTGCAAGTTTTTTGGAAAATAAAAGCGCAAGTAAAGAAAAAGAAGAACTTCTTTTTCTGATACTGCTAGCAAGATT  
 AGTAAGTCGGGAACAGCTGCTTCTTCAGACAAACAAGAAAAAATACAAGTGATGTTACAGGTGACGCCAAAAAGC  
 ATACTAGTAGCCCTTACATGCTTGCTGATGCCCTTATTGTTAGTGATACTACTAATAGAGATAGAGATAAGCAAGA  
 AAATAAAGATAAATTAAATGAAGAAGATAAAAAAAGCTTAATGCTTTTTTTAGCACAACTAAAACATATCAATCT  
 AGCCTAGATTCCATTTATAACAAATATACAGGCTATTATAATACCATTGATACCTATGGCAGCTGTGATACGTATC  
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 CAGCTCAAAGTGCTGCCGATGACGAAAAGAAAAGAAATATAGATAATTTAAAAATAGTTAGAGATGTTCTTCTTAT  
 TATTAAAAAACTATTGAGAAAAGCCAGCCGATCTTATGCTGATGCTTTTGCTATTGCAACATCTAGCTTATCTTGT  
 AGCGAATTTAAGCAAGCTGTTAAAGAGTTTAATGATGCTGCTAAACAATATGCTAATGGAAATAAAGGAGACAATG  
 CTGTCAATGTTATTGTAGGCACTATTTCTAGTATGCCTTATGTCAAATTTAAAGATGAGTTTGCAAGAGCAAAAAT  
 GTTTGCTCGTAATTATAGAGGAGACGAGGTAGACAAGATGATAAGAGCTATCGACAAG

f31-2.aa

KNKEVLMKRK	SNICISLLVT	ILFVSCKFFG	NKSASKEKEE	TSFSDTASKI	SKSGTAASSD
KQEKNTSDVT	GDAKKHTSSP	YMLADALIVS	DTNDRDRDKQ	ENKDKLNEED	KKKLNAFFST
TKTYQSSLD	IYNKYTGYYN	TIDTYGSCDT	YRIECFSVGP	SEKRKQALAD	LEKLKLEDEK
TQLSTMLKSA	VPSYKKNLND	DSIAQYKEAI	KQAIEAESKI	ETVKDYATAQ	SAADDEKRN
IDNLKIVRDV	LLIIKKTIEK	ASRSYADAF	IATSSLSCSE	FKQAVKEFND	AAKQYANGNK
GDAVNVIVG	TISSMPYVKF	KDEFARAKMF	ARNYRGDEV	KMIRAIDKLC	DVYKVAL

t31-2.aa

CKFFGNKSASKEKEETSFSDDTASKISKSGTAASSDKQEKNTSDVTGDAKKHTSSPYMLADALIVSDTTNDRDRDKQE  
 NKDKLNEEDKKKLNAFFSTTKTYQSSLDIYNKYTGYYNTIDTYGSCDTYRIECFSVGPSEKRKQALADLEKLKLD  
 EKYTQLSTMLKSAVPSYKKNLDDSIQYKEAIKQAIEAESKIETVKDYATAQSAADDEKRNIDNLKIVRDVLLI  
 IKKTIEKASRSYADAFIATSSLSCSEFKQAVKEFNDAKQYANGNKGDNAVNVIVGTISSMPYVKFKDEFARAKM  
 FARNYRGDEVDMIRAIDK

f32-4.nt

TAAGGAAATA	TGAGGAATAT	TAGCAATTGT	ATCAAATATA	TTATATTAAC	AATGCTTATT
GGATTATTAA	TTTTTTGTTG	TGCAACCTTT	GTTTGCTTGA	TTGGAATTTT	TTATTCAAAT
AACTTTAAAG	AAGAGCGGAA	TTATTCAATA	AGCCCAATAG	ATAGTGTTAT	TATGCGTAAA
TGTTATTTTA	AAGAATTTAA	GTCTGGACTT	ATTAAAAGCG	TATTCTTTAA	GAAATTAGAT

TABLE 1. Nucleotide and Amino Acid Sequences

GTAAATGTTA ACTCTAAAAA TTTTAAGGAG CTAAATAAGG TAGATAAACA AAATCTGCTA  
 AATTCTTATC CATCTTATCA TATGGAGTTT GTCGTAGTTG ATAATGGATT TTTAATGAAT  
 TTTAAAAATG TTATTTTAA TGGTATAGAT GATGCTAAAT TATACGATCA ACGTGATATG  
 GTTTACGGAG GATTTAGATA CTCAAAAGAG GCTTATTTCC AAATTATTGG CAATTATGAT  
 GTTAAATTAA ATAAAATGAA ACAATATACT CCAGCAATTG TAGTAAATGT TTTCAAAATT  
 AACATTAATG ATGCTTTATT TAACTCGTTA TTAAAGCAAA AAACCTTTAA AGTTACTTTG  
 ATTTCCCATATAATAAAGA GTATATTTTA CAACTAATA ATTTCTTATC AAAGTATAAT  
 TTTCAAACAC CAGAAAAGGA GAATAGTTCT TACTAA

t32-4.nt

AAATAACTTTAAAGAAGAGCGGAATTATTCAATAAGCCCAATAGATAGTGTTATTATGCGTAAATGTTATTTTAA  
 GAATTTAAGTCTGGACTTATTAAAAGCGTATTCTTTAAGAAATTAGATGTAAATGTTAACTCTAAAAATTTAAGG  
 AGCTAAATAAGGTAGATAAAACAAAATCTGCTAAATTCTTATCCATCTTATCATATGGAGTTTGTCTAGTTGATAA  
 TGGATTTTAAATGAATTTTAAAAATGTTATTTTAAATGGTATAGATGATGCTAAATTATACGATCAACGTGATATG  
 GTTTACGGAGGATTTAGATACTCAAAGAGGCTTATTTCCAAATTATTGGCAATTATGATGTTAAATTAAATAAAA  
 TGAAACAATATACTCCAGCAATTGTAGTAAATGTTTTCAAAATTAACATTAATGATGCTTTATTTAACTCGTTATT  
 AAAGCAAAAACTTTAAAAGTTACTTTGATTTCCCATATAATAAAGAGTATATTTTACAACTAATAATTTCTTA  
 TCAAAGTATAATTTTCAAACACCAGAAAAGGAGAATAGTTCTTAC

f32-4.aa

GNMRNISNCI KYIILTMLIG LLIFCCATFV WLIGIFYSN FKEERNYSIS PIDSVIMRKC  
 YFKEFKSGLI KSVFFKKLDV NVNSKNFKEL NKVDKQNLN SYPSYHMEFV VVDNGFLMNF  
 KNVIFNGIDD AKLYDQDMV YGGFRYSKEA YFQIIGNYDV KLNKMKQYTP AIVVNVFKIN  
 INDALFNSLL KQKTLKVTLI SHNNKEYILO TNNFLSKYNF QTPEKENSSY

t32-4.aa

NNFKEERNYSISPIDSVIMRKC YFKEFKSGLIKSVFFKKLDV NVNSKNFKELNKVDKQNLN SYPSYHMEFVVVDN  
 GFLMNFKNVIFNGIDD AKLYDQDMV YGGFRYSKEA YFQIIGNYDV KLNKMKQYTP AIVVNVFKIN INDALFNSLL  
 KQKTLKVTLISHNNKEYILO TNNFLSKYNF QTPEKENSSY

f4-15.nt

TAAATGAGCA AAAAAGTAAT TTTAATATTA CTAGAAATTT TGATCTTGTC TTGTGATTTA  
 TCTATAAATA AAGAACAAAA AACCAAAGAA AAAACATCTG AAAAGCAAGA ATCTGAAAAA  
 CAAAATATTG AAAAACAAGA GCCTGAAAAA CAGAAACAAA ATGCAGCAAA AATAATCCCT  
 ACGGTATCAA TTCAAACGGT AGAAATAAGG GAATCAAATC AAATTCCAAA AAGCATTGAG  
 AAGTACTACA AGCAAGCTTA TCCGATTCAA ACATTCACTC TTGATTTTAG CATCACAAGA  
 GAAAAGGAAT TTCTAAAACC AGAAGATAAA ATCTTGCCCA CACAGGGGAA AGTGGAGTCT  
 TTGAGCATCT TAATAAATAA AAAATTGTTA GACTTTAAAG CCCCAGAAAA TCCAAAAAGC  
 TCAACTTTAA AAAATTTCAA AGAAATTAAG AATATTGAGA ATTTCTTCCA AAATCAAGAC  
 TTATTATTTG TCTTAACCTT TAAAGATAAA AATAACAACA AACTATTAA CATCATGCTC  
 AATCCCCCAA ACGACATCCA AAAACCCAAA GATTATATTT TAAAAGACCT TAAAGACACA  
 ATTAATAAAGG GTACTGGTGA GAAATACTTA AATCCTATCT ATAGATTTCA AATAAAAAAC  
 AAAAAAGATT ATCATTCAT AGATTACAAC AAAGTGAATA TTAGCGAAAA AACAATAGAA  
 TTGGACCTAC TGCCCTCACA ACAAGTCTTT CAAATGAATA AAAATTTTAC TAAAATTTTA  
 GACACAATAA CAGACTTAA TAATCTAAAA TTAGTAATTC AAAAGAATT AGTGTA

t4-15.nt

TTGTGATTTATCTATAAATAAAGAACAAAAACCAAAGAAAAACATCTGAAAAGCAAGAATCTGAAAAACAAAT  
 ATTGAAAAACAAGAGCCTGAAAAACAGAAACAAAATGCAGCAAAAAATAATCCCTACGGTATCAATTCAAACGGTAG  
 AAATAAGGGAATCAAATCAAATTCAAAAAGCATTGAGAAGTACTACAAGCAAGCTTATCCGATTCAAACATTCAC  
 TCTTGATTTTAGCATCACAAGAGAAAAGGAATTTCTAAAACCAGAAAGATAAAATCTTGCCACACAGGGGAAAGTG

TABLE 1. Nucleotide and Amino Acid Sequences

GAGTCTTTGAGCATCTTAATAAATAAAAAATTGTTAGACTTTAAAGCCCCAGAAAATCCAAAAAGCTCAACTTTAA  
 AAAATTTCAAAGAAATTAATAATATTTGAGAATTTCTTCCAAAATCAAGACTTATTATTTGTCTTAACCCTTAAAGA  
 TAAAAATAACAACAACACTATTAACATCATGCTCAATCCCCCAAACGACATCCAAAAACCCAAAGATTATATTTTA  
 AAAGACCTTAAAGACACAATTAATAAAGGGTACTGGTGAGAAATACTTAAATCCTATCTATAGATTTCAAATAAAAA  
 ACAAAAAAGATTATCATTCAATAGATTACAACAAAGTGACTATTAGCGAAAAACAATAGAATTGGACCTACTGCC  
 TCACGAACAAGTCTTTCAAATGAATAAAAAATTTCACTAAA

f4-15.aa

MSKKVILILL EILILSCDLS INKEQKTKEK TSEKQSEKQ NIEKQEPEKQ KQNAAKIIP  
 VSIQTVEIRE SNQIPKSIEK YYKQAYPIQT FTLDFSITRE KEFLKPEDKI LPTQGKVESL  
 SILINKKLLD FKAPENPKSS TLKNFKEIKN IENFFQNQDL LFVLTLKDN NNNTINIMLN  
 PPNDIQPKPD YILKDLKDTI KKGTEGEKYN PIYRFQIKNK KDYHSIDYNK VTISEKTIEL  
 DLLPHEQVFQ MNKNFTKILD TITDLNNLKL VIQKELV

t4-15.aa

CDLSINKEQKTKEKTSEKQSEKQNIKEQEPEKQKQNAAKIIPVSIQTVEIRESNQIPKSIEKYYKQAYPIQTFT  
 LDFSITREKEFLKPEDKILPTQGKVESLSILINKKLLDFKAPENPKSSTLKNFKEIKNIENFFQNQDLLFVLTLKD  
 KNNNTINIMLNPPNDIQPKPDYILKDLKDTIKKGTEGEKYNPIYRFQIKNKDYHSIDYNKVTISEKTIELDLLP  
 HEQVFQMNKNFTK

f4-50.nt

TAGAAGGAGG AAAAAATGAA AATTGGAAAG CTAAATTCAA TAGTTATAGC CTTGTTTTTT  
 AAACCTATTGG TCGCATGTAG TATTGGATTA GTAGAAAGAA CAAATGCAGC TCTTGAATCG  
 TCCTCTAAGG ATTTAAAAAA CAAAATTTTA AAAATAAAAA AAGAAGCCAC GGGAAAAAGGT  
 GTACTTTTTG AAGCTTTTAC AGGTCTTAAA ACCGGTTCCA AGGTAACAAG TGGTGGACTA  
 GCCTTAAGAG AAGCAAAAGT ACAAGCCATT GTTGAAACAG GAAAGTTCCT TAAGATAATA  
 GAAGAAGAAG CTTTAAAGCT TAAAGAACT GGAAACAGTG GTCAATTCTT GGCTATGTTT  
 GACTTAATGC TTGAGGTTGT AGAATCGCTA GAAGACGTTG GAATAATAGG CTTAAAAGCC  
 CGTGTTTTAG AGGAATCTAA AAATAATCCT ATAAACACAG CTGAAAGATT GCTTGCGGCT  
 AAAGCTCAA TAGAAAATCA ACTTAAAGTG GTTAAGGAAA AACAAAATAT TGAAAATGGT  
 GGAGAGAAAA AAAATAATAA AAGCAAAAAA AAGAAATAA

t4-50.nt

ATGTAGTATTGGATTAGTAGAAAGAACAAATGCAGCTCTTGAATCGTCCTCTAAGGATTTAAAAACAAAATTTTA  
 AAAATAAAAAAAGAAGCCACGGGAAAAGGTGTACTTTTTGAAGCTTTTACAGGTCTTAAACCGGTTCCAAGGTAA  
 CAAGTGGTGGACTAGCCTTAAGAGAAGCAAAAGTACAAGCCATTGTTGAAACAGGAAAGTTCCTTAAGATAATAGA  
 AGAAGAAGCTTTAAAGCTTAAAGAACTGGAAACAGTGGTCAATTCTTGGCTATGTTTGACTTAATGCTTGAGGTT  
 GTAGAATCGCTAGAAGACGTTGGAATAATAGGCTTAAAGCCCGTGTTTTAGAGGAATCTAAAAATAATCCTATAA  
 ACACAGCTGAAAGATTGCTTGCGGCTAAAGCTCAAATAGAAAATCAACTTAAAGTGTTAAGGAAAAACAAAATAT  
 TGAAAATGGTGGAGAGAAAAAAATAATAAAGCAAAAAAAGAAA

f4-50.aa

KEEKMIGKL NSIVIALFFK LLVACSIGLV ERTNALESS SKDLKNKILK IKKEATGKGV  
 LFEAFTGLKT GSKVTSGLA LREKVQAIV ETGKFLKIE EEALKLKETG NSGQFLAMFD  
 LMLEVESLE DVGIIGLKAR VLEESKNNPI NTAERLLAAK AQIENQLKVV KEKQNIENG  
 EKKNNKSKK K

t4-50.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CSIGLVERTNAALESSSKDLKNKILKIKKEATGKGVLFEAFTGLKTGSKVTSGLLALREAKVQAIVETGKFLKIIIE  
 EEALKLKETGNSGQFLAMFDLMLEVESLEDVGIIGLKARVLEESKNNPINTAERLLAAKAQIENQLKVVKEKQNI  
 ENGGEKNNKSKKKK

f4-66.nt

TAATTTTAA AATTAAATA TTTACATAAT AGTAATGTGT GTGGGAGACG TATGAAAAAT  
 ATTTTATTAT TTGTTATTTT ATTATTCCTT TCTTGTAAG AATTAAATTA TTCTGATCTT  
 AGGAGAAGGC CTTCAAAGGT TTTAAATGCT TCTAATGGTG CATCAAATAA AGAACTTAAA  
 ATTTCTTTTG TAGATCTTTT AAATGATGAT CAAAAAGAAG CTTTGTTTTT TCTTGAACAG  
 GTAGTTCTTG ATAGCAATCC CGACAAGTTT AATCAAATTT TTAATTTAAA TGAAGAGAAG  
 GTAAAAGAAA TGCTTGTTAC TGTGTGTTAAG TGTTTAAAGG CCAAAAGAAA GGCTAAAATG  
 GCTCTTGAGA GCTCAAATGT TGCAAATGTT GCCAATGCTA AACAGCAATT GCTACAGGTT  
 GAAAAAACTT ACATAGATAA TTTGCGACAA TCTTTTATGA CTACTAAAAA CATTTGAAGAG  
 GCTTGTAATC TTGTAAAAAA TTATGATGCA TCTGCTTCGT TTAA

t4-66.nt

TTGTAAAGAATTTAATTATCTGATCTTAGGAGAAGGCCTTCAAAGGTTTTAAATGCTTCTAATGGTGCATCAAAT  
 AAAGAACTTAAATTTCTTTTGTAGATCTTTAAATGATGATCAAAAAAGAAGCTTTGTTTTTTCTTGAACAGGTAG  
 TTCTTGATAGCAATCCCGACAAGTTTAATCAAATTTTAAATTTAAATGAAGAGAAGGTAAAAGAAATGCTTGTTAC  
 TGTTGTAAAGTGTTTAAAGGCCAAAAGAAAGGCTAAATGGCTCTTGAGAGCTCAAATGTTGCAAATGTTGCCAAT  
 GCTAAACAGCAATTGCTACAGGTTGAAAAACTTACATAGATAATTTGCGACAATCTTTTATGACTACTAAAAACA  
 TTGAAGAGGCTTGTAATCTTGTAATAAATTATGATGCATCTGCTTCGTTT

f4-66.aa

FLKFKYLHNS NVCGRRMKNI LLFVILLFFS CKEFNYSDLR RRPSKVLNAS NGASNKELKI  
 SFVDSLNDQ KEALFFLEQV VLDSNPDKFN QIFNLNEEKV KEMLVTVVKC LKAKRKAKMA  
 LESSNVANVA NAKQQLLQVE KTYIDNLRQS FMTTKNIEEA CNLVKNYDAS ASF

t4-66.aa

CKEFNYSDLRRRPSKVLNASNGASNKELKISFVDSLNDQKEALFFLEQVVLDSNPDKFNQIFNLNEEKVKEMLVT  
 VVKCLKAKRKAKMALESSNVANVANAKQQLLQVEKTYIDNLRQSFMTTKNIEEACNLVKNYDASASF

f42-1.nt

TAATTATTAA AATCTAAGGA GAAGAGATTT ATGAACAAAA AATTTTCTAT TTCATTATTA  
 TCTACAATAT TAGCCTTCTT GTTAGTATTA GGTTGTGATT TGTCAGCAA TAATGCTGAA  
 AACAAAATGG ATGATATTTT TAATTTAGAA AAGAAATACA TGGATAATTC AAATTATAAA  
 TGTTTAAAGTA AAAATGAGGC TATAGTTAAA AATTCTAAAA TTAAATTAGG TGTAATAAT  
 ACTAGAAGTC GTTCTTATTC TTCTAGAGAG ACTAATGTTT CGGATTCCTA TAATAAAACC  
 TATTCATATT GCAAAAGCAA CTGA

t42-1.nt

TTGTGATTTGTCAAGCAATAATGCTGAAAACAAAATGGATGATATTTTAAATTTAGAAAAGAAATACATGGATAAT  
 TCAAATTATAAATGTTTAAAGTAAAAATGAGGCTATAGTTAAAAATCTAAAAATTAATTAGGTGTAAATAATACTA  
 GAAGTCGTTCTTATCTTCTAGAGAGACTAATGTTTCGGATTCTATAATAAAACCTATTCATATTGCAAAAGCAA  
 C

f42-1.aa

LLKSKEKRFM NKKFSISLLS TILAFLLVLG CDLSSNNAEN KMDDIFNLEK KYMDNSNYKC  
 LSKNEAIVKN SKIKLGVNNT RRSYSSRET NVSDSYNKTY SYCKSN

TABLE 1. Nucleotide and Amino Acid Sequences

t42-1.aa

CDLSSNNAENKMDIDFNLEKKYMDNSNYKCLSKNEAIVKNSKIKLGVNNTRSRYSYSSRETNVSDSYNKTYSYCKSN

f43-3.nt

TGAATATTAA TAATAAAAAA AGGAATAANA ATGAAAATTA TCAACATATT ATTTTGTTTA  
 TTTTACTAA TGCTAAACAG CTGTAATTCCT AATGATACTA ATACTAGCCA AACAAAAAGT  
 AGACAAAAAC GTGATTTAAC CCAAAAAGAA GCAACACAAG AAAAACCATA ATCTAAAGAA  
 GACCTGCTTA GAGAAAAGCT ATCTGAAGAC CAAAAACAC ATCTTGACTG GTTAAAAACC  
 GCTTTAAGTG GTGCTGGAGA ATTTGATAAA TTTTATAGGAT ATGACGAAGA CAAAAATAAA  
 GGTGCACTTA ATCATATAAA GAGTGAACCT GATAAGTGTA CTGGGGATAA TTCTGAACAA  
 CAAAAAGCA CCTTCAAAGA GGTGGTTAAG GGGGCTCTTG GTGGCGGTAT AGATAGTTTT  
 GCAACTAGTG CAAGTAGTAC CTGCCAAGCT CAGCAATAA

t43-3.nt

CTGTAATTCTAATGATACTAATACTAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGCAACA  
 CAAGAAAAACCAAAATCTAAAGAAGACCTGCTTAGAGAAAAGCTATCTGAAGACCAAAAAACACATCTTGACTGGT  
 TAAAAACCGCTTTAACTGGTGCTGGAGAATTTGATAAATTTTATAGGATATGACGAAGACAAAAATAAAGGTGCACT  
 TAATCATATAAAGAGTGAACCTTGATAAGTGACTGGGGATAATTCTGAACAACAAAAAAGCACCTTCAAAGAGGTG  
 GTTAAGGGGGCTCTTGGTGCGGTATAGATAGTTTTGCAACTAGTGCAAGTAGTACCTGCCAAGCTCAGCAA

f43-3.aa

ILIIKKGIXM KIINILFCLF LLMLNSCNSN DTNTSQTCSR QKRDLTQKEA TQEKPKSKED  
 LLREKLSEDQ KTHLDWLKTA LTGAGEFDKF LGYDEDKIKG ALNHIKSELD KCTGDNSEQQ  
 KSTFKEVVKG ALGGGIDSFA TSASSTCQAQ Q

t43-3.aa

CNSNDTNTSQTCSRQKRDLTQKEATQEKPKSKEDLLREKLSEDQKTHLDWLKTALTGAGEFDKFLGYDEDKIKGAL  
 NHIKSELDKCTGDNSEQQKSTFKEVVKGALGGGIDSFATSASSTCQAQ

f45-2.nt

TAGGAGAGAA TAATTATGAA TAAAAAACA TTGATTATTT GTGCTGTTTT TCGCTGATA  
 ATTTCTTGCA AGAATTTTGC AACTGGTAAA GATATAAAC AAAATTCAGA AGGGAAAATT  
 AAAGGATTTG TAAATAAGAT TTTAGATCCA GTAAAGGATA AAATTGCTTC AAGTGGTACA  
 AAAGTAGATG AAGTAGCAA AAAATTACAA GAAGAAGAA AAGAAGAATT AATGCAGGGC  
 GATGATCCTA ATGGCAGTGG AATAAATCCG CCACCAAGTAT TGCCGGAATA TATTCACAAT  
 AATGCATTAG TATTAAGAGC AATAGAACA AGTGATGGTC AACAAGAAAA AAAAGTAGAA  
 GAAGCTGAAG CTAAAGTTGA AGAAAAATA GAAAAACAAG AGAATACAGA AGAAAAACAT  
 AAAGAAAAAG AAATAATAGA CGAACAAAA AAACAAGAAT TAGCTAAAGC TAAAGAAGAA  
 GAACAACAAA AAGAACAAAA AAGACATCAA GAAGAGCAAC AAAGAAAAAGC TAAAGCAGAA  
 AAAGAAAAAA GAGAAAGAGA AGAGGCAGAA CAACAAAAAC GACAACAAGA AGAGGAAGAA  
 AAAAGGCAAG TTGATAACCA AATTAAAAACA CTTATAGCTA AAATAGATGA GATCAATGAA  
 AATATTGATG TTATAAATG GCAAACGACT GTAGGCCAC AAGGCGTTAT AGATAGAATT  
 ACTGGGCCTG TGTATGATGA TTTTACCAAT GGCAATAATT CTATACGCGA AACTTGGGAG  
 GGGTTAGAAG AGGAATCAGA AGACGAAGGA TTAGGAAAAT TATTGAAAGA ATTGAGTGAT  
 GCTAGGGACG CGCTAAGAAC TAAATTAAAT GAAGGCAATA AACCATATAC TGGTTACGAA  
 GAGCCTAAGT TAAAGAAAG TGTAATGTG AGCGAAATTA AAGAAGATT AGAAAAATTA  
 AAATCAAAAT TAGAAGAAGT TAAAAAATAT CTTAAAGATA GTTCTAAATT TGAAGAAATT  
 AAAGGATACA TCAGTGACAG TCAGTAA

t45-2.nt

TABLE 1. Nucleotide and Amino Acid Sequences

TTGCAAGAATTTTGCAACTGGTAAAGATATAAAACAAAATTCAGAAGGGAAAATTAAAGGATTTGTAAATAAGATT  
TTAGATCCAGTAAAGGATAAAATTGCTTCAAGTGGTACAAAAGTAGATGAAGTAGCAAAAAATTACAAGAAGAAG  
AAAAAGAAGAATTAATGCAGGGCGATGATCCTAATGGCAGTGGAAATAATCCGCCACCAGTATTGCCGGAAAATAT  
TCACAATAATGCATTAGTATTAAAAGCAATAGAACAAAAGTGATGGTCAACAAGAAAAAAGTAGAAGAAGCTGAA  
GCTAAAGTTGAAGAAAAATAAGAAAAACAAGAGAATACAGAAGAAAAACATTAAAGAAAAAGAAATAATAGACGAAC  
AAAACAAACAAGAATTAGCTAAAGCTAAAGAAGAAGAACAAAAAGAACAACAAAAAGACATCAAGAAGAGCAACA  
AAGAAAAGCTAAAGCAGAAAAAGAAAAAGAGAAAGAGGCGAGAACAACAAAAACGACAACAAGAAGAGGAA  
GAAAAAAGGCAAGTTGATAACCAATTAAACACTTATAGCTAAAAATAGATGAGATCAATGAAAATATTGATGTTA  
TAAATGGCAAACGACTGTAGGCCACAAGGCGTTATAGATAGAATTACTGGGCCTGTGTATGATGATTTTACCAA  
TGGCAATAATTCTATACGCGAAACTTGGGAGGGGTTAGAAGAGGAATCAGAAGACGAAGGATTAGGAAAATTATTG  
AAAGAATTGAGTGATGCTAGGGACGCGCTAAGAACTAAATTAAATGAAGGCAATAAACCATATACTGGTTACGAAG  
AGCCTAAGTTAAAAAGAAAGTGTAATGTTAGCGAAATTAAAGAAAGATTAGAAAAATTAAATCAAATTAGAAGA  
AGTTAAAAAATATCTTAAAGATAGTTCTAAATTTGAAGAAATTAAAGGATACATCAGTGACAGTCAG

f45-2.aa

ERIIMNKKTL IICAVFALII SCKNFATGKD IKQNSEGKIK GFVNKILDPV KDKIASSGTK  
VDEVAKKLQE EEKEELMQGD DPNGSGINPP PVLPENIHNN ALVLKAIEQS DGQKEKKVEE  
AEAKVEENKE KQENTENIK EKEIIDEQNK QELAKAKEEE QQKEQKRHQE EQQRKAKAEK  
EKREEREEAQ QKRQQEEEEK RQVDNQIKTL IAKIDEINEN IDVIKWQTTV GPQGVIDRIT  
GPVYDDFTNG NNSIRETWEG LEESEDEGL GKLLKELSDA RDALRTKLNE GNKPYTGYYE  
PKLKESVNVN EIKEDLEKLK SKLEEVKKYL KDSSKFEEIK GYISDSQ

t45-2.aa

CKNFATGKDIKQNSEGKIKGFVNKILDPVKDKIASSGKTVDEVAKKLQEEKEELMQGDDPNSGINPPVLPENI  
HNNALVLKAIEQSDGQKEKKVEEAEAKVEENKEKQENTENIKEKEIIDEQNKQELAKAKEEEQQKEQKRHQEEQQ  
RKAKAEKEKREEREEAEQQKRQQEEEEKQVDNQIKTLIAKIDEINENIDVIKWQTTVGPQGVIDRITGPVYDDFTN  
GNNSIRETWEGLEEESEDEGLGKLLKELSDARDALRTKLNEGKNPYTGYYEPLKESVNVSEIKEDLEKLKSKLEE  
VKKYLKDSSKFEEIKGYISDSQ

f47-2.nt

TGAATATTAA TAATAAAAAA AGGAGTAACA ATGAAAATCA TCAACATATT ATTTTGTATA  
TCTTTGCTAC TACTAAATAG CTGTAATTCC AATGATAATG ACACTTTAAA AAACAATGCC  
CAACAAACAA AAAGCAGGAA AAAACGTGAT TTAAGCCAAG AAGAACTGCC ACAACAAGAA  
AAAATCACTT TAACATCCGA CGAAGAAAAA ATGTTTACTT CATTAATCAA TGTGTTTAAA  
TACACAATTG AAAAATTAAA CAATGAAATA CAAGGGTGCA TGAATGGAAA CAAAAGTAAA  
TGTAATGACT TCTTTGATTG GCTTCTTGAA GATATTCAA AACAAAAAGA ATTAGCTGGT  
GCTTTTACCA AGGTTTACAA CTTCTTAAAA TCAAAAGCAC AAAATGAAAC TTTTGATACT  
TATATTAAAG GAGCTATTGA TTGTAAAAA AACACTCCAC AAGATTGTAA TAAAAATAAT  
GAAATATGGG GAGGTGGACA ACTTANTAGN GCAATATTTT AG

t47-2.nt

CTGTAATTCCAATGATAATGACACTTTAAAAACAATGCCCAACAAACAAAAAGCAGGAAAAACGTGATTTAAGC  
CAAGAAGAACTGCCACAACAAGAAAAAATCACTTTAACATCCGACGAAGAAAAAATGTTTACTTCATTAATCAATG  
TGTTTAAATACACAATTGAAAAATTAAACAATGAAATACAAGGGTGCATGAATGGAAACAAAAGTAAATGTAATGA  
CTTCTTTGATTGGCTTTCTGAAGATATT  
CAAAAACAAAAAGAATTAGCTGGTGCTTTTACCAAGGTTTACAACCTTCTTAAAAATCAAAGCACAAAATGAACTT  
TTGATACTTATATTAAAGGAGCTATTGATTGTAAAAAAACACTCCACAAGATTGTAATAAAAAATAATGAA

f47-2.aa

ILIIKKGVTM KIINILFCIS LLLNSCNSN DNDTLKNNQ QTKSRKKRDL SQEELPQOEK

TABLE 1. Nucleotide and Amino Acid Sequences

ITLTSDEEKM FTSLINVKY TIEKLNNEIQ GCMNGNKS KC NDFFDWLSED IQKQKELAGA  
FTKVYNFLKS KAQNETFD TY IKGAIDCKKN TPQDCNK NNE IWGGGQLXXA IF

t47-2.aa

CNSNDNDTLKNNAQQTKSRKKRDL SQEELPQQEKITLTSDEEKMFTSLINVKY TIEKLNNEIQGCMNGNKS KCND  
FFDWLSEDIQKQKELAGAF TKVYNFLKSKAQNETFD TYIKGAIDCKKNTPQDCNK NNE

f49-2.nt

TAAATGTTCA AAACAATCAT TAAACAAAAA AATATGAAAA AAATTTCAAG TGCAATTTTA  
TTAACAACTT TCTTTGTTTT TATTAATTGT AAAAGCCAAG TTGCTGATAA GGCGAGTGTG  
ACGGGGATTG CTAAGGGAAT AAAGGAGATT GTTGAAGCTG CTGGGGGGAG TGAAAAGCTG  
AAAGTTGCTG CTGCTGAAGG GGAGAATAAT GAAAAGGCAG GGAAGTTGTT TGGGAAGGCT  
GGTGTGTTA ATGCTGGGGA CAGTGAGGCT GCTAGCAAGG CGGCTGGTGC TGT TAGTGCT  
GTTAGTGGGG AGCAGATATT AAGTGCATT GTTAAGGCTG CTGCTGAGGC TGC GCAGGAT  
GGAGAGAAGC CTGGGGAGGC TAAAAATCCG ATTGCTGCTG CTATTGGGAA GGGTAATGAG  
GATGGTGCGG AGTTTAAGGA TGAGATGAAG AAGGATGATC AGATTGCTGC TGCTATTGCT  
TTGAGGGGGA TGGCTAAGGA TGGAAAGTTT GCTGTGAAGA ATGATGAGAA AGGGAAGGCT  
GAGGGGGCTA TTAAGGGAGC TGGCGAGTTG TTGGATAAGC TGGTAAAAGC TGTAAAGACA  
GCTGAGGGGG CTCAAGTGG TACTGCTGCA ATTGGAGAAG TTGTGGCTGA TGATAATGCT  
GCGAAGGTTG CTGATAAGGC GAGTGTGAAG GGGATTGCTA AGGGGATAAA GGAGATTGTT  
GAAGCTGCTG GGGGGAGTAA AAAGCTGAAA GTTGTCTGCTG CTAAAGAGGG CAATGAAAAG  
GCAGGGAAGT TGTTTGGGAA AGTTGATGCT GCTCATGCTG GGGACAGTGA GGCTGCTAGC  
AAGGCGGCTG GTGCTGTTAG TGCTGTTAGT GGGAGCAGA TATTAAGTGC GATTGTTAAG  
GCTGCTGGTG CGGCTGCTGG TGATCAGGAG GGAAAGAAGC CTGGGGATGC TAAAAATCCG  
ATTGCTGCTG CTATTGGGAA GGGTGATGCG GAGAATGGTG CGGAGTTTAA TCATGATGGG  
ATGAAGAAGG ATGATCAGAT TGCTGCTGCT ATTGCTTTGA GGGGGATGGC TAAGGATGGA  
AAGTTTGCTG TGAAGAGTGG TGGTGGTGAG AAAGGGAAGG CTGAGGGGGC TATTAAGGGA  
GCTGCTGAGT TGTTGGATAA GCTGGTAAAA GCTGTAAAGA CAGCTGAGGG GGCTTCAAGT  
GGTACTGATG CAATTGGAGA AGTTGTGGCT AATGCTGGTG CTGCAAAGGT TGCTGATAAG  
GCGAGTGTGA CGGGGATTGC TAAGGGGATA AAGGAGATTG TTGAAGCTGC TGGGGGGAGT  
GAAAAGCTGA AAGTTGCTGC TGCTACAGGG GAGAGTAATA AAGGGGCAGG GAAGTTGTTT  
GGGAAGGCTG GTGCTGGTGC TAATGCTGGG GACAGTGAGG CTGCTAGCAA GGCGGCTGGT  
GCTGTTAGTG CTGTTAGTGG GGAGCAGATA TTAAGTGCGA TTGTTAAGGC TGCTGATGCG  
GCTGATCAGG AGGGAAAGAA GCCTGGGGAT GCTANAAATC CGATTGCTGC TGCTATTGGG  
AAGGGTNATG NGGAGAATGG TGCGGAGTTT AANNATGANG GATGA

t49-2.nt

TTGTAAAAGCCAAGTTGCTGATAAGGCGAGTGTGACGGGGATTGCTAAGGGAATAAAGGAGATTGTTGAAGCTGCT  
GGGGGGAGTGAAAAGCTGAAAAGTTGCTGCTGCTGAAGGGGAGAATAATGAAAAGGCAGGGAAGTTGTTTGGGAAGG  
CTGGTGCTGGTAATGCTGGGGACAGTGAGGCTGCTAGCAAGGCGGCTGGTGCTGTTAGTGCTGTTAGTGGGGAGCA  
GATATTAAAGTGCGATTGTTAAGGCTGCTGGTGAGGCTGCGCAGGATGGAGAGAAGCCTGGGGAGGCTAAAAATCCG  
ATTGCTGCTGCTATTGTTAAGGGAAGGTAATGAGGATGGTGCGGAGTTTAAGGATGAGATGAAGAAGGATGATCAGATTG  
CTGCTGCTATTGCTTTGAGGGGGATGGCTAAGGATGGAAAGTTTGTGCTGTGAAGAATGATGAGAAAGGGAAGGCTGA  
GGGGGCTATTAAAG

f49-2.aa

MFKTIKQKN MKKISSAILL TTFVFINCK SQVADKASVT GIAKGIKEIV EAAGGSEKLK  
VAAAEENNE KAGKLFKAG AGNAGDSEAA SKAAGAVSAV SGEQILSAIV KAAGEAAQDG  
EKPGEAKNPI AAAIGKGNED GAEFKDEMCK DDQIAAAIAL RGMADGKFA VKNDEKGKAE  
GAIKGAGELL DKLVKAVKTA EGASSGTAAI GEVVADDNAA KVADKASVKG IAKGIKEIVE  
AAGGSKKLKV AAAKEGNEKA GKLFKVDAA HAGDSEAASK AAGAVSAVSG EQILSAIVKA  
AGAAAGDQEG KKP GDAKNPI AAAIGKDAE NGAEFNHDGM KKDDQIAAAI ALRGMADGK

TABLE 1. Nucleotide and Amino Acid Sequences

FAVKSGGGEK GKAEGAIGKA AELLDKLVKA VKTAEGASSG TDAIGEVVAN AGAAKVADKA  
SVTGIAGKIK EIVEAAGGSE KLKVAAATGE SNKGAGKLFG KAGAGANAGD SEAASKAAGA  
VSAVSQEIL SAIVKAADAA DQEGKKPGDA XNPAAAAIGK GXXENGAEFX XXG

t49-2.aa

CKSQVADKASVTGIAGKIKEIVEAAGGSEKLKVAAAEKENNEKAGKLFGKAGAGNAGDSEAASKAAGAVSAVSQEIQ  
ILSAIVKAAGEAAQDGEKPGKAKNPAAAAIGKGNEDGAEFKDEMKKDDQIAAAIALRGMADGKFAVKNDEKKGKAE  
GAIK

f5-14.nt

TAGAAATTCA AAACAAAGGA GAAAACAAAA AGTATGAATA AAAAAATATT GATTATTTTT  
GCTGTTTTTG CACTTATAAT TTCTTGTAAG AATTATGCAA CTGGTAAAGA TATAAAACAA  
AATGCAAAAG GGAAATTAAG AGGATTTTTTA GATAAGGTTT TAGATCCAGC AAAAGATAAA  
ATTACTTCAA GTAGTTCAA AGTAGATGAA TTAGCAAAAA AATTACAAGA AGAAGATGAA  
GATAATGAAT TAATGCAGGG CGATGATCCT AATAACAGAG CAATAGCACT GTTACCAGTA  
TTGCCGGAAG ATAGTCATGA CAATCCACCA GTACCAAAAG TAAAAGCAGC AGCACAAAGT  
GGTGGTCAAC AAGAAGACCA AAAAGCAAAA GAATCTAAAG ATAAAGTTGA GGAAGAAAAA  
GAAGTTGTAG AGGAGAAAAA AGAAGAACAA GATAGTAAAA AAGAAAAAGT GGAGAAGCAA  
AGTCAAAAGC AAAAAGAAGA AGAGAGAAAC TCTAAAGAAG AACAACAAAA ACAAGAAGAA  
GCAAAAGCTA GAGCAGATAG AGAAAGAGAA GAACGACTAA AACAACAAGA ACAAAAAAGA  
CAACAGGAAG AAGCTAGGGT TAAAGCAGAA AAAGAAAAAC AAGAAAGAGA GGAACAACAA  
AAACAAGAAG AAGAAAAGAA AGTTAAATAT AAAATTAAAA CACTTACAGA CAAAATAGAT  
GAAATAAATA AGGATATTGA TGGTATAAAT GGTAACAA TGTAGGAGC AGAAGAAGTT  
ATAGATAAAA TTACGGGGCC TGTATATGAT GATTTTACTG ATGGGAATAA AGCTATATAC  
AAAACCTGGG GAGATTTAGA GGATGAAGAA GGCGAAGAAT TAGGAAAATT ATTGAAAGAA  
TTGAGTGATA CTAGACATAA TTTAAGAACC AAATTAAATG AGGGTAATAA AGCATATATT  
GTTCTAGAAA AGGAGCCTAA TTTAAAAGAA AATGTAAATG TTAGTGATAT TCAATCAGAT  
TTAGAAAAAT TAAATCAGG ATTAGAAGAA GTTAAAAAAT ATTTTGAAAA TGAAGATAAT  
TTTGAAGAAA TTAAAGGATA CATTGAGGAT AGTAATTCAT ATTGA

t5-14.nt

TTGTAAAAATTATGCAACTGGTAAAGATATAAAACAAAATGCAAAAGGGAAAAATTAAAGGATTTTTAGATAAGGTT  
TTAGATCCAGCAAAAGATAAAATTACTTCAAGTAGTTCAAAAGTAGATGAATTAGCAAAAAAATTACAAGAAGAAG  
ATGAAGATAATGAATTAATGCAGGGCGATGATCCTAATAACAGAGCAATAGCACTGTTACCAGTATTGCCGGAAGAA  
TAGTCATGACAATCCACCAGTACCAAAAGTAAAAGCAGCAGCACAAAGTGGTGGTCAACAAGAAGACCAAAAAGCA  
AAAGAATCTAAAGATAAAGTTGAGGAAGAAAAAGAAGTTGTAGAGGAGAAAAAGAAGAACAAGATAGTAAAAAAG  
AAAAAGTGGAGAAGCAAAGTCAAAAGCAAAAAGAAGAAGAGAGAAACTCTAAAGAAGAACAACAAAAACAAGAAGA  
AGCAAAAGCTAGAGCAGATAGAGAAAAGAGAAGAACGACTAAAACAACAAGAACAAGAAAGACAAACAGGAAGAAGCT  
AGGGTTAAAGCAGAAAAAGAAAAACAAGAAAGAGAGGAACAACAACAAGAAAGAAGAAAGAAAGTTAAATATA  
AAATTAACACACTTACAGACAAAATAGATGAAATAAATAAGGATATTGATGGTATAAATGGTAAAACAAATTGTAGG  
AGCAGAAGAAGTTATAGATAAAATTACGGGGCCTGTATATGATGATTTTACTGATGGGAATAAAGCTATATACAAA  
ACTTGGGGAGATTTAGAGGATGAAGAAGCGGAAGAATTAGGAAAATTATTGAAAGAATTGAGTGATACTAGACATA  
ATTTAAGAACCAAAATTAAATGAGGGTAATAAAGCATATATTGTTCTAGAAAAGGAGCCTAATTTAAAAAGAAATGT  
AAATGTTAGTGATATTCAATCAGATTTAGAAAAATTAAATCAGGATTAGAAGAAGTTAAAAAATATTTTGAAAT  
GAAGATAATTTTGAAGAAATTAAAGGATACATTGAGGATAGTAATTCATAT

f5-14.aa

KFKTKKTKS MNKKILIIFA VFALIISCKN YATGKDIQON AKGKIKGFLD KVLDPKDKI  
TSSSSKVDEL AKKLQEEDED NELMQGDDPN NRAIALLPVL PENSHDNPPV PKVKAQAQSG  
GQQEDQKAKE SKDKVEEKE VVEEKKEEQD SKKEKVEKQS QKQKEEERN SKEEQKQEEA  
KARADRERE RLKQEQKQK QEEARVKA EKQEREQQK QEEKKVKYK IKTLTDKIDE  
INKDIDGING KTIVGAEEVI DKITGPVYDD FTDGNKAIYK TWGDLEDEEG EELGKLLKEL



TABLE 1. Nucleotide and Amino Acid Sequences

SDTRHNLRTK LNEGKNKAYIV LEKEPNLKEN VNVSDIQSDL EKLKSGLEEV KKYFENEDNF  
EEIKGYIEDS NSY

t5-14.aa

CKNYATGKDIKQNAKGKIKGFLDKVLDPAKDKITSSSSKVDLAKKLQEEDEDNELMQGDDPNNRALALLPVLPEN  
SHDNPPVPVKVAAAQSGGQQEDQKAKESKDKVEEKEVVEEKKEEQDSKKEKVEKQSQKQKEEERNSKEEQQKQEE  
AKARADREREERLKQQEQKRQQEEARVKAKEKQEREQQKQEEKKVKYKIKTLTDKIDEINKDIDGINGKTIVG  
AEEVIDKITGPVYDDFTDGNKAIYKWTGDLDEDEGEELGKLLKELSDTRHNLRTKLNNEGKNKAYIVLEKEPNLKENV  
NVSDIQSDLEKLKSGLEEVKKYFENEDNFEEIKGYIEDSNSY

f5-15.nt

TAACCTTATGA ATAAGAAAAT GAAAATGTTT ATTATTTGTG CTGTTTTTGC ATTGATGATT  
TCTTGCAAGA ATTATGCAAG TGGTGAAAAT CTAAAAAATT CAGAACAAAA TCTAGAAAGT  
TCAGAACAAA ATGTAAAAAA AACAGAACAA GAGATAAAAA AACAAAGTTGA AGGATTTTTTA  
GAAATTCTAG AGACAAAAGA TTTATCTAAA TTAGATGAAA AAGATACAAA AGAAATTGAA  
AAACAAATTC AAGAATTTAA GAATAAAATA GAAAAATTAG ATTCTAAAAA AACTTCTATT  
GAAACATATT CTGAGTATGA AGAAAAAATA AACAAAATAA AAGAAAAATT GAAAGGAAAA  
GGACTTGAAG ATAAATTTAA GGAGCTTGAA GAGAGTTTAG CAAAGAAAAA GGGGGAGAGA  
AAAAAAGCTT TACAAGAGGC CAAACAGAAA TTTGAAGAAT ATAAAAACA AGTAGATACT  
TCAACTGGGA AAACCAAGG CGACAGGTCT AAAAACCAG AGTGGTGTGG AGTGCAAGCT  
TGGCAGTGTG CCAATGAATT AGGTTTGGGT GTAAGTTATT CTAATGGCGG CAGTGACAAC  
AGCAATACTG ATGAATTAGC AAACAAAGTT ATAGATGATT CTCTTAAAAA GATTGAAGAA  
GAACCTAAGG GAATAGAAGA AGATAAAAA GAATAA

t5-15.nt

TTGCAAGAATTATGCAAGTGGTGAAAAATCTAAAAAATTCAGAACAAAATCTAGAAAGTTCAGAACAAAATGTAAAA  
AAAACAGAACAAGAGATAAAAAACAAGTTGAAGGATTTTTAGAAATTCAGAGACAAAAGATTTATCTAAATTAG  
ATGAAAAAGATACAAAAGAAATTGAAAACAAATTCAGAATTAAGAATAAAATAGAAAAATTAGATTCTAAAAA  
AACTTCTATTGAAACATATTCTGAGTATGAAGAAAAATAAACAAAATAAAAGAAAAATGAAAGGAAAAGGACTT  
GAAGATAAATTTAAGGAGCTTGAAGAGAGTTTAGCAAAGAAAAAGGGGGAGAGAAAAAAGCTTTACAAGAGGCCA  
AACAGAAATTTGAAGAATATAAAAAACAAGTAGATACTTCAACTGGGAAAACCTCAAGGCGACAGGTCTAAAAACCG  
AGGTGGTGTGGAGTGCAAGCTTGGCAGTGTGCCAATGAATTAGGTTTGGGTGTAAGTTATTCTAATGGCGGCAGT  
GACAACAGCAATACTGATGAATTAGCAAACAAGTTATAGATGATTCTCTTAAAAAGATTGAAGAAGAACTTAAGG  
GAATAGAAGAAGATAAAAAAGAA

f5-15.aa

LMNKKMKMFI ICAVFALMIS CKNYASGENL KNSEQNLESS EQNVKKTEQE IKKQVEGFLE  
ILETKDLSKL DEKDTKEIEK QIQELKNKIE KLDSKKTSIE TYSEYEEKIN KIKEKLKGKG  
LEDKFKELEE SLAKKKGERK KALQEAKQKF EYKKQVDTs TGKTQGDRSK NRGVGVQAW  
QCANELGLGV SYNGGSDNS NTDELANKVI DSLKKIEEE LKGIEEDKKE

t5-15.aa

CKNYASGENLKNSEQNLESSEQNVKKTEQEIKKQVEGFLEIETKDLSKLDEKDTKEIEKQIQELKNKIEKLDSKK  
TSIETYSEYEEKINKIKEKLKGKLEDKFKELEESLAKKKGERKKALQEAKQKFEEYKKQVDTSTGKTQGDRSKNR  
GGVGVQAWQCANELGLGVSYNGGSDNSNTDELANKVIDDSLKKIEEELKGIEEDKKE

f51-2.nt

TAATTGTTTG GGGTTGTGGT AAACCTTAAGG CTTATGGAGT GGATTATGAA TAAAAAATG  
AAAATATTTA TTATTTGTGC TGTATTTGTG CTGATAAGTT CTTGCAAGAT TGATGCAACT  
GGTAAAGATG CAACTGGTAA AGATGCAACT GGTAAAGATG CAACTGGTAA AGATGCAACT  
GGTAAAAATG CAGAACAAA TATAAAAGGG AAAGTTCAAG GATTTTTAGA AAAGATTTTA

TABLE 1. Nucleotide and Amino Acid Sequences

GATCCAGTAA AGGATAAAAT TGCTTCAAAT GGTCCAATAG CAGATGAATT GGCAAAAAAA  
 TTACAAGAAG AAGAAAAGGT AAATAACGGG GAAGAAGAAA ATGATAAAGC TGTCTTTTAA  
 GGAGAAGAAT CAAAAGAGGA TGAAGAAGAA AATGAGCAAG CTGTTAATTT AGAAGAAAAA  
 AATGCGGAAG AGGATAAGAA AGTTGTTAAT TTAGAAGAGA AAGAATTAGA AGTTAAAAAA  
 GAGACTGAAG AAGATGAAGA TAAAGAAGAA ATAGAGAAAC AAAACAAGA AGTGGAAAAA  
 GCACAAGAAA GAAAACAACG ACAAGAAGAA AAGAAACGAA AAAACAAGA ACAGCAAGAA  
 GAAAAGAAAC GAAAACGACA AGAACAAAGA AAAGAAAGGA GAGCTAAAAA CAAAATTAAA  
 AAACTTGCGG ATAAAAATAGA TGAGATAAGT TGGAATATTG ATGGTATAGA AAGTCAAACA  
 AGTGTAAGAC CGAAAGCAGT TATAGATAAA ATTACGGGGC CTGTATATGA TTATTTTACC  
 GATGACAACA AAAAAGCTAT ATATAAAACA TGGGGAGATT TAGAAGATGA AGAAGGCGAA  
 GGATTGGGAA AATTATTGAA AGAATTGAGT GATACTAGAG ATGAGTTAAG AACCAAATTA  
 AATAAAGATA ATAAAAATA TTATGCCCAT GAAAATGAGC CTCCTCTAAA AGAAAATGTA  
 GATGTCAGCG AAATTAAAGA AGATTTAGAA AAAGTAAAT CAGGATTAGA AAAGGTTAAA  
 GAATATCTTA AAGACAATTC TAAATTTGAA GAAATTAAAG GATACATCAG TTACAGTCAG  
 TAA

t51-2.nt

TTGCAAGATTGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCAACTGGTAAAGATGCA  
 ACTGGTAAAAATGCAGAACAAATATAAAAGGGAAAGTTCAAGGATTTTATAGAAAAGATTTTAGATCCAGTAAAGG  
 ATAAATTGCTTCAAATGGTCCAATAGCAGATGAATTGGCAAAAAAATTACAAGAAGAAGAAAGGTAAATAACGG  
 GGAAGAAGAAAATGATAAAGCTGTCTTTTATAGGAGAAGAATCAAAAGAGGATGAAGAAGAAAATGAGCAAGCTGTT  
 AATTTAGAAGAAAAAATGCGGAAGAGGATAAGAAAGTTGTTAATTTAGAAGAGAAAGAATTAGAAGTTAAAAAAG  
 AGACTGAAGAAGATGAAGATAAAGAAGAAATAGAGAAACAAAAACAAGAAGTGGAAAAAGCACAAGAAAGAAAAACA  
 ACGACAAGAAGAAAAGAAACGAAAAAACAAGAACAGCAAGAAGAAAAGAAACGAAACGACAAGAACAAGAAAA  
 GAAAGGAGAGCTAAAAACAAAATTAAAAAACTTGCGGATAAAATAGATGAGATAAGTTGGAATATTGATGGTATAG  
 AAAGTCAAACAAGTGTAACCGAAAGCAGTTATAGATAAAATTACGGGGCCTGTATATGATTATTTTACCGATGA  
 CAACAAAAAAGCTATATATAAACATGGGGAGATTTAGAAGATGAAGAAGGCGAAGGATTGGGAAAATTATTGAAA  
 GAATTGAGTGATACTAGAGATGAGTTAAGAACCAAAATTAATAAAGATAATAAAAAATATTATGCCCATGAAAATG  
 AGCCTCCTCTAAAAGAAAATGTAGATGTCAGCGAAATTAAGAAGATTTAGAAAAAGTAAATCAGGATTAGAAAA  
 GGTTAAAGAATATCTTAAAGACAATTCTAAATTTGAAGAAATTAAGGATACATCAGTTACAGTCAG

f51-2.aa

LFGVVVNLRL MEWIMNKKMK IFIICAVFVL ISSCKIDATG KDATGKDATG KDATGKDATG  
 KNAEQNIKKG VQGFLEKILD PVKDKIASNG PIADELAKKL QEEKVNNGE EENDKAVFLG  
 EESKEDEEEN EQAVNLEEK AEDDKVVNL EEKELEVKE TEDEDKEEI EKQKQVEKA  
 QERKQREEK KRKKQEQEE KKRKRQEQRK ERRAKNKKK LADKIDEISW NIDGIESQTS  
 VKPKAVIDKI TGPVYDYFTD DNKKAIYKTW GDLEDEEGEG LGKLLKELSD TRDELRTKLN  
 KDNKKYYAHE NEPLKENVD VSEIKEDLEK VKSGLEKVKE YLKDNSKFEE IKGYISYSQ

t51-2.aa

CKIDATGKDATGKDATGKDATGKDATGKNAEQNIKGVQGFLEKILDPVKDKIASNGPIADELAKKLQEEKVNNG  
 EEENDKAVFLGEESKEDEEENEQAVNLEEKNAEDDKVVNLEEKELEVKE TEDEDKEEIEKQKQVEKAQERKQ  
 RQEEKKRKKQEQEEKKRKRQEQRKERRAKNKKKLADKIDEISWNIDGIESQTSVKPKAVIDKITGPVYDYFTDD  
 NKKAIYKTWGDLEDEEGEGLGKLLKELSDTRDELRTKLNKDNKKYYAHENEPPLKENVDVSEIKEDLEKVKSGLEK  
 VKEYLKDNSKFEEIKGYISYSQ

f6-21.nt

TAGGCAAAAT TTAAATTTAT AAAAATTGT AAGGATGCTT GTATGAAAAT ATTGATAAAA  
 AAGTTAAAAG TTGTATTATT TCTCAATTTA ATTTTACTTA TTTCTTGTGT TAATGAAAGT  
 AATAGAAACA AATTGGTTTT TAAGCTAAAT ATTGGAAGTG AGCCTGCTAC TTTAGATGCT  
 CAATTAATAA ACGATACGGT TGGATCAGGG ATTGTAAGCC AAATGTTTCT TGGCATTTTA  
 GATGGAGATC CCAGGACTGG AGGATACAGA CCGGACTTG CTAAAAGTTG GGATATTTCT

TABLE 1. Nucleotide and Amino Acid Sequences

GATGACGGAG TAGTTTATAC GTTTCATTTA AGAGATAATC TTGTTTGGAG TGATGGAGTT  
TCCATTACTG CCGAAGAATA A

t6-21.nt

TTGTGTTAATGAAAGTAATAGAAACAAATTGGTTTTTAAGCTAAATATTGGAAGTGAGCCTGCTACTTTAGATGCT  
CAATTAATAAACGATACGGTTGGATCAGGGATTGTAAGCCAAATGTTTCTTGGCATTTTAGATGGAGATCCCAGGA  
CTGGAGGATACAGACCGGGACTTGCTAAAAGTTGGGATATTTCTGATGACGGAGTAGTTTATACGTTTCATTTAAG  
AGATAATCTTGTTTGGAGTGATGGAGTTTCCATTACTGCCGAAGAA

f6-21.aa

AKFKFIKTCK DACMKILIKK LKVVLFLNLI LLISCVNESN RNKLVFKLNI GSEPATLDAQ  
LINDTVGSGI VSQMFLGILD GDPRTGGYRP GLAKSWDISD DGVVYTFHLR DNLVWSDGVS  
ITAEE

t6-21.aa

CVNESNRNKLVFKLNIGSEPATLDAQLINDTVGSGIVSQMFLGILDGDPRTGGYRPLAKSWDISDDGVVYTFHLR  
DNLVWSDGVSITAEE

f6-27.nt

TAAAGAAAAG CTTGCATAAA AAGTATAACA AATTCTTTAA TAATTAAAAT CAAAAAGAAT  
ATAATTATTG CACTAAAATT AAATTTATAC AGTTATATAG AATCACTTAA GGAACAAAAA  
ATGAAATACC TTAAAAACAT TTCCTTATTT TTGTTAATTT TAGGTTGCAA ATCCATCCCA  
AATGGTAATT TCAATCTACA CGATACAAAC CATAAATTAG GAAAACTAAA ATTTCAAGAA  
GACTCGATAA TAAGCAGAAA TTATGATAAT AAAATATCCA TTGTGGGAGT ATACAACCCCT  
TTAACAGAAA AAGAAAATTT TAAAGTCAAT ATTTTCATCA AAAAAAAGG ATTACAAATA  
GATCCTGAAA ATATTTTGAT AAATGAAGAA AAAATTAATT ATTCAAAATA TAAAGCAGAA  
CTCAAAGTAA AATCTAGCTT TAATAAAAGC ATTATCAGTA TTTCCTAAC TAATTCAAGA  
GATCTATTAA CCTACATTTA CGATAAAAGC ACAGGGAAAT ACATTAACAT TGACTTTAAG  
GACAATTGGA ACGTATCGCA CAGTATAAAA TTTAATAAGG AGTATATTTT AGCATATATA  
ACAGATTTTG ATAAAGAAAT TAAAATATCT AAAAATATTT TGCAAAAACG TATTGATAAT  
AGAAAAATTG AAATTGAAAA AACAGAGCTT AAAACAGAAT ATAATGAAAT AGAGGATTAT  
TACATCTACA GTATGAAAAT TCCAAAATTA TTTGAAAAAT CAGACGCTCC CTCTGAAACT  
TACGAAACAT TTGTTATAGC AAATTATTAC CCCTGTGAAA ATTTAAATAT ACTGTTTTTG  
AATTAAAGCT TATACTCTGA TAAATTACGC TTTCTAACT CTATTTATGA TGAGAATGAT  
AGAAAATTAA AAATGGAGCC TCCTGTGAGA GCCTTAAAGA ATTCAAAAAC AATAAAGAA  
ACATTAAATA TAGTATTAAG TCCTCAAAAA ATAATAGAGC TAGCAAAAAA CATTGAAAAA  
GATATTACTC TAAAATTAA ATCTTACGGA GAAAAGGGAG AATTCACATT TGAAATATAT  
AAACCACTTC TTTTAAAATT CTTAAAAGAA GTAGATCATT GCATAAAAAA TTTGCAATCA  
AGTAGGCATA AATTTTAA

t6-27.nt

TTGCAAAATCCATCCCAAATGGTAATTTCAATCTACACGATACAAACCATAAATTAGGAAAACTAAAATTTCAAGAA  
GACTCGATAATAAGCAGAAATTATGATAATAAAATATCCATTGTGGGAGTATACAACCCTTTAACAGAAAAAGAA  
ATTTTAAAGTCAATATTTTCATCAAAAAAAGGATTACAAATAGATCCTGAAAATATTTTGATAAATGAAGAAAA  
AATTAATTATTCAAAATATAAAGCAGAACTCAAAGTAAATCTAGCTTTAATAAAAGCATTATCAGTATTTCACTA  
ACTAATTCAGAGATCTATTAACCTACATTTACGATAAAAGCACAGGGAAATACATTAACATTGACTTTAAGGACA  
ATTGGAACGTATCGCACAGTATAAAATTTAATAAGGAGTATATTTTAGCATATATAACAGATTTTGATAAAGAAAT  
TAAAATATCTAAAAATATTTTGCAAAAAACGTATTGATAATAGAAAAATTGAAATTGAAAAACAGAGCTTAAAACA  
GAATATAATGAAATAGAGGATTATTACATCTACAGTATGAAAATTCCAAAATTATTTGAAAAATCAGACGCTCCCT  
CTGAACTTACGAAACATTTGTTATAGCAAATTATTACCCCTGTGAAAATTTAAATATACTGTTTTTTGAATTTAAG  
CTTATACTCTGATAAATTACGCTTTCTAACTCTATTTATGATGAGAATGATAGAAAATTTAAAATGGAGCCCTCT

TABLE 1. Nucleotide and Amino Acid Sequences

GTGAGAGCCTTAAAGAATTCAAAAACAATAAAAAGAAACATTAAATATAGTATTAAGTCCTCAAAAAATAATAGAGC  
TAGCAAAAACATTGAAAAAGATATTACTCTAAAATTAAAATCTTACGGAGAAAAGGGAGAATTACATTTGAAAT  
ATATAAACCACTTCTTTTAAAATTCTTAAAAGAAGTAGATCATTGCATAAAAAATTTGCAATCAAGTAGGCATAAA  
TTT

f6-27.aa

RKACIKSITN SLIIKIKKNI IIALKLNLYS YIESLKEQKM KYLKNISLFL LILGCKSIPN  
GNFNLHDTNH KLGKLFQED SIISRNNDNK ISIVGVYNPL TEKENFKVNI FIKKKGLQID  
PENILINEEK INYSKYKAEL KVKSSFNKS IISLSTNSRD LLTYIYDKST GKYINIDFKD  
NWNVSHSIKF NKEYILAYIT DFDKEIKISK NILQKRIDNR KIEIEKTELK TEYNEIEDYY  
IYSMKIPKLF EKSDAPSETY ETFVIANYP CENLNILFLN LSLYSDKLRF LNSIYDENDR  
KLKMEPPVRA LKNSKTIKET LNIVLSPQKI IELAKNIEKD ITLKLKSYGE KGEFTFEIYK  
PLLLKFLKEV DHCINKLQSS RHKF

t6-27.aa

CKSIPNGNPNLHDTNHKLGKLFQEDSIISRNNDNKISIVGVYNPLTEKENFKVNI FIKKKGLQIDPENILINEEK  
INYSKYKAELKVKSSFNKSIIISLSTNSRDLLTYIYDKSTGKYINIDFKDNWNVSHSIKF NKEYILAYITDFDKEI  
KISKNILQKRIDNRKIEIEKTELKTEYNEIEDYYIYSMKIPKLF EKSDAPSETYETFVIANYP CENLNILFLNLS  
LYSDKLRF LNSIYDENDRKLKMEPPVRALKNSKTIKETLNIVLSPQKIIELAKNIEKDITLKLKSYGEKGEFTFEI  
YKPLLLKFLKEVDHCINKLQSSRHKF

f6-5.nt

TAAATGAAGA AGTTTTTAAT ATCCGTTTAT TTTTATTGT TTTATGGTTG TTCAACTATA  
TCTTTGGTAA AAATACCAGA AAAAGATAAA ATAAATTTAA CTGTTTTATC ATCTTTAATG  
AATTATCCTG ATTTGAAGAT TTCAAATTTT AAAATAAAAG ACTACGAACA TTTGCATTAT  
TCATCTGATT TTGAAAGCTT GAGTGATACT AAAAATAGTG CTTATATTTA CGTTGATGAA  
TCTAGTTTCA ATAATAATAT TAATTTTAT AAAGATCTTT TTATTTATAA TAAGAAATTA  
TATAGAATAC TTATTGCTTA TAGCTTGACC CAAGGTGCAT CTTTTAAGGC AGAAGTTTTA  
TCTTATCTTG AAAAACAAAA AATTATGAAA AATTTTTCAT TGAAAATAAA TTTTCCAAC  
GCTAAAAAAT TTATGGATAA TAAGTATTGG ATTGTAATTG CAAAAACCA TTTAGATTCT  
CTTGTTAAGA GTAAAAATTA TTTAGTCTTG GCGAATGTAA AGATGGAATA TATACTCAA  
AAGTTTTTAA CTTGA

t6-5.nt

TTGTTCAACTATATCTTTGGTAAAAATACCAGAAAAAGATAAAATAAATTTAACTGTTTTATCATCTTTAATGAAT  
TATCCTGATTTGAAGATTTCAAATTTTAAAAATAAAAGACTACGAACATTTGCATTATTCATCTGATTTTGAAAGCT  
TGAGTGATACTAAAAATAGTGCTTATATTTACGTTGATGAATCTAGTTTCAATAATAATATTAATTTTATTAAAGA  
TCTTTTATTATTAATAAGAAATTATATAGAATACTTATTGCTTATAGCTTGACCAAGGTGCATCTTTTAAGGCA  
GAAGTTTTATCTTATCTTGAAAAACAAAAAATTATGAAAAATTTTTCATTGAAAAATAAATTTTCCAACCTGCTAAAA  
AATTTATGGATAATAAGTATTGGATTGTAATTGCAAAAAACCATTTAGATTCTCTTGTTAAGAGTAAAAAT

f6-5.aa

MKKFLISVYF LLFYGCSTIS LVKIEPKDKI NLTVLSSLMN YPDLKISNFK IKDYEHLHYS  
SDFESLSDTK NSAYIYVDES SFNNNINFIK DLFYNNKKLY RILIAVSLTQ GASFKAEVLS  
YLEKQKIMKN FSLKINFPTA KKFMDNKYWI VIAKNHLDL VKSKNYLVLA NVKMEYILKK  
FLT

t6-5.aa

CSTISLVKIEPKDKINLTVLSSLMNYPDLKISNFKIKDYEHLHYSSDFESLSDTKNSAYIYVDESSFNNNINFIK  
DLFIYNNKKLYRILIAVSLTQ GASFKAEVLSYLEKQKIMKNFSLKINFPTAKKFMDNKYWIVIAKNHLDL SVKSKN

TABLE 1. Nucleotide and Amino Acid Sequences

f7-30.nt

TAGAGACGAA GTCACAAGCA AAATGTTAAA AGATTTACAA AATCAAGTTC AAGGGGGCAA  
 ATAATGAAAA ATTTAAAGAC AAAAATTAAT TTTT TAGGGA TATTTTGGCT ACTGTTACTA  
 TTTCTTTCTT GCGAATCAAT ACCATCACTT CCCCCAAAAC CAACCCTAAC AAACAAAGAA  
 GATATTGAAA ATTTAATGCT CGATGAAGCA GAAC TTTTTA GATACTCAAC CGCACTAAAT  
 GTTTGGCTTT TGACTGTAAA ATCTTATGTG ATCAAATACT ATCCTAATGA CAAATTTCCCT  
 GTGTTTGAAA ATTTTGATCC CGTGT TTTGGC GATGAAAATG GAACTAAAGA AACAAATATA  
 CTAAAAAATC GAATTACCTA CTACAATCGA TACATAGAAA AAACCGAACC GATTGTATTT  
 GGGTGT TACA AAAAATACAG CAGAAGATAA

t7-30.nt

TTGCGAATCAATACCATCACTTCCCCAAAACCAACCCTAACAAACAAAGAAGATATTGAAAATTTAATGCTCGAT  
 GAAGCAGAACTTTT TAGATACTCAACCGCACTAAATGTTTGGCTTTTGACTGTAAAATCTTATGTGATCAAATACT  
 ATCCTAATGACAAATTTCTGTGTTGAAAATTTTGATCCCGTGT TTTGGCGATGAAAATGGAAC TAAAGAAACAAA  
 TATACTAAAAAATCGAATTACCTACTACAATCGATACATAGAAAAAACCGAACCGATTGTATTTGGGTGTTACAAA  
 AAATACAGCAGAAGA

f7-30.aa

RRSHKQNVKR FTKSSSRGQI MKNLKT KINF LGIFWLLLLF LSCESIPSLP QKPTLTNKED  
 IENLMLDEAE LFRYALNVL WLLTVKSYVI KYYPNDKFPV FENFDPVFGD ENGTKETNIL  
 KNRITYYNNRY IEKTEPIVFG CYKKYSRR

t7-30.aa

CESIPSLPQKPTLTNKEDIENLMLDEAE LFRYALNVLWLLTVKSYVIKYYPNDKFPVFENFDPVFGDENGTKETN  
 ILKNRITYYNNRYIEKTEPIVFGCYKKYSRR

f76-1.nt

TGAATATTAA TAATAAAAAA AGGAGTAACA ATGAAAATTA TCAACATATT ATTTTGT TTG  
 TTTT TACTAA TGCTAAACGG CTGTAATTC T AATGATACAA ATACCAAGCA GACAAAAAGC  
 AGACAAAAGC GTGATTTAAC CCAAAAAGAA GCAACACAAG AAAAACCTAA ATCTAAATCT  
 AAAGAAGACC TGCTTAGAGA AAAGCTATCT GATGATCAAA AAACACAAC T GACTGGTTA  
 AAAACCGCTT TAACTGGTGT TGGAAAATTT GATAAATTC T TAGAAAATGA TGAAGGCAAA  
 ATTAAATCAG CACTTGAACA TATAAAGACT GAAC T TGATA AATGTAATGG AAATGATGAA  
 GGAAAAACA CCTTCAAAAC TACCGTTCAA GGGTTTTTTA GCGGCGGCAA TATAGATAAT  
 TTTGCAGATC AAGCAACTGC TACCTGCAAT TAA

t76-1.nt

CTGTAATTCTAATGATACAAAATACCAAGCAGACAAAAAGCAGACAAAAGCGTGATTTAACCCAAAAAGCAACA  
 CAAGAAAAACCTAAATCTAAATCTAAAGAAGACCTGCTTAGAGAAAAGCTATCTGATGATCAAAAAACACAACCTG  
 ACTGGTTAAAAACCGCTTTAACTGGTGT TGGAAAATTTGATAAATTC TTAGAAAATGATGAAGGCAAAATTAATC  
 AGCACTTGAACATATAAAGACTGAACTTGATAAATGTAATGGAATGATGAAGGAAAAACACCTTCAAAACTACC  
 GTTCAAGGGTTTTTTAGCGGCGGCAATATAGATAATTTTGCAGATCAAGCAACTGCTACCTGCAAT

f76-1.aa

ILIIKKGVTM KIINILFCLF LLMLNGCNSN DTNTKQTKSR QKRDLTQKEA TQEKPKSKSK  
 EDLLREKLS DQKTQLDWLK TALTGVGKFD KFLNDEGKI KSALEHIKTE LDKCNGNDEG  
 KNTFKTTVQG FFSGGNIDNF ADQATATCN

t76-1.aa

TABLE 1. Nucleotide and Amino Acid Sequences

CNSNDTNTKQTKSRQKRDLTQKEATQEKPKSKSKEDLLREKLSDQKTQLDWLKTALTGVGKFDKFLNDEGKIKS  
ALEHIKTELDKCNGNDEGNKNTFKTTVQGFSSGGNIDNFADQATATCN

f8-10.nt

TAAGTAAGGA GAATATTTAT GAAATATAAT ACGATTATAA GCATATTTGT TTGTTTGT  
TTAACTGCTT GCAATCCAGA TTTTAACACA AATAAGAAAA GAACCTAAG TAAGGGGATA  
ATTTCAAATC AAGATGCAGA TTCTGATAAA ATAATAAAAA ATAAATTACT TGATGATTTA  
ATAAATTTAA TAGAAAAAGC GAATGCAGAT AGAGAAAAAT ATGTAAAAAA AATGGAAGAA  
GAACCTTCGG ATCAATATGG AATGTTGGCT GTTTTGGAG GTATGTATTG GGCAGAATCA  
CCACGGGAAT TAATATCTGA TACAGGTAGT GAGAGATCTA TTAGGTATAG AAGGCGTGT  
TATAGTATTT TATTAAATGC TATTGAACT AATGAATTAA AGAAATTTTC AGAAATTAGA  
ATACTGTCAA TAAAAGTACT AGAAATATTT AGCCTATTTA ATCTATTTGG AAGTACTCTT  
GATGATGTGG TTGTTCACTT ATATTCCAAA AAAGATACTC TAGGTAACT AGATATTTCA  
AATTTAAAAA GACTTAAAAA TTTGTTTGAA AAATTATTAT CTATAAAAAA AATCGTTTCA  
AAGATGTCAA AACGCTTTTT ATTGGATTAT CAAAATAATG AAAATTTTAT AAAACAGAT  
AACGCCAAGC TTGGATCTTA TGTGGTTGCA CTTTCCAATC AAATTCAAGA AAAATATAAT  
GAAGCAGAAA GGCTGAAAAG CGAGATAATT TTAATATATA CCCTTTAA

t8-10.nt

TTGCAATCCAGATTTTAACACAAATAAGAAAAGAACTCTAAGTAAGGGGATAATTTCAAATCAAGATGCAGATTCT  
GATAAAATAATAAAAAATAAATTACTTGATGATTTAATAAATTTAATAGAAAAAGCGAATGCAGATAGAGAAAAAT  
ATGTAAAAAAATGGAAGAAGAACCTTCGGATCAATATGGAATGTTGGCTGTTTTGGAGGTATGTATTGGGCAGA  
ATCACCACGGGAATTAATATCTGATACAGGTAGTGAGAGATCTATTAGGTATAGAAGGCGTGTATTAGTATTTTA  
TTAAATGCTATTGAACTAATGAATTAAAGAAATTTTCAGAAATTAGAACTGTCAATAAAAGTACTAGAAATAT  
TTAGCCTATTTAATCTATTGGAAGTACTCTTGATGATGTGGTTGTTCACTTATATTCCAAAAAGATACTCTAGG  
TAACTAGATATTTCAAATTTAAAAAGACTTAAAAATTTGTTTGAAAAATTTATTATCTATAAAAAACAATCGTTTCA  
AAGATGTCAAACGCTTTTTATTGGATTATCAAATAATGAAAAATTTTATAAAAAACAGATAACGCCAAGCTTGGAT  
CTTATGTGGTTGCACTTTCCAATCAAATTCAAGAAAAATATAATGAAGCAGAAAGGCTGAAA

f8-10.aa

VRRIFMKYNT IISIFVCLFL TACNPDFNTN KKRTLSKGII SNQDADSDKI IKNKLLDDLI  
NLIEKANADR EKYVKMEEE PSDQYGMLAV FGGMYWAESP RELISDTGSE RSIRYRRRVY  
SILLNAIETN ELKKFSEIRI LSIKVEIFS LFNLFGSTLD DVVHLYSKK DTLGKLDISN  
LKRLKNLF EK LLSIKTIVSK MSKRLLLDYQ NNENFIKTDN AKLGSYVVAL SNQIQEKEYNE  
AERLKSEIIL IYTL

t8-10.aa

CNPDFNTNKKRTLSKGII SNQDADSDKI IKNKLLDDLINLIEKANADREKYVKMEEE PSDQYGMLAV FGGMYWAE  
SPRELISDTGSE RSIRYRRRVYSILLNAIETNELKKFSEIRI LSIKVEIFS LFNLFGSTLD DVVHLYSKK DTLG  
KLDISNLKRLKNLF EK LLSIKTIVSK MSKRLLLDYQ NNENFIKTDN AKLGSYVVAL SNQIQEKEYNEAERLK

f8-14.nt

TAATATATAT TCTTGATTAA GGGAAAGGAG AGTATTTTAA TGAAAAAAA AATGTTTTTA  
TATACATTGT TAACGATAGG ATTGATGTCT TGTAATCTAA ATTCTAAAT ATCTGGTAAT  
AAAGAGGAAC AAAAAATAA CAATGATATA AAAGAAGCTT TAAATGGCGT TCAAGAAAAT  
GCTATTAATA ATTTATATGG AAATAAAAAA GAAAAAAAAG ATTTTATTAA AAATTCGGAA  
AAATTGAAAG ACAAGGGTTT AGACGTGACC ACCCTCCCT TAGAACCTGT AGTGGCGCCC  
TCCGTAGAAT CTGCGGTGTC TTTAGGAGAA TCTAATAATA GGATTGGTAT ACCAACCATT  
TCAATTGAGC ATAATCAAAA AAAAGAGATA AAAGAAGAGG ATTTTTTCCC TTCTACTGAG  
GAAGAAAAGC AAGCGGATAA AGCAATTAAA GATATAGAGA ATCTTATTGG AGAATCTGGA

TABLE 1. Nucleotide and Amino Acid Sequences

TTTCCCGAGT TAATTGAGAA TGTGTGCTCA CTTAAACATG AATATACTTT AATAAGAAGT  
 GATTTTTATG ATGTGATAAC TAAGATTCAG AATAAAAAA TATCACTAAT GAAAAATTCT  
 CATAATAATA GAAATAAAAT AAGGGAAC TAACAATTGC AAAATAATTT AAAGATAGGA  
 GACGAAC TTG ATAAAATTAT GGGTTGCATT GATACTGCAG AACAAGAGAT AAGATCTGCC  
 GCTTCTTTT TTGATGAAGC TAAGGAAAGC TTAAAAGAAG GTATTATTAA AAGATTGGAA  
 AAAAGTAAAA ATAGGGCAGC ATCACAATTA TCTAAAAAGG CTTTAAATAG AGCAGAGGAT  
 GCTTTAAGGT GCTTAGAAAA TTATTCTTCT AAAAAAGGTG AGGCAATAGG AAGAAGAAGC  
 TTTATAAAAG AAGTTGTTGA ACAGGCAAAA AATGCTTTAA GTAAGTCTTA A

t8-14.nt

TTGTAATCTAAATCTAAATTATCTGGTAATAAAGAGGAACAAAAAATAACAATGATATAAAAGAAGCTTTAAAT  
 GGCGTTCAAGAAAATGCTATTAATAATTTATATGGAAATAAAAAAGAAAAAAGATTTTATTAAAAATTCGGAAA  
 AATTGAAAGACAAGGGTTTAGACGTGACCACCTCCCTTAGAACCTGTAGTGGCGCCCTCCGTAGAATCTGCGGT  
 GTCTTTAGGAGAATCTAATAATAGGATTGGTATACCAACCATTTCATTGAGCATAATCAAAAAAAGAGATAAAA  
 GAAGAGGATTTTTTCCCTTCTACTGAGGAAGAAAAGCAAGCGGATAAAGCAATTAAAGATATAGAGAATCTTATTG  
 GAGAATCTGGATTTCCCGAGTTAATTGAGAATGTGTGCTCACTTAAACATGAATATACTTTAATAAGAAGTGATTT  
 TTATGATGTGATAACTAAGATTCAGAATAAAAAAATATCACTAATGAAAAATTCTCATAATAATAGAAATAAAAA  
 AGGGAAC TAGTACAATTGCAAAATAATTTAAAGATAGGAGACGAAC TTGATAAAATTATGGGTTGCATTGATACTG  
 CAGAACAAGAGATAAGATCTGCCGCTTTCTTTTTTGATGAAGCTAAGGAAAGCTTAAAGAAGGTATTATTAAAG  
 ATTGGAAGAAAGTAAAAATAGGGCAGCATCACAATTATCTAAAAAGGCTTTAAATAGAGCAGAGGATGCTTTAAGG  
 TGCTTAGAAAATTATTCTTCTAAAAAAGGTGAGGCAATAGGAAGAAGAAGCTTTATAAAAGAAGTTGTTGAACAGG  
 CAAAAATGCTTTAAGTAAGTCT

f8-14.aa

YIFLIK GKES IFMKKKMFLY TLLTIGLMSC NLNSKLSGNK EEQKNNNDIK EALNGVQENA  
 INNLYGNKKE KKDFIKNSEK LKDKGLDVT LPLEPVVAPS VESAVSLGES NNRIGIPTIS  
 IEHNQKKEIK EEDFFPSTEE EKQADKAID IENLIGESGF PELIENVCSL KHEYTLIRSD  
 FYDVITKIQN KKISLMKNSH NNRNKIRELV QLQNNLKIGD ELDKIMGCID TAEQEIRSA  
 FFFDEAKESL KEGIIKRLEK SKNRAASQLS KKALNRAEDA LRCLENYSSK KGEAIGRRSF  
 IKEVVEQAKN ALSKS

t8-14.aa

CNLNSKLSGNKEEQKNNNDIKEALNGVQENAINNLYGNKKEKKDFIKNSEKLKDKGLDVTT LPLEPVVAPSVESAV  
 SLGESNNRIGIPTISIEHNQKKEIKEEDFFPSTEEEEKQADKAID IENLIGESGFPELIENVCSLKHEYTLIRSD  
 YDVITKIQNKKISLMKNSHNNRNKIRELVQLQNNLKIGDELDKIMGCIDTAEQEIRSAFFFFDEAKESLKEGIIKR  
 LEKSKNRAASQLSKKALNRAEDALRCLENYSSKKGEAIGRRSFIKEVVEQAKNALSKS

f01A.nt BB001

TGATTAATTTTTTTTAAAGATTACGTTTTGAAAAGAAACAAAATTTGGAAAACGTTAAACTGTTTCAAATAACTT  
 TACTGTTCTCATGCTCTTTTATTCTAAATCAAACAACACAGAAGCGATAAGTGAATTACAATCAAGCCCTATTAA  
 ACTTGGAATAATTAAGTTTACAAAAACAGAAAAGATTGTAAGCACCCAAAATCTTCAAACCTTACAACAAAGC  
 CAGTTCTTTAAATGAAAAAGAAAAAATAATTAATAAAATTCACACAAGAATTTGATGAGAATGAAAAATTGATTA  
 ATAAATAGGTCCAAATATCGAAATGTTTGCTCAAACAATAAACACGGATATTCAAATAATCGAACCTAATGATCA  
 ATTTGGAATAAATAAACTTTATTACAGAAAAAAGACAATAATATTGACTTTATGTTAAAGACAATCGACTT  
 AGAAGATTATTTTACTCATCTTTAAATTATGATGAAAATAAAATCAAAAAATTAGCCACAATACTCGCGCAAACAT  
 CAAGCTCAAACGACTACCATTACACACTTATTGGTTTAATTTTTTGGACAGGATTTAAATCCAAGAAGCATTGGA  
 AAGCGCTGTTAATTTTTAACTAAAGACGAGCAAAAGCGCTAATTTTTTAATTTTAGAACAAAAACAGTAAAAGAG  
 ATTCAGGAAAATTTTGAATACTAATGCAAGAGAGAAATTCATGGATAAAAAATCGTCGATAACATTATTGGCGAAT  
 ATGACAAAAATACGGGAGGATGCAAAGCTGATGGAAAAATCTCGGAGAAGTAATAAGGGTTGGATACGAGCATGA  
 ACTCGACTCAAATAAAAGTATGCAAATTTTAAACAATATTGAAACACCGCTAAAAACCTGTTGTGACCACATACAC  
 TACTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t01A.nt BB001

TGCTCTTTTTATTCTAAATCAAAACAACACAGAAGCGATAAGTGAATTACAATCAAGCCCTATTAAACTTGGAAAAA  
 TTAAAGTTTTACAAAAAACAGAAAAAGATTGTAAGCACCCAAAATCTTCAAACTTACAACAAAGCCAGTTC'TTTAA  
 AAATGAAAAAGAAAAATAATTAAAAAAATTGCACAAGAATTTGATGAGAATGAAAAATTGATTAATAAAATAGGT  
 CCAATATCGAAATGTTTGCTCAAAACAATAAACACGGATATTCAAAAAATCGAACCTAATGATCAATTTGGAATAA  
 ATAAACTTTTATTCACAGAAAAAAAAGACAATAATATTGACTTTTATGTTAAAAGACAATCGACTTAGAAGATTATT  
 TTACTCATCTTTAAATTATGATGAAAAATAAATCAAAAAATTAGCCACAATACTCGCGCAAACATCAAGCTCAAAC  
 GACTACCATTACACACTTATTGGTTAATTTTGGACAGGATTTAAAATCCAAGAAGCATTGAAAGCGCTGTTA  
 ATATTTTAACTAAAGACGAGCAAAAAGCGCCTAATTTTAAATTTTAGAACAAAAACAGTAAAAGAGATTTCAGGAAAA  
 TTTTGAAAACTAATGCAAGAGAGAAAAATTCATGGATAAAAAATCGTCGATAACATTATTGGCGAATATGACAAAAAT  
 ACGGGAGGATGCAAGCTGATGAAAAAATTCGCGAGAAGTAATAAGGGTTGGATACGAGCATGAACTCGACTCAA  
 ATAAAAGTATGCAATTTTAAACAATATTGAAACACCGCTAAAAACCTGTTGTGACCACATACACTAC

f01A.aa BB001

LIFFKDYVLKRNIWKTLKLFQITLLFSCSFYSKSNTEAISELQSSPIKLGKIKVLQKTEKIVSTQNQLQNLOQSQ  
 FFKNEKEKIIKKIAQEFDENEKLINKIGPNIEFQAQTINTDIQKIEPNDQFGINKTLFTEKKDNNIDFMLKDNRLR  
 RLFYSSLNYDENKIKKLATILAQTSSSN DYHYTLIGLIFWTGFKIQEAFESAVNILTKDEQKRLIFNFRKTQVKEI  
 QENFEKLMQERN SWIKIVDNIIGEYDKNTGGCKADGKILGEVIRVGYEHEDLSNKSMSQILNNIETPLKTCDDHIHY

t01A.aa BB001

CSFYSKSNTEAISELQSSPIKLGKIKVLQKTEKIVSTQNQLQNLOQSQFFKNEKEKIIKKIAQEFDENEKLINKIG  
 PNIEFQAQTINTDIQKIEPNDQFGINKTLFTEKKDNNIDFMLKDNRLRLFYSSLNYDENKIKKLATILAQTSSSN  
 DYHYTLIGLIFWTGFKIQEAFESAVNILTKDEQKRLIFNFRKTQVKEIQENFEKLMQERN SWIKIVDNIIGEYDKN  
 TGGCKADGKILGEVIRVGYEHEDLSNKSMSQILNNIETPLKTCDDHIHY

f02A.nt BB002

TAATTAATACTGGTTTTAATTTATAAGGAGAGTATTTTGAAAAAGCCAACTAAATATAATCAAGATTAATATTA  
 TTACAATGATATTAACCTTTAATTTGCATCTCATGTGCACCTTTTAACAAAATCAATCCCAAGGCAAATGAAAACAC  
 CAAGCTTAAAAAAAACACCAGACTGAAAAAACCCGCCAATCCAGGGGAAAACATCCAAAATTTTAAAGATAAATCT  
 GGAGACCTTGGCGCTTCTGATGAAAAATTTATGGGAAC TACCGCTTCAGAGCTAAAAGCAATTGGTAAGGAGCTAG  
 AAGATCGAAAAATCAATACGATATACAAATAGCCAAAATTACTAATGAAGAATCTAACCTATTAGATACTTATAT  
 TCGGGCTTATGAACTAGCTAACGAAAAATGAAAAATGCTTTTAAAAAGATTTCTTCTTTCATCTTTAGATTATAAA  
 AAAGAAAACATAGAGACATTAAAAGAAATTC'TTGAAAACTCATAAATAATTACGAAAACGACCCCAAAATTGCTG  
 CAAATTTCTTTATCGCATAGCGCTGGATATTCAATTTAAAAC'TGGAAAAGCACTTAAAATCAATAAATGAAAACT  
 GGACACTCTAAGCAAAGAAAATTCAAAAGAAGATTTAGAGGCGTTGCTAGAACAAAGTAAAATCTGCCTTACAGCTA  
 CAAGAAAAGTTTAAAAAACCCCTAAACAAAAC'TCTTGAAGATTACCGTAAAAATACTAACAACATTCAGAAAATA  
 AAGTACTAGCAGAACACTTTAATAAATATTACAAAGACTCTGATTCTTTACAATCTGCCTTTTATTAA

t02A.nt BB002

TGTGCACCTTTTAACAAAATCAATCCCAAGGCAAATGAAAACACCAAGCTTAAAAAAAACACCAGACTGAAAAAAC  
 CCGCCAATCCAGGGGAAAACATCCAAAATTTTAAAGATAAATCTGGAGACCTTGGCGCTTCTGATGAAAAATTTAT  
 GGGAAC TACCGCTTCAGAGCTAAAAGCAATTGGTAAGGAGCTAGAAGATCGAAAAAATCAATACGATATACAAATA  
 GCCAAAATTACTAATGAAGAATCTAACCTATTAGATACTTATATTCGGGCTTATGAACTAGCTAACGAAAATGAAA  
 AAATGCTTTTAAAAAGATTTCTTCTTTCATCTTTAGATTATAAAAAAGAAAACATAGAGACATTAAAAGAAATTC  
 TGAAAACTCATAAATAATTACGAAAACGACCCCAAAATTCCTTGCAATTTCTTTATCGCATAGCGCTGGATATT  
 CAATTTAAAAC'TGGAAAAGCACTTAAAATCAATAAATGAAAACTGGACACTCTAAGCAAAGAAAATTCAAAAGAAG  
 ATTTAGAGGCGTTGCTAGAACAAAGTAAAATCTGCCTTACAGCTACAAGAAAAGTTTAAAAAACCCCTAAACAAAAC  
 TCTTGAAGATTACCGTAAAAATACTAACAACATTCAGAAAATAAAGTACTAGCAGAACACTTTAATAAATATTAC  
 AAAGACTCTGATTCTTTACAATCTGCCTTTTAT

f02A.aa BB002



TABLE 1. Nucleotide and Amino Acid Sequences

LILVLIYKESILKKAKLNI IKINIITMILT LICISCAPFNKINPKANENTKLKKNTRLKKPANPGENIQNFKDKSG  
DLGASDEKFMGTTASELKAIGKELED RKNQYDIQIAKITNEESNLLD TYIRAYELANENEMLLKRFLSSLDYKK  
ENIETLKEILEKLINNYENDPKIAANFLYRIALDIQLKLEKHLKSINEKLD TLSKENSKEDELEALLEQVKSALQLQ  
EKFKKTLNKTLEDYRKNTNNIQENKVLAEHFNKYYKDSDSLQSAFY

t02A.aa BB002

CAPFNKINPKANENTKLKKNTRLKKPANPGENIQNFKDKSGDLGASDEKFMGTTASELKAIGKELED RKNQYDIQI  
AKITNEESNLLD TYIRAYELANENEMLLKRFLSSLDYKKENIETLKEILEKLINNYENDPKIAANFLYRIALDI  
QLKLEKHLKSINEKLD TLSKENSKEDELEALLEQVKSALQLQEKFKKTLNKTLEDYRKNTNNIQENKVLAEHFNKYY  
KDSDSLQSAFY

f03A.nt BB006

TGATTTAATGTAAATTTTAATTACCGCCTAAAAAAGGCTTTAAATGGTATAAAGGAAGAAGATCTAATGGTATTTA  
GAACATATAAACATTTGGAAC TAATAATGCTGCCCATGTTAATGCTGAGTTGCGCTTTTTTTAAGAAACCACAATC  
TGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTACATTTAATATCAGGCAAATTTCAAAT  
AAAAAATTGCCAATCATAAATAGTAATCATGACGTAAC TTGGATAAAAAACAAAGGCAATGACAATCTTAGGCGAAG  
ATGGAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATAATATCTCCTGTAAAAATGGATGGAAA  
ATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAAC TAAAAATGGAGATGATGAATATGAAATTGAAGAT  
GTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAAT TCTCTTTAGCTGTTGAAAATTCACAAGAAGAAG  
GATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAAAAATGCTTTTAAATTAACATATAAAAA  
TGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTACTCAAGAACTAAAATTTATAAAATT  
TCTCTTAATTCAAAATTAATTATTGAATTTTTAAAGAAGTGCTAAAAGAAAAT TCTATATTAAAGACATAGCTG  
GAGATTTATTTGAAGATATATAA

t03A.nt BB006

TGCGCTTTTTTTAAGAAACCACAATCTGTACATCAAGACAGCAATACTGGCAAACCAATAAGCGATGAAAAATTAC  
ATTTAATATCAGGCAAATTTCAAATAAAAAATTGCCAATCATAAATAGTAATCATGACGTAAC TTGGATAAAAAAC  
AAAGGCAATGACAATCTTAGGCGAAGATGGAAGAAATACCAGAATTTAAAAACAAATTTGGATATTCTTATATA  
ATATCTCCTGTAAAAATGGATGGAAAATATAGTTATTACGCGTCATTATTAATACTTTTTGAAACAAC TAAAAATG  
GAGATGATGAATATGAAATTGAAGATGTTAAATTTGTAACAGCTGGTTCCACCCTAGAACTTAAAAAT TCTCTTT  
AGCTGTTGAAAATTCACAAGAAGAAGGATATGTTACTGCATACCCATTTGGAATATTGATGAGTGACGAGATTAA  
AATGCTTTTTAAATTAACATATAAAAAATGGTCATTGGAATTATATGCTTGCAGATTTAACTGTCAAAAATAAACTTA  
CTCAAGAACTAAAATTTATAAAAAATTTCTCTTAATTCAAAATTAATTATTGAATTTTTTAAAGAAGTGCTAAAAGA  
AAATTCATATTAAAAAGACATAGCTGGAGATTTATTTGAAGATATA

f03A.aa BB006

FNVNFNRYRLKKALNGIKEEDLMVFR TYKHLELIMLPMLMLS CAFFKKPQSVHQDSNTGKPI SDEKLHLISGKISNK  
KLPIINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYIISPVKMDGKYSYASLLILFETTKNGDDEYEIEDV  
KFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIKNAFKLTYKNGHWN YMLADLTVKNKLTQETKIYKIS  
LNSKLIIEFLKEVLKENSILKDIAGDLFEDI

t03A.aa BB006

CAFFKKPQSVHQDSNTGKPI SDEKLHLISGKISNKKLPIINSNHDVTWIKTKAMTILGEDGKEIPEFKNKFGYSYI  
ISPVKMDGKYSYASLLILFETTKNGDDEYEIEDVKFVTAGSTLELKNSLLAVENSQEEGYVTAYPFGILMSDEIK  
NAFKLTYKNGHWN YMLADLTVKNKLTQETKIYKISLNSKLIIEFLKEVLKENSILKDIAGDLFEDI

f04A.nt BB011

TAATTACCAAAGATAAGTAAACTTGCAAATAAACTACACGTATTGAAAGTAGATTTGAAATTTCCATTATATTTA  
TATATAATGGCACTAAATATCTGAAAATGAAGGAGAAGCGGGTGGGCAATAAAATTTTTTATATTT CAGTGGTTTT  
AATTTTAATAGTTGGTTGCGACTGGGGAAC TATTAAAGATAAAAGTACAGAAATTTCCAAGCTATTAAGAACGGAC

TABLE 1. Nucleotide and Amino Acid Sequences

AAAGATAAGACTAAAAATCAAGATAGAATAGAATTGGGTGAAGATAATTTTGTATCTAAAAATAATATGTCTACTA  
CTGATACGGGCATTACTAGTTTAGGAAGTCTAAACAACCTTGGATTTAATTAATCGTTCACAGCGGGTCAGTGAACC  
ACCTATAATCTCAAATGAGAAAGCCATAGCTACTCAAGCAAAAGTAGATTTAATGAACAACATTAATGTTACTATA  
ATAAAACCCAAAACCAGCTCAAAATTTGGGAAATTCCTTTAAACAATACTACTACTGAAGATAGTGTGAAGTTTTTAT  
CAATTGAAAACCAAGAGTGGCTTATTAGTAAAAAGATTTTGGCCAGTAAGTTGGAAAATTTAGAAAGCTTTCTAAA  
AACACAACACGAAAAAGAAGCTTTTAAGACGGCTAAAACCTATACAAAGTCTCATTAGTAATTCCAATATGGGTAAA  
GAAATTATTAAGTTTAAGGAAGAATATTACAACTTTTATAATTTGTTTGAAGGCATACAAACAAAATTCATAGTC  
AAAGGAATTCATTTATAAAAGATACTAAATTTGGGGAAAATAGACAAAAAATGCAGTTATATTTAAATCCTTTTC  
ATCTATAGAGAAAGAAATTAGAGATTTGAATTATAAGTTGNGTGAAATCCAAAGTAATTTTCAAATTCAGATGTT  
AGCTGGAATAATGCAAACCTCTCTTTTAAAAGAATCTATAGAAAAATTAATTCAGGCAATTGAAAAAAGGTATGACA  
ATGAGAGTAGAAAAGCAAGGTCAAATTTGGTGGACCTGCTAATAGATGGGATAAAAAATCAAGCTGACAATTTTGCTAA  
GGATGCAAGTATAAGGCAGAACATTCAGCAAATGATTTGGAAAATGCAGCCAACTATTTTAGATATAGTTGTTCA  
AATGAAAAAGAAGCTAAAAAGCTATTAGAAGAAATTAAAAAAAGATTTGTACGAATTGGTATTAGCCTATAA

t04A.nt BB011

TGCGACTGGGGAACCTATTAAAGATAAAAGTACAGAAATTTCCAAGCTATTAAGAACGGACAAAGATAAGACTAAAA  
ATCAAGATAGAATAGAATTGGGTGAAGATAATTTTGTATCTAAAAATAATATGTCTACTACTGATACGGGCATTAC  
TAGTTTAGGAAGTCTAAACAACCTTGGATTAAATTAATCGTTCACAGCGGGTCAGTGAACCACCTATAATCTCAAAT  
GAGAAAGCCATAGCTACTCAAGCAAAAGTAGATTTAATGAACAACATTAATGTTACTATAATAAAACCCAAAACCAG  
CTCAAAATTTGGGAAATTCCTTTAAACAATACTACTACTGAAGATAGTGTGAAGTTTTTATCAATTGAAAACCAAGA  
GTGGCTTATTAGTAAAAAGATTTTGGCCAGTAAGTTGGAAAATTTAGAAAGCTTTCTAAAAACACAACACGAAAA  
GAAGCTTTTAAGACGGCTAAAACCTATACAAAGTCTCATTAGTAATTCCAATATGGGTAAAGAAATTTAAGTTTA  
AGGAAGAATATTACAACTTTTATAATTTGTTTGAAGGCATACAAACAAAATTCATAGTCAAAGGAATTCATTTAT  
AAAAGATACTAAATTTGGGGAAAATAGACAAAAAATGCAGTTATATTTAAATCCTTTTCATCTATAGAGAAAGAA  
ATTAGAGATTTGAATTATAAGTTGNGTGAAATCCAAAGTAATTTCAAATTCAGATGTTAGCTGGAATAATGCAA  
ACTCTCTTTTAAAAGAACTATAGAAAAATTAATTCAGGCAATTGAAAAAAGGTATGACAATGAGAGTAGAAAGCA  
AGGTCAAATTTGGTGGACCTGCTAATAGATGGGATAAAAAATCAAGCTGACAATTTTGCTAAGGATGCAAGTATAAG  
GCAGAACATTCAGCAAATGATTTGGAAAATGCAGCCAACTATTTTAGATATAGTTGTTCAAATGAAAAAGAAGCTA  
AAAAGCTATTAGAAGAAATTAAAAAAAGATTTGTACGAATTGGTATTAGCCTA

f04A.aa BB011

LPKISKLANKTTRIESRFEISIIIFIYNGTKYLMKEKRVGNKIFYISVVLILIVGCDWGTIKDKSTEISKLLRTDK  
DKTKNQDRIELGEDNFVSKNNMSTTDTGITSLSLNNLDLINRSQRVSEPPIIISNEKAIATQAKVDLMNNINVTII  
NPKPAQNLGNSLNNNTTSDSVKFLSIENQEWLISKILPSKLENLESFLKTQHEKEAFKTAQTIQSLISNSNMKE  
IIFKEEYKLYNLFEGIQQKFHSQRNSFIKDTKFGENRQKNAVIFKSFSSIEKEIRDLNLYKLXEIQSNFQIADVS  
WNNANSLKESIEKLIQAIKRYDNESRKQGQIGGPANRWDKNQADNFAKDAKYKAEHSANDLENAANYFRYSCSN  
EKEAKKLLLEEIKKRFVRIGISL

t04A.aa BB011

CDWGTIKDKSTEISKLLRTDKDKTKNQDRIELGEDNFVSKNNMSTTDTGITSLSLNNLDLINRSQRVSEPPIIISN  
EKAIATQAKVDLMNNINVTIINPKPAQNLGNSLNNNTTSDSVKFLSIENQEWLISKILPSKLENLESFLKTQHEK  
EAFKTAQTIQSLISNSNMKEIIFKEEYKLYNLFEGIQQKFHSQRNSFIKDTKFGENRQKNAVIFKSFSSIEKE  
IRDLNLYKLXEIQSNFQIADVSWNNANSLKESIEKLIQAIKRYDNESRKQGQIGGPANRWDKNQADNFAKDAKYK  
AEHSANDLENAANYFRYSCSNEKEAKKLLLEEIKKRFVRIGISL

f05A.nt BB009

TAAATAAATTGTAGGATAAAAAATGAAACAAAAATACGAAAACCTATTTTAAAAAAGATTAAATTTTAAACCTATTAA  
TATTTTTACTACTAGCATGCTCAAGCGAATCCATATTTTACAATTAGGAAATCTGCAAAAAATAAAACATGAATA  
CAATATTTTGGGCAGTTCAAGTCCAAGAGGAATTTCTCTAGTAGGAGAACTCTCTACATTGCAGCCATGCATTTA  
TTTAAAAAAGAAAACGGCAAGATTGAAAAAATTGATTTGAGCAATTCCTATGAGTTTATAAACGACATTGTAAATA  
TATCTGGA AAAACCTATCTTTTAGCGCAAAACAAAGAAGAAGATTAGAAGTTTGCAGCTAAATGGAAGAGATTG  
GACATTAAAATTTAAAAAACCGCTAAAAGCATATAAATCTTAAATCCGTAGAAGAGATGGCGTAA

TABLE 1. Nucleotide and Amino Acid Sequences

t05A.nt BB009

TGCTCAAGCGAATCCATATTTTCACAATTAGGAAATCTGCAAAAAATAAAACATGAATACAATATTTTGGGCAGTT  
CAAGTCCAAGAGGAATTTCTCTAGTAGGAGAACTCTCTACATTGCAGCCATGCATTTATTTAAAAAAGAAAACGG  
CAAGATTGAAAAAATTGATTTGAGCAATTCTTATGAGTTTATAAACGACATTGTAAATATATCTGGAAAAACCTAT  
CTTTTAGCGCAAAACAAAGAAGAAGAATTAGAAGTTTGCGAGCTAAATGGAAAAGATTGGACATTAATAATTTAAAA  
AACCGCTAAAAGCATATAAATTCCTTAAAATCCGTAGAAGAGATGGCG

f05A.aa BB009

INCRIKMKQKYENYFKRLILNLLIFLLACSSSESIFSQGLNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLF  
KKENGKIEKIDLSNSYEFINDIVNISGKTYLLAQNKKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVEEMA

t05A.aa BB009

CSSSESIFSQGLNLQKIKHEYNILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTY  
LLAQNKKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVEEMA

f06A.nt BB014

TAAGGAGCATATATGAGGATTTTGGTTGGCGTTTGTATAATAGCATTGGCTTTATTGGGTGTTATTTGCCTGATA  
ATCAGGAACAAGCTGTTCAAACCTTTTTTTGAGAATTCGGAAAGTAGTGATATGGGTTCGATGAGATTGTTACTGA  
AGGCATATTTTCTAGTTTAAATTTATATGCGTCTGAACATCGTTTATTGGTTGAGATAAAAAAGACTTTAATTAGT  
TTAAAAGATCCCTAATTATCNNGNTGTAGTACNCCCAGTGAGTGACTATAATGAGGAGTATTTTAATAAATTCCTTC  
TAGATTTAGGGTCTGAGCAATCTAAAGACCTGATTAAGTTGTTTATTATGGTAAAAAATGAGCAGAACAATAATA  
ATTTATGCGTATAGTTTCGTTGGCTGTATTTCATGTATAGAGGAGTTATATTTCTCTAGATATTAAGTATTCTGGCGAG  
GGGAGCCATGAGTATAATCGTAATATGCCTAGACCCACTGCTTATGAACAATATTTAAAAGTGAAGAGGTATGATT  
ATAATAGCCCAGTTTCTATTTTACCTACATAA

t06A.nt BB014

TGTTATTTGCCTGATAATCAGGAACAAGCTGTTCAAACCTTTTTTTGAGAATTCGGAAAGTAGTGATATGGGTTCGG  
ATGAGATTGTTACTGAAGGCATATTTTCTAGTTTAAATTTATATGCGTCTGAACATCGTTTATTGGTTGAGATAAA  
AAAGACTTTAATTAGTTTAAAGATCCTAATTATCNNGNTGTAGTACNCCCAGTGAGTGACTATAATGAGGAGTAT  
TTTAATAAATTCCTTCTAGATTTAGGGTCTGAGCAATCTAAAGACCTGATTAAGTTGTTTATTATGGTAAAAAATG  
AGCAGAACAATAATAAATTTATGCGTATAGTTTCGTTGGCTGTATTTCATGTATAGAGGAGTTATATTCTCTAGATAT  
TAAGTATTCTGGCGAGGGGAGCCATGAGTATAATCGTAATATGCCTAGACCCACTGCTTATGAACAATATTTAAAA  
GTGAAGAGGTATGATTATAAT

f06A.aa BB014

GAYMRILVGVCIIALALLGCYLPDNQEAVQVTFENSESSDMGSDEIVTEGIFSSLKLYASEHRLLEIKKTLISL  
KDPNYXXVVPVSDYNEEYFNKFFLDLGSEQSKDLIKLFIMVKNEQNNKFMRIVRWLYSCIEELYSLDIKYSSEG  
SHEYNRNMPRPTAYEQYLKVKRYDYNPVSILPT

t06A.aa BB014

CYLPDNQEAVQVTFENSESSDMGSDEIVTEGIFSSLKLYASEHRLLEIKKTLISLKDPPNYXXVVPVSDYNEEY  
FNKFFLDLGSEQSKDLIKLFIMVKNEQNNKFMRIVRWLYSCIEELYSLDIKYSSEGSGHEYNRNMPRPTAYEQYLK  
VKRYDYN

f07A.nt BB023

TAAAGTATTTTATTTTTTTTTTATTATCCACTGTTCTTTTTGCTCAAGAGACTGATGGATTAGCAGAGGGTTCTAAAA  
GGGCAGAGCCTGGAGAATTAGTTTTAGATTTTGCCGAGCTTGCAAGAGATCCAAGTTCAACTAGACTTGATCTTAC

TABLE 1. Nucleotide and Amino Acid Sequences

AAATTATGTTGATTATGTATATTCGGGCGCTTCTGGTATTGTTAAGCCGGAAGATATGGTTGTAGATCTTGGGATA  
 AATAATTGGAGCGTTTTACTTACTCCTTCTGCAAGGTTGCAGGCTTACGTTAAAAATTCAGTTGTTGCGCCCGCTG  
 TTGTTAAGAGTGAGTCAAAAAGGTACGCAGGTGATACTATTTTAGGGGTAAGAGTTTGTTCCTCAAGCTATTCTCA  
 ATCATCTGCTATGATTATGCCACCATTAAAAATTCCTTTTTATTTCAGGGGAAAGTGGCAATCAATTTTATAGGCAA  
 GGTCTTATTGATAACATTAAAAACCATGAAAGAAATTAAGGTATCTGTTTATAGTTTAGGGTATGAGATAGATCTTG  
 AGGTTTTATTTGAAGATATGAATGNCATGGAATATGCTTNNTCTATGGGTACTTTAAAGTTTAAAGGGTGGGCTGA  
 TTTAATTTGGTCAAATCCTAACTATATTCCTAATATATCATCCAGAATTATTAAAGACGATGTTCCAAATTATCCT  
 CTTGCTTCAAGTAAAATGAGATTTAAGGCTTTTAGAGTTTCAAAGTCACACAGTTCAAAGAGCAAAATTTTCATCT  
 TTTATGTTAAAGATTTAAGAGTTCTTTATGATAAGTTGAGTGTTCATAGATTCTGATATTGACAGTGAGTCTGT  
 ATTTAAAGTTTATGAGACTAGCGGAACGAATCCCTTCGTAAATTAAAGGCACACGNAACNTTTAAAAGNGTTTAA  
 AAGCTTAGAGAAAAAATTTCTATGCCTGAAGGCTCTTTCCAAAACCTTGTAGAAAAGATTGAGAGTGAAAAACCTG  
 AAGAATCATCTCCGAAAAATTAG

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GAGGGTCTAAAAGGGCAGAGCCTGGAGAATTAGTTTTAGATTTTGCCGAGCTTGCAAGAGATCCAAGTTCAACTA  
 GACTTGATCTTACAAATTATGTTGATTATGTATATTCGGGCGCTTCTGGTATTGTTAAGCCGGAAGATATGGTTGT  
 AGATCTTGGGATAAATAATTGGAGCGTTTTACTTACTCCTTCTGCAAGGTTGCAGGCTTACGTTAAAAATTCAGTT  
 GTTGCGCCCGCTGTTGTTAAGAGTGAGTCAAAAAGGTACGCAGGTGATACTATTTTAGGGGTAAGAGTTTGTTC  
 CAAGCTATTCTCAATCATCTGCTATGATTATGCCACCATTAAAAATTCCTTTTTATTTCAGGGGAAAGTGGCAATCA  
 ATTTTATAGGCAAAGGTCTTATTGATAACATTAAAAACCATGAAAGAAATTAAGGTATCTGTTTATAGTTTAGGGTAT  
 GAGATAGATCTTGAGGTTTTATTTGAAGATATGAATGNCATGGAATATGCTTNNTCTATGGGTACTTTAAAGTTTA  
 AAGGGTGGGCTGATTTAATTTGGTCAAATCCTAACTATATTCCTAATATATCATCCAGAATTATTAAAGACGATGT  
 TCCAAATTATCCTCTTGCTTCAAGTAAAATGAGATTTAAGGCTTTTAGAGTTTCAAAGTCACACAGTTCAAAGAG  
 CAAAATTTTCATCTTTTATGTTAAAGATTTAAGAGTTCTTTATGATAAGTTGAGTGTTCATAGATTCTGATATTG  
 ACAGTGAGTCTGTATTTAAAGTTTATGAGACTAGCGGAACGAATCCCTTCGTAAATTAAAGGCACACGNAACNTT  
 TAAAAGNGTTTTAAAGCTTAGAGAAAAAATTTCTATGCCTGAAGGCTCTTTCCAAAACCTTGTAGAAAAGATTGAG  
 AGTGAAAAACCTGAAGAATCATCTCCGAAAAAT

f07A.aa BB023

SILFFLLSTVLFAQETDGLAEGSKRAEPGELVLDFAEELARDPSSTRLDLTNYVDYVYSGASGIVKPEDMVVDLGIN  
 NWSVLLTPSARLQAYVKNSVAVPVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKG  
 LIDNIKTMEIKVSVYSLGYEIDLEVLFDNMNXMEYAXSMGTLKFKGWADLIWSNPNIIPNIISSRIKDDVPNYPL  
 ASSKMRFKAFRVSKSHSSKEQNFIFYVKDLRVLYDKLSVSDIDSESFVKVYETSGTESLRKLKAHXTFKXVLK  
 LREKISMPEGSFQNFVEKIESEKPEESSPKN

t07A.aa BB023

EGSKRAEPGELVLDFAEELARDPSSTRLDLTNYVDYVYSGASGIVKPEDMVVDLGINNWSVLLTPSARLQAYVKNSV  
 VAVPVKSESKRYAGDTILGVRVLFPSYSQSSAMIMPPFKIPFYSGESGNQFLGKGLIDNIKTMEIKVSVYSLGY  
 EIDLEVLFDNMNXMEYAXSMGTLKFKGWADLIWSNPNIIPNIISSRIKDDVPNYPLASSKMRFKAFRVSKSHSSKE  
 QNFIFYVKDLRVLYDKLSVSDIDSESFVKVYETSGTESLRKLKAHXTFKXVLKLREKISMPEGSFQNFVEKIE  
 SEKPEESSPKN

f08A.nt BB024

TGAATATTAATAATAAAAAAGGAGTAACAATGAAAATCATCAACATATTATTTTGTATTATTTTACTAATGCTAA  
 ACGGCTGTAATTCTAATGATAATGACACTTTAAAAACAATGCCCAACAAACAAAAGACGGGGAAAGCGTGATTT  
 AACCCAAAAGAAACAACAAGAAAAACCAAAATCTAAAGAAGAATACTTAGAGAAAAGCTATCTGACGATCAA  
 AAAACACATCTTGACTGGTTAAAACCCGCTTTAACTGGTGGTGGAGAATTTGACAAATTTTAGAAAATGATGATG  
 ATAAAATAAAATCAGCACTTGATCATATAAAACTCAACTTGATAGTTGTAATGGTGATCAAGCAGAACAAACAAA  
 AACCACCTTTCAAACCTGTGGTTACAGAATTCCTTAAAAATGGTGATATAGATAATTTTGCAACTGGAGCGGTTAGT  
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t08A.nt BB024

TABLE 1. Nucleotide and Amino Acid Sequences

TGTAATTCTAATGATAATGACACTTTAAAAACAATGCCCAACAAACAAAAAGACGGGGAAAGCGTGATTTAACCC  
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CTTTCAAACTGTGGTTACAGAATCTTTAAAAATGGTGATATAGATAATTTTGCAACTGGAGCGGTTAGTAAC TG  
CAATAATGGTGGC

f08A.aa BB024

ILIIKKGVMTMKIINILFCLFLLMLNGCNSNDNDTLKNNAAQQT KRRGKRDLTQKETTTQEKPKSKEELLREKLSDDQK  
THLDWLKPALTGAGEFDKFLNDDDKIKSALDHIKTQLDSCNGDQAEQQTTFKTVVTEFFKNGDIDNFATGAVSN  
CNNGG

t08A.aa BB024

CNSNDNDTLKNNAAQQT KRRGKRDL51TQKETTTQEKPKSKEELLREKLSDDQKTHLDWLKPALTGAGEFDKFLNDD  
DKIKSALDHIKTQLDSCNGDQAEQQTTFKTVVTEFFKNGDIDNFATGAVSNCNNGG

f09A.nt BB025

TGAATATTAATAATAAAAAAGGAATAATAATGAAAATTATCAACATATTATTTTGTATTATTTTACTAATGCTAA  
ACGGCTGTAATTCTAATGATACTAATAATAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGC  
AACACAAGAAAAACCTAAATCTAAAGAAGAACTTCTTAGAGAAAAGCTAAATGATAATCAAAAAACACACCTTGAC  
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CACTTGATCATATAAAGAGTGAACCTTGACAGTTGTACTGGAGATAAGGTTGAAAATAAAAATACCTTCAAGCAGGT  
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t09A.nt BB025

TGTAATTCTAATGATACTAATAATAGCCAAACAAAAAGTAGACAAAAACGTGATTTAACCCAAAAAGAAGCAACAC  
AAGAAAAACCTAAATCTAAAGAAGAACTTCTTAGAGAAAAGCTAAATGATAATCAAAAAACACACCTTGACTGGTT  
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GATCATATAAAGAGTGAACCTTGACAGTTGTACTGGAGATAAGGTTGAAAATAAAAATACCTTCAAGCAGGTCTGTC  
AGGAGGCCCTTAAAGGGGGCATAGACGGCTTTGAAAATACTGCAAGTAGTACGTGCAAAAATTCA

f09A.aa BB025

ILIIKKGIIMKIINILFCLFLLMLNGCNSNDTNNSQTKSRQKRDLTQKEATQEKPKSKEELLREKLNDNQKTHLDW  
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t09A.aa BB025

CNSNDTNNSQTKSRQKRDLTQKEA51TQEKPKSKEELLREKLNDNQKTHLDWLKEALGNDGEFNKFLGYDESKI  
KALDHIKSELDSCTGDKVENKNTFKQVVQEALKGGIDGFENTASSTCKNS

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

Query	GenSeq Access No.	GenSeq Gene Description	BLAST Score	BLAST P-Value
f01A.aa	gil2690256	(AE000790) antigen, P35, putative [Borrelia burgdorferi]	1523	5.90E-206
f02A.aa	gil2690286	(AE000790) B. burgdorferi predicted coding region BBA69 [Borrelia]	1320	2.10E-174
f02A.aa	gil2690285	(AE000790) B. burgdorferi predicted coding region BBA68 [Borrelia]	278	7.50E-71
f02A.aa	gil2690105	(AE000789) B. burgdorferi predicted coding region BBI38 [Borrelia]	151	8.40E-54
f02A.aa	gil2690092	(AE000789) antigen, P35, putative [Borrelia burgdorferi]	151	2.70E-48
f02A.aa	gil2690183	(AE000787) antigen, P35, putative [Borrelia burgdorferi]	155	4.20E-22
f02A.aa	gil2690106	(AE000789) B. burgdorferi predicted coding region BBI39 [Borrelia]	154	1.30E-21
f03A.aa	gil2688051	(AE001127) antigen, S2, putative [Borrelia burgdorferi]	1223	7.60E-164
f03A.aa	gil1063419	S2 gene product [Borrelia burgdorferi]	116	3.00E-22
f03A.aa	gil2690227	(AE000790) antigen, S2 [Borrelia burgdorferi] >pirD70207ID70207	116	9.70E-22
f03A.aa	gil2690128	(AE000788) protein p23 [Borrelia burgdorferi] >pirC70257IC70257	110	5.70E-19
f03A.aa	gil2689956	(AE000785) protein p23 [Borrelia burgdorferi] >pirD70225ID70225	104	7.90E-15
f04A.aa	gil2690078	(AE000784) B. burgdorferi predicted coding region BBH18 [Borrelia]	1873	5.60E-250
f04A.aa	gil2690192	(AE000787) B. burgdorferi predicted coding region BB113 [Borrelia]	167	1.40E-15
f05A.aa	gil2687919	(AE001117) B. burgdorferi predicted coding region BB0028 [Borrelia]	696	4.20E-92
f06A.aa	gil2690129	(AE000788) outer membrane protein [Borrelia burgdorferi]	884	4.80E-124
f06A.aa	gil2690089	(AE000789) conserved hypothetical protein [Borrelia burgdorferi]	731	2.20E-118
f06A.aa	gil520783	unknown [Borrelia burgdorferi] >gil551742 unknown [Borrelia]	337	4.30E-58
f07A.aa	gil2688608	(AE001168) flagellar filament outer layer protein (flaA) [Borrelia]	1668	2.50E-224
f07A.aa	gil1575447	FlaA protein [Borrelia burgdorferi] >gil1019754 orf [Borrelia]	1645	3.60E-221
f07A.aa	gil152896	flagellar filament surface antigen [Spirochaeta aurantia]	144	1.70E-38
f07A.aa	gil155059	endoflagellar sheath protein [Treponema pallidum]	139	3.80E-28
f07A.aa	gil433524	flagellin FlaA1 [Serpulina hyodysenteriae] >gil904393 endoflagellar	119	3.00E-26
f07A.aa	pirA32814	flagellar filament surface antigen - Spirochaeta aurantia	116	9.40E-11
f08A.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	508	2.10E-78
f08A.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	547	4.00E-70
f08A.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	303	3.70E-51

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f08A.aa	gil209843	lipoprotein [Borrelia burgdorferi]	395	2.20E-49
f08A.aa	gil209849	lipoprotein [Borrelia burgdorferi]	219	2.60E-27
f08A.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	234	4.30E-27
f08A.aa	gil209831	lipoprotein [Borrelia burgdorferi]	209	1.10E-22
f08A.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	200	1.80E-22
f08A.aa	gil209857	lipoprotein [Borrelia burgdorferi]	200	2.50E-21
f08A.aa	gnllPIDle26 8244	surface-exposed lipoprotein [Borrelia afzelii]	142	1.80E-11
f09A.aa	gil209843	lipoprotein [Borrelia burgdorferi]	453	8.60E-67
f09A.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	379	1.00E-56
f09A.aa	gil209873	lipoprotein [Borrelia burgdorferi]	282	1.10E-45
f09A.aa	gil209837	lipoprotein [Borrelia burgdorferi]	357	7.10E-44
f09A.aa	gil209849	lipoprotein [Borrelia burgdorferi]	143	1.60E-13
f09A.aa	gnllPIDle26 8244	surface-exposed lipoprotein [Borrelia afzelii]	111	3.60E-13
f09A.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	142	5.40E-13
f101.aa	gil2688708	(AE001176) conserved hypothetical protein [Borrelia burgdorferi]	1099	4.50E-152
f105.aa	gil2688693	(AE001175) B. burgdorferi predicted coding region BB0758 [Borrelia]	1276	2.20E-177
f11-12.aa	gil2690139	(AE000788) B. burgdorferi predicted coding region BBK01 [Borrelia]	1473	4.70E-193
f11-12.aa	gil2690030	(AE000786) B. burgdorferi predicted coding region BBG01 [Borrelia]	1066	1.40E-138
f11-12.aa	gil2690074	(AE000784) B. burgdorferi predicted coding region BBH37 [Borrelia]	173	6.20E-93
f11-12.aa	gil2690188	(AE000787) B. burgdorferi predicted coding region BB108 [Borrelia]	192	2.70E-75
f11-4.aa	gil2690150	(AE000788) B. burgdorferi predicted coding region BBK12 [Borrelia]	1144	2.70E-147
f11-4.aa	gil2690145	(AE000788) B. burgdorferi predicted coding region BBK07 [Borrelia]	852	5.70E-127
f11-4.aa	gil2690095	(AE000789) B. burgdorferi predicted coding region BB110 [Borrelia]	153	1.30E-34
f11-4.aa	gil2690197	(AE000787) B. burgdorferi predicted coding region BB131 [Borrelia]	115	1.40E-12
f11-4.aa	gil2690219	(AE000787) B. burgdorferi predicted coding region BB145 [Borrelia]	115	1.40E-12
f112-1.aa	gil2690054	(AE000784) B. burgdorferi predicted coding region BBH06 [Borrelia]	573	7.00E-75
f12.aa	gil2688785	(AE001182) B. burgdorferi predicted coding region BB0838 [Borrelia]	6008	0
f129.aa	gil2688685	(AE001174) B. burgdorferi predicted coding region BB0739 [Borrelia]	987	6.20E-133
f14-8.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	385	2.70E-75

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f14-8.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BB134 [Borrelia burgdorferi]	330	2.60E-66
f14-8.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	287	4.00E-64
f14-8.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BB116 [Borrelia burgdorferi]	172	1.10E-38
f14-8.aa	gil2690115	(AE000789) B. burgdorferi predicted coding region BB128 [Borrelia burgdorferi]	173	1.70E-28
f14-8.aa	gil2690116	(AE000789) B. burgdorferi predicted coding region BB129 [Borrelia burgdorferi]	163	8.20E-24
f14-8.aa	gil2690207	(AE000787) B. burgdorferi predicted coding region BB102 [Borrelia burgdorferi]	220	1.90E-23
f14-8.aa	gil2690099	(AE000789) B. burgdorferi predicted coding region BB115 [Borrelia burgdorferi]	140	3.60E-12
f14-8.aa	gil2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	111	1.00E-11
f142.aa	gil2688655	(AE001172) glutamate transporter (gluP) [Borrelia burgdorferi]	2233	7.199999999999999e-311
f142.aa	gnlPIDle233874	hypothetical protein [Bacillus subtilis] >gnlPIDle1182902	727	2.60E-156
f142.aa	gnlPIDld1016231	Proton/sodium-glutamate symport protein (Glutamate-aspartate)	762	6.60E-146
f142.aa	gil1574711	proton glutamate symport protein (gluP) [Haemophilus influenzae]	903	2.10E-131
f142.aa	gil2983758	(AE000735) proton/sodium-glutamate symport protein [Aquifex]	111	8.40E-36
f142.aa	gil143000	proton glutamate symport protein [Bacillus stearothermophilus]	125	1.20E-30
f142.aa	gil143002	proton glutamate symport protein [Bacillus caldotenax]	125	1.90E-28
f142.aa	gnlPIDle1183024	proton/sodium-glutamate symport protein [Bacillus subtilis]	122	2.20E-25
f142.aa	gnlPIDld1022697	glutamate transporter [Caenorhabditis elegans]	121	1.80E-22
f142.aa	gil1255318	coded for by C. elegans cDNA cm08h9; coded for by C. elegans cDNA	121	2.10E-22
f142.aa	gil2388712	(AF017105) amino acid transporter [Chlamydia psittaci]	135	3.60E-22
f142.aa	gil2655021	(AF018259) glutamate transporter 5A [Ambystoma tigrinum]	125	7.70E-22
f142.aa	gnlPIDle149542	gluT-R gene product [Clostridium perfringens]	199	4.60E-21
f142.aa	gil396412	gluP [Escherichia coli] >gil147160 proton-glutamate [Escherichia coli]	109	7.90E-21
f147.aa	gil2688656	(AE001172) NADH oxidase, water-forming (nox) [Borrelia burgdorferi]	2245	7.20E-303
f147.aa	gil642030	NADH oxidase [Serpulina hyodysenteriae]	318	9.20E-105
f147.aa	gil2650234	(AE001077) NADH oxidase (noxA-2) [Archaeoglobus fulgidus]	303	2.90E-93



TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f147.aa	gil2792490	(AF041467) coenzyme A disulfide reductase [Staphylococcus aureus]	194	2.60E-90
f147.aa	gil2650383	(AE001088) NADH oxidase (noxA-1) [Archaeoglobus fulgidus]	286	3.30E-88
f147.aa	gnllPIDId10 09320	H2O-forming NADH Oxidase [Streptococcus mutans]	369	4.30E-85
f147.aa	gil49023	NADH peroxidase [Enterococcus faecalis] >pirS18332S18332 NADH	638	3.20E-83
f147.aa	gil1591361	NADH oxidase (nox) [Methanococcus jannaschii] >pirA64381A64381	535	4.80E-83
f147.aa	gil2622461	(AE000898) NADH oxidase [Methanobacterium thermoautotrophicum]	303	8.40E-72
f147.aa	gil47045	NADH oxidase [Enterococcus faecalis] >pirS26965S26965 NADH oxidase	547	8.80E-71
f147.aa	gil2650233	(AE001077) NADH oxidase (noxA-3) [Archaeoglobus fulgidus]	312	2.00E-63
f147.aa	gil1674132	(AE000044) Mycoplasma pneumoniae, NADH oxidase; similar to	175	7.00E-61
f147.aa	gil1045969	NADH oxidase [Mycoplasma genitalium] >pirD64230D64230 NADH	164	4.10E-51
f147.aa	gil2648692	(AE000975) NADH oxidase (noxA-5) [Archaeoglobus fulgidus]	143	2.00E-40
f147.aa	gil2983379	(AE000709) NADH oxidase [Aquifex aeolicus]	162	5.50E-30
f150.aa	gil2688659	(AE001172) conserved hypothetical protein [Borrelia burgdorferi]	1319	2.70E-179
f150.aa	gil2983887	(AE000743) hypothetical protein [Aquifex aeolicus]	238	1.40E-25
f150.aa	gil2581796	(AF001974) putative TrkA [Thermoanaerobacter ethanolicus]	175	5.80E-23
f150.aa	gil1377829	unknown [Bacillus subtilis] >gnllPIDId1007628 orf4 [Bacillus	212	1.50E-21
f150.aa	gnllPIDId11 85982	similar to hypothetical proteins [Bacillus subtilis]	181	6.00E-17
f150.aa	gnllPIDId10 11497	hypothetical protein [Synechocystis sp.] >pirS75999S75999	128	3.70E-11
f152.aa	gil2688660	(AE001172) K+ transport protein (ntpI) [Borrelia burgdorferi]	2200	2.40000000 001213e- 313
f152.aa	gil2983882	(AE000743) K+ transport protein homolog [Aquifex aeolicus]	239	3.60E-106
f152.aa	gnllPIDId11 84940	similar to Na+-transporting ATP synthase [Bacillus subtilis]	158	6.60E-64
f152.aa	gnllPIDId11 85983	similar to Na+-transporting ATP synthase [Bacillus subtilis]	131	3.40E-62
f152.aa	gnllPIDId10 18749	Na+ -ATPase subunit J [Synechocystis sp.] >pirS75455S75455	141	1.70E-55

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f152.aa	gnlPIDd10 04799	Na+ -ATPase subunit J [Enterococcus hirae]	209	4.00E-45
f152.aa	gil2581795	(AF001974) putative TrkG [Thermoanaerobacter ethanolicus]	149	2.20E-29
f152.aa	gil1674061	(AE000036) Mycoplasma pneumoniae, Na(+) translocating ATPase	104	4.00E-28
f152.aa	gil1046024	Na+ ATPase subunit J [Mycoplasma genitalium] >pirF64235IF64235	114	2.80E-27
f152.aa	gil567062	HKT1 [Triticum aestivum] >pirS47582IS47582 high-affinity potassium	137	2.00E-17
f154.aa	gil2688664	(AE001172) B. burgdorferi predicted coding region BB0722 [Borrelia	2456	0
f157.aa	gil2688641	(AE001171) rod shape-determining protein (mreB-2) [Borrelia	2300	0
f157.aa	gil143657	endospore forming protein [Bacillus subtilis]	224	2.60E-61
f157.aa	gil580938	internal open reading frame (AA 1-290) [Bacillus subtilis]	224	2.60E-61
f157.aa	gil2982781	(AE000670) rod shape determining protein RodA [Aquifex aeolicus]	333	5.40E-61
f157.aa	gil580937	spoVE gene product (AA 1-366) [Bacillus subtilis] >gnlPIDle1185111	224	7.70E-59
f157.aa	gil147695	rod-shape-determining protein [Escherichia coli] >gil1778551	340	6.10E-58
f157.aa	gnlPIDle32 8589	sfr [Streptomyces coelicolor]	362	6.40E-58
f157.aa	gil1572976	rod shape-determining protein (mreB) [Haemophilus influenzae]	307	4.00E-56
f157.aa	gnlPIDle11 85075	similar to cell-division protein [Bacillus subtilis]	203	2.60E-45
f157.aa	gil1469784	putative cell division protein fisW [Enterococcus hirae]	231	6.90E-45
f157.aa	gil1016213	strong sequence similarity to FisW, RodA, and SpoV-E [Cyanophora	206	3.00E-41
f157.aa	gnlPIDd10 19002	rod-shape-determining protein [Synechocystis sp.]	184	1.60E-38
f157.aa	gil146039	cell division protein [Escherichia coli] >gil40857 FisW protein	104	8.30E-35
f157.aa	gil1574692	cell division protein (fisW) [Haemophilus influenzae]	114	3.30E-33
f157.aa	gil1165286	FisW [Borrelia burgdorferi] >gil2688164 (AE001137) cell division	170	6.20E-32
f17-6.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BB116 [Borrelia	1250	1.70E-164
f17-6.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BB134 [Borrelia	142	3.40E-59
f17-6.aa	gil2690115	(AE000789) B. burgdorferi predicted coding region BB128 [Borrelia	447	6.70E-56
f17-6.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	182	1.10E-34
f17-6.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	196	6.60E-34

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f17-6.aa	gi2690114	(AE000789) B. burgdorferi predicted coding region BB127 [Borrelia	176	1.00E-16
f17-6.aa	gnllPID10 12343	gene required for phosphorylation of oligosaccharides/ has	178	2.80E-15
f17-6.aa	gi2690207	(AE000787) B. burgdorferi predicted coding region BB102 [Borrelia	114	3.50E-13
f17-6.aa	gnllPID1e32 9895	(AJ000496) cyclic nucleotide-gated channel beta subunit	152	1.10E-11
f170.aa	gi2688652	(AE001171) B. burgdorferi predicted coding region BB0708 [Borrelia	524	2.60E-73
f186.aa	gi2688622	(AE001169) B. burgdorferi predicted coding region BB0689 [Borrelia	792	1.80E-105
f186.aa	gi2688622	(AE001169) B. burgdorferi predicted coding region BB0689 [Borrelia	792	1.80E-105
f19-2.aa	gi2690120	(AE000789) B. burgdorferi predicted coding region BB134 [Borrelia	1341	2.70E-177
f19-2.aa	gi2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	347	7.00E-53
f19-2.aa	gi2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	254	7.70E-53
f19-2.aa	gi2690100	(AE000789) B. burgdorferi predicted coding region BB116 [Borrelia	142	6.60E-50
f19-2.aa	gi2690115	(AE000789) B. burgdorferi predicted coding region BB128 [Borrelia	144	7.60E-34
f19-2.aa	gi2690116	(AE000789) B. burgdorferi predicted coding region BB129 [Borrelia	183	2.20E-21
f19-2.aa	gi2690207	(AE000787) B. burgdorferi predicted coding region BB102 [Borrelia	171	2.00E-16
f19-2.aa	gi2690099	(AE000789) B. burgdorferi predicted coding region BB115 [Borrelia	166	1.20E-15
f19-2.aa	gi2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	122	5.70E-14
f19-4.aa	gi2690116	(AE000789) B. burgdorferi predicted coding region BB129 [Borrelia	1129	1.30E-150
f19-4.aa	gi2690099	(AE000789) B. burgdorferi predicted coding region BB115 [Borrelia	260	3.00E-30
f19-4.aa	gi2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	180	1.80E-23
f19-4.aa	gi2690120	(AE000789) B. burgdorferi predicted coding region BB134 [Borrelia	183	1.50E-21
f19-4.aa	gi2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	192	1.20E-19
f19-4.aa	gi2690207	(AE000787) B. burgdorferi predicted coding region BB102 [Borrelia	149	8.90E-14
f19-4.aa	gi2690098	(AE000789) B. burgdorferi predicted coding region BB114 [Borrelia	138	8.00E-12
f19-6.aa	gi2690115	(AE000789) B. burgdorferi predicted coding region BB128 [Borrelia	995	1.20E-131
f19-6.aa	gi2690100	(AE000789) B. burgdorferi predicted coding region BB116 [Borrelia	447	3.00E-55
f19-6.aa	gi2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	219	2.00E-36
f19-6.aa	gi2690120	(AE000789) B. burgdorferi predicted coding region BB134 [Borrelia	144	3.50E-34
f19-6.aa	gi2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	130	6.30E-12
f196.aa	gi2688620	(AE001169) methyl-accepting chemotaxis protein (mcp-5) [Borrelia	3093	0

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f196.aa	gil2688621	(AE001169) methyl-accepting chemotaxis protein (mcp-4) [Borrelia]	615	1.90E-83
f196.aa	gil496484	tlpC gene product [Bacillus subtilis] >pirI40496I40496 methylation	180	6.90E-28
f196.aa	gnllPIDId10 07002	methyl-accepting chemotaxis protein TlpC [Bacillus subtilis]	180	4.90E-27
f196.aa	gnllPIDId11 73493	methyl-accepting chemotaxis protein [Bacillus subtilis]	162	5.10E-25
f196.aa	gil882594	ORF_f506 [Escherichia coli] >gil1789453 (AE000389) aerotaxis	204	1.70E-24
f196.aa	gil148350	tas [Enterobacter aerogenes] >pirID32302ID32302 probable aspartate	179	1.80E-24
f196.aa	gil1066850	putative [Rhodobacter capsulatus] >pirJC4735JC4735	207	1.80E-24
f196.aa	gil154381	chemoreceptor [Salmonella typhimurium] >pirA47178A47178	230	2.00E-24
f196.aa	gil459690	transmembrane receptor [Bacillus subtilis] >gnllPIDId1185997	212	1.40E-23
f196.aa	gil805015	MCPA protein [Rhodobacter sphaeroides] >pirIS70094IS54262	237	2.10E-23
f196.aa	gil40424	mcpA gene product [Caulobacter crescentus] >pirS23064IS23064 mcpA	238	7.30E-23
f196.aa	gil144913	sensory transducer protein [Clostridium thermocellum]	227	8.90E-23
f196.aa	gil1061063	Trg sensory transducer protein [Escherichia coli]	211	2.40E-20
f196.aa	gnllPIDId10 15762	Methyl-accepting chemotaxis protein III (MCP-III) (Ribose and	211	2.50E-20
f197.aa	gil2688621	(AE001169) methyl-accepting chemotaxis protein (mcp-4) [Borrelia]	3724	0
f197.aa	gil2688620	(AE001169) methyl-accepting chemotaxis protein (mcp-5) [Borrelia]	615	8.40E-83
f197.aa	gil1066850	putative [Rhodobacter capsulatus] >pirJC4735JC4735	227	9.80E-27
f197.aa	gil882594	ORF_f506 [Escherichia coli] >gil1789453 (AE000389) aerotaxis	217	1.00E-26
f197.aa	gil154381	chemoreceptor [Salmonella typhimurium] >pirA47178A47178	239	2.80E-25
f197.aa	gil496484	tlpC gene product [Bacillus subtilis] >pirI40496I40496 methylation	202	5.10E-25
f197.aa	gnllPIDId10 07002	methyl-accepting chemotaxis protein TlpC [Bacillus subtilis]	202	5.10E-25
f197.aa	gil2564665	(AF022807) putative methyl accepting chemotaxis protein [Rhizobium]	212	7.20E-24
f197.aa	gil459691	transmembrane receptor [Bacillus subtilis] >gnllPIDId1185996	215	1.10E-23
f197.aa	gil43218	serine chemoreceptor [Escherichia coli] >bbsI127562 serine	236	2.80E-23
f197.aa	gil537197	CG Site No. 63; alternate gene name cheD [Escherichia coli]	236	2.90E-23
f197.aa	gil148077	methyl-accepting chemotaxis protein I [Escherichia coli] >gil2367378	236	2.90E-23
f197.aa	gnllPIDId10	transducer [Pseudomonas aeruginosa]	178	4.20E-23

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

09948				
f197.aa	gil148349	tse [Enterobacter aerogenes] >pir[C32302]C32302 serine transducer	234	5.50E-23
f197.aa	gil2626835	chemotactic transducer [Pseudomonas aeruginosa]	177	5.70E-23
f200.aa	gil2688600	(AE001168) ribose/galactose ABC transporter, permease protein	1887	5.10E-266
f200.aa	gnlPIDle311453	unknown [Bacillus subtilis] >gnlPIDle1184234 similar to	283	1.50E-63
f200.aa	gil2649711	(AE001042) ribose ABC transporter, permease protein (rbsC-1)	202	1.10E-47
f200.aa	gil2130609	(AF000308) putative polytopic protein [Mycoplasma fermentans]	119	2.10E-27
f200.aa	gnlPIDle311493	unknown [Bacillus subtilis] >gnlPIDle1184235 similar to	112	1.10E-18
f200.aa	gil950073	membrane forming protein [Mycoplasma capricolum] >pir[S77790]S77790	161	5.60E-16
f200.aa	gil2688599	(AE001168) ribose/galactose ABC transporter, permease protein	108	2.00E-14
f208.aa	gil2688610	(AE001168) B. burgdorferi predicted coding region BB0674 [Borrelia	1726	6.70E-244
f21-4.aa	gil1197833	Bbk2.11 [Borrelia burgdorferi] >pir[S70531]S70531 bbk2.11 protein	474	3.00E-70
f21-4.aa	gil2627267	ErpL [Borrelia burgdorferi]	477	6.30E-69
f21-4.aa	gil1707281	putative outer membrane protein [Borrelia burgdorferi]	503	6.60E-66
f21-4.aa	gil896042	OspF [Borrelia burgdorferi] >pir[S70532]S70532 outer surface protein	503	6.60E-66
f21-4.aa	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	489	3.00E-60
f21-4.aa	gil1707290	putative outer surface protein [Borrelia burgdorferi]	342	3.20E-49
f21-4.aa	gil1663633	ErpK [Borrelia burgdorferi]	268	1.70E-48
f21-4.aa	gil466482	outer surface protein F [Borrelia burgdorferi] >pir[40287]40287	321	3.80E-38
f21-4.aa	gil896038	Bbk2.10 precursor [Borrelia burgdorferi] >pir[S70534]S70534 bbk2.10	121	3.90E-34
f21-4.aa	gil896040	Bbk2.10 precursor [Borrelia burgdorferi] >pir[S70533]S70533 bbk2.10	118	2.30E-33
f21-4.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	107	3.30E-33
f21-4.aa	gil2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	118	6.00E-14
f210.aa	gil2688603	(AE001168) conserved hypothetical protein [Borrelia burgdorferi]	867	2.60E-116
f210.aa	gil2688604	(AE001168) chemotaxis response regulator (cheY-3) [Borrelia	733	1.40E-97
f210.aa	gil1408274	CheY [Borrelia burgdorferi]	720	9.00E-96
f210.aa	gil1765976	chemotaxis protein Che Y [Treponema pallidum]	405	6.60E-52
f210.aa	gil142682	chemotactic response protein [Bacillus subtilis] >gnlPIDle1185224	184	8.00E-30
f210.aa	gil940149	CheY [Thermotoga maritima]	171	1.50E-27

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f210.aa	gil2649557	(AE001031) chemotaxis response regulator (cheY) [Archaeoglobus]	168	1.50E-26
f210.aa	gil620085	cheY gene product [Listeria monocytogenes]	183	3.00E-26
f210.aa	gnlPIDe24 9646	YneI [Bacillus subtilis] >gil870926 response regulator	166	4.00E-24
f210.aa	gil149620	ORF2 [Leptospira borgpetersenii] >splP240861YLB3_LEPIN HYPOTHETICAL	121	4.70E-22
f210.aa	gil1408275	orfX; putative OrfX protein [Borrelia burgdorferi]	208	9.20E-22
f210.aa	gil994802	cheY gene product [Halobacterium salinarum] >pirIS58645IS58645 CheY	139	8.90E-18
f210.aa	gil143598	spo0F [Bacillus subtilis] >gil143601 Spo0F protein [Bacillus]	113	4.70E-11
f216.aa	gil2688586	(AE001167) conserved hypothetical protein [Borrelia burgdorferi]	804	1.20E-109
f216.aa	gil1575446	orfA [Borrelia burgdorferi]	472	1.10E-91
f219.aa	gil2688594	(AE001167) B. burgdorferi predicted coding region BB0664 [Borrelia]	1122	3.10E-148
f22.aa	gil2688779	(AE001181) B. burgdorferi predicted coding region BB0832 [Borrelia]	1400	4.90E-188
f22.aa	gil2688779	(AE001181) B. burgdorferi predicted coding region BB0832 [Borrelia]	1400	4.90E-188
f221.aa	gil2688596	(AE001167) B. burgdorferi predicted coding region BB0662 [Borrelia]	692	2.60E-93
f229.aa	gil2688591	(AE001167) oxygen-independent coproporphyrinogen III oxidase,	863	7.80E-120
f24-1.aa	gil2039285	putative vls recombination cassette Vls6 [Borrelia burgdorferi]	924	1.80E-114
f24-1.aa	gil2039284	putative vls recombination cassette Vls5 [Borrelia burgdorferi]	867	6.30E-107
f24-1.aa	gil2039287	putative vls recombination cassette Vls8 [Borrelia burgdorferi]	824	1.50E-104
f24-1.aa	gil2039289	putative vls recombination cassette Vls10 [Borrelia burgdorferi]	829	7.50E-102
f24-1.aa	gil2039320	vmp-like sequence protein VlsE [Borrelia burgdorferi]	644	1.10E-98
f24-1.aa	gil2039288	putative vls recombination cassette Vls9 [Borrelia burgdorferi]	783	8.20E-96
f24-1.aa	gil2039330	vmp-like sequence protein VlsE [Borrelia burgdorferi]	742	6.30E-95
f24-1.aa	gil2039336	vmp-like sequence protein VlsE [Borrelia burgdorferi]	509	1.50E-92
f24-1.aa	gil2039286	putative vls recombination cassette Vls7 [Borrelia burgdorferi]	754	6.60E-92
f24-1.aa	gil2039324	vmp-like sequence protein VlsE [Borrelia burgdorferi]	488	8.10E-86
f24-1.aa	gil2039316	vmp-like sequence protein VlsE [Borrelia burgdorferi]	531	1.70E-85
f24-1.aa	gil2039312	vmp-like sequence protein VlsE [Borrelia burgdorferi]	531	1.20E-83
f24-1.aa	gil2039326	vmp-like sequence protein VlsE [Borrelia burgdorferi]	476	2.00E-82
f24-1.aa	gil2039332	vmp-like sequence protein VlsE [Borrelia burgdorferi]	474	5.10E-82
f24-1.aa	gil2039328	vmp-like sequence protein VlsE [Borrelia burgdorferi]	420	3.50E-59

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f253.aa	gi2688567	(AE001165) Na+/H+ antiporter (nhaC-1) [Borrelia burgdorferi]	2247	0
f253.aa	gi2688566	(AE001165) Na+/H+ antiporter (nhaC-2) [Borrelia burgdorferi]	609	6.40E-155
f253.aa	gi2209268	Na+/H+ antiporter [Bacillus firmus] >pirA41594/A41594	158	9.40E-15
f253.aa	gi1574661	Na+/H+ antiporter (nhaC) [Haemophilus influenzae]	143	4.20E-14
f253.aa	gnlPIDle11 85625	similar to Na+/H+ antiporter [Bacillus subtilis]	137	1.20E-11
f253.aa	gnlPIDle32 4972	hypothetical protein [Bacillus subtilis] >gnlPIDle1182969	133	2.00E-11
f265.aa	gi2688555	(AE001164) conserved hypothetical protein [Borrelia burgdorferi]	1196	9.90E-161
f269.aa	gi2688560	(AE001164) B. burgdorferi predicted coding region BB0624 [Borrelia]	1654	5.50E-226
f28-2.aa	gi2690174	(AE000788) B. burgdorferi predicted coding region BBK47 [Borrelia]	1683	2.80E-222
f28-2.aa	gi2690161	(AE000788) B. burgdorferi predicted coding region BBK49 [Borrelia]	1068	2.20E-163
f28-3.aa	gi2690138	(AE000788) immunogenic protein P37, putative [Borrelia burgdorferi]	281	6.00E-48
f28-3.aa	gi2690127	(AE000788) immunogenic protein P37 [Borrelia burgdorferi]	209	3.20E-28
f28-3.aa	gi2459605	immunogenic protein P37 [Borrelia burgdorferi]	208	4.50E-28
f28-3.aa	gi2690137	(AE000788) immunogenic protein P37, putative [Borrelia burgdorferi]	172	5.50E-17
f29.aa	gi2688764	(AE001180) B. burgdorferi predicted coding region BB0826 [Borrelia]	869	8.20E-116
f290.aa	gi2688537	(AE001162) serine-type D-Ala-D-Ala carboxypeptidase (dacA)	2046	1.50E-281
f290.aa	gi143439	DD-carboxypeptidase [Bacillus subtilis] >pirB42708/B42708	161	6.60E-36
f290.aa	gnlPIDle11 85617	D-alanyl-D-alanine carboxypeptidase (penicillin binding	161	6.60E-36
f290.aa	gnlPIDle10 16562	Probable penicillin-binding protein. [Escherichia coli]	131	3.30E-28
f290.aa	spP37604/ DACD_SA LTY	PENICILLIN-BINDING PROTEIN 6B PRECURSOR	135	9.10E-28
f290.aa	gi1572974	penicillin-binding protein 5 (dacA) [Haemophilus influenzae]	145	3.00E-27
f290.aa	gi1580849	D-alanine carboxypeptidase [Bacillus stearothermophilus]	170	4.10E-27
f290.aa	gi1778549	penicillin-binding protein 5 [Escherichia coli] >gi141212 precursor	152	3.20E-26
f290.aa	gi142820	penicillin-binding protein 5 [Bacillus subtilis]	137	4.60E-26
f290.aa	gi1410134	penicillin-binding protein [Bacillus subtilis] >gnlPIDle1185588	137	4.60E-26
f290.aa	gi141218	precursor [Escherichia coli]	136	1.30E-25

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f290.aa	gnlPIDd10 15262	Penicillin-binding protein 6 precursor (D-alanyl-D-alanine	136	1.30E-25
f290.aa	gil1864022	penicillin binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f290.aa	gnlPIDle15 4145	penicillin binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f290.aa	gnlPIDle26 4682	penicillin-binding protein 4 [Staphylococcus aureus]	155	5.10E-22
f291.aa	gil2688538	(AE001162) L-lactate permease (lctP) [Borrelia burgdorferi]	2473	0
f291.aa	gnlPIDle27 4704	lactate permease [Streptococcus iniae]	586	1.20E-132
f291.aa	gil882504	ORF_f560 [Escherichia coli] >gil1789347 (AE000380) f560; This 560 aa	345	3.60E-95
f291.aa	gil2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori]	359	1.10E-94
f291.aa	gil2313224	(AE000535) L-lactate permease (lctP) [Helicobacter pylori]	348	2.90E-93
f291.aa	gil404693	L-lactate permease [Escherichia coli] >gil466741 aug is 3rd start	331	7.20E-82
f291.aa	gnlPIDle31 3006	hypothetical protein [Bacillus subtilis] >gnlPIDle1186107	330	9.00E-80
f291.aa	gnlPIDd10 22632	lactate permease [Bacillus subtilis]	300	1.70E-61
f291.aa	gnlPIDle11 82258	L-lactate permease [Bacillus subtilis] >pirF69649F69649	300	1.10E-60
f291.aa	gnlPIDd10 09575	homologue of L-lactate permease of E. coli [Bacillus	265	6.40E-56
f291.aa	gil2649804	(AE001049) L-lactate permease (lctP) [Archaeoglobus fulgidus]	170	1.50E-47
f291.aa	gnlPIDle28 3914	L-lactate permease [Sulfolobus solfataricus]	163	2.60E-44
f291.aa	gil1574148	L-lactate permease (lctP) [Haemophilus influenzae]	173	6.00E-35
f296.aa	gil2688517	(AE001161) chaperonin, putative [Borrelia burgdorferi]	1276	4.40E-177
f296.aa	gil840643	mucZ gene product [Coxiella burnetii] >pir140852I40852 mucZ	101	7.90E-12
f3.aa	gil2688797	(AE001183) B. burgdorferi predicted coding region BB0844 [Borrelia	1604	1.40E-211
f30.aa	gil2688765	(AE001180) B. burgdorferi predicted coding region BB0825 [Borrelia	1343	2.00E-181
f301.aa	gil2688521	(AE001161) methyl-accepting chemotaxis protein (mcp-3) [Borrelia	2756	0
f301.aa	gil1805311	methyl-accepting chemotaxis protein B [Treponema denticola]	211	7.00E-20



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f301.aa	gil2688522	(AE001161) methyl-accepting chemotaxis protein (mcp-2) [Borrelia	189	2.80E-18
f301.aa	gil2367665	(AF016689) Mcp-2 [Treponema pallidum]	189	3.50E-17
f301.aa	gil2352917	(AF012922) methyl-accepting chemotaxis protein [Treponema	187	5.70E-17
f301.aa	gil1354776	MCP-1 [Treponema pallidum]	189	5.90E-17
f301.aa	gil2619023	(AF027868) YoaH [Bacillus subtilis] >gnlPIDle1185333 similar to	184	2.80E-16
f301.aa	gil1654421	transducer HtB protein [Halobacterium salinarum]	177	2.20E-15
f301.aa	gil415694	chemoreceptor [Desulfovibrio vulgaris] >pirG36943IG36943	163	3.50E-15
f301.aa	gil459691	transmembrane receptor [Bacillus subtilis] >gnlPIDle1185996	163	4.90E-15
f301.aa	gil2104730	ORF2 [Desulfurococcus sp. SY]	173	5.80E-15
f301.aa	gil2914132	methyl accepting chemotaxis homolog [Treponema denticola]	170	1.10E-14
f301.aa	gil459689	transmembrane receptor [Bacillus subtilis] >gnlPIDle1185998	164	1.30E-14
f301.aa	gil496484	tlpC gene product [Bacillus subtilis] >pirI40496I40496 methylation	170	3.80E-14
f301.aa	gil2313163	(AE000530) methyl-accepting chemotaxis transducer (tlpC)	170	6.30E-14
f308.aa	gil2688527	(AE001161) B. burgdorferi predicted coding region BB0592 [Borrelia	1227	1.70E-176
f31-2.aa	gil2690202	(AE000787) B. burgdorferi predicted coding region BB136 [Borrelia	1771	7.20E-235
f31-2.aa	gil2690200	(AE000787) B. burgdorferi predicted coding region BB134 [Borrelia	423	4.60E-88
f31.aa	gil2688766	(AE001180) B. burgdorferi predicted coding region BB0824 [Borrelia	957	7.80E-133
f314.aa	gil2688509	(AE001160) pfs protein (pfs-2) [Borrelia burgdorferi]	1329	7.40E-180
f314.aa	gil2690087	(AE000789) pfs protein (pfs) [Borrelia burgdorferi]	335	1.50E-77
f314.aa	gil2688288	(AE001143) pfs protein (pfs-1) [Borrelia burgdorferi]	266	1.00E-65
f314.aa	gil2738591	(AF012886) Pfs [Buchnera aphidicola]	115	1.70E-52
f314.aa	gil1552737	similar to purine nucleoside phosphorylase (deoD) [Escherichia	133	6.90E-52
f314.aa	gnlPIDle11	similar to purine nucleoside phosphorylase [Bacillus	157	1.20E-49
	83957			
f314.aa	gil147158	pfs [Escherichia coli] >gil457107 ORF [Escherichia coli] {SUB 9-219}	133	2.50E-42
f314.aa	gil1574146	pfs protein (pfs) [Haemophilus influenzae] >pirC64169IC64169 pfs	110	2.70E-37
f314.aa	gil2267164	(AF009177) pfs protein homolog [Helicobacter pylori]	118	3.30E-23
f314.aa	gil2313168	(AE000530) pfs protein (pfs) [Helicobacter pylori]	115	1.00E-22
f314.aa	gil1777939	Pfs [Treponema pallidum]	102	1.90E-20
f314.aa	gil2689970	(AE000785) B. burgdorferi predicted coding region BBE07 [Borrelia	191	1.50E-19
f314.aa	gnlPIDle24	unknown [Mycobacterium tuberculosis] >sp Q10889 Y05A_MYCTU	105	7.60E-16



f32-4.aa	gil2690221	(AE000787) B. burgdorferi predicted coding region BBJ47 [Borrelia	1192	4.00E-163
f32-4.aa	gil2689979	(AE000785) B. burgdorferi predicted coding region BBE16 [Borrelia	103	4.10E-11
f32.aa	gil2688767	(AE001180) B. burgdorferi predicted coding region BB0823 [Borrelia	623	1.80E-81
f32.aa	gil2688767	(AE001180) B. burgdorferi predicted coding region BB0823 [Borrelia	623	1.80E-81
f320.aa	gil2688497	(AE001159) carboxypeptidase, putative [Borrelia burgdorferi]	1373	6.40E-186
f320.aa	gil2529473	(AF006665) YokZ [Bacillus subtilis]	136	9.80E-28
f320.aa	gil2415396	(AF015775) carboxypeptidase [Bacillus subtilis] >gnlPIDle1185433	136	1.90E-27
f320.aa	gil1209528	D,D-carboxypeptidase [Enterococcus faecalis] >spIQ47746VANY_ENTFA	148	3.30E-16
f320.aa	gil155044	van Y [Transposon Tn1546] >gil149126 D,D-carboxypeptidase [Plasmid	142	1.60E-13
f328.aa	gil2688502	(AE001159) CTP synthase (pyrG) [Borrelia burgdorferi]	869	6.10E-119
f328.aa	gil1591801	CTP synthase (pyrG) [Methanococcus jannaschii] >pirE644461E64446	325	6.20E-59
f328.aa	gil2650385	(AE001088) CTP synthase (pyrG) [Archaeoglobus fulgidus]	304	4.20E-54
f328.aa	gil1399854	CTP synthetase [Synechococcus PCC7942] >spiQ54775IPYRG_SYNP7 CTP	313	3.30E-52
f328.aa	gnlPIDld10 19032	CTP synthetase [Synechocystis sp.] >pirS75840IS75840 CTP	295	1.80E-50
f328.aa	gil143597	CTP synthetase [Bacillus subtilis] >gil853762 CTP synthase [Bacillus	274	1.60E-49
f328.aa	gil2983754	(AE000735) CTP synthetase [Aquifex aeolicus]	271	1.50E-46
f328.aa	gil1574630	CTP synthetase (pyrG) [Haemophilus influenzae] >pirF64181IF64181	234	1.90E-44
f328.aa	gil413755	CTP synthetase [Spiroplasma citri] >spiP52200IPYRG_SPICI CTP	231	3.00E-44
f328.aa	gil2621483	(AE000826) CTP synthase [Methanobacterium thermoautotrophicum]	257	2.80E-40
f328.aa	gil950067	CTP synthase [Mycoplasma capricolum] >pirS77767IS77767 CTP synthase	220	4.10E-39
f328.aa	gil904007	cytidine triphosphate synthetase precursor [Giardia intestinalis]	219	2.00E-38
f328.aa	gil147478	CTP synthetase (EC 6.3.4.2) [Escherichia coli]	217	2.90E-38
f328.aa	gil882674	CTP synthetase [Escherichia coli] >gil1789142 (AE000361) CTP	214	7.70E-38
f328.aa	gil38688	CTP synthase [Azospirillum brasilense] >pirI39496IS25101 CTP	132	3.20E-37
f342.aa	gil2688495	(AE001158) B. burgdorferi predicted coding region BB0563 [Borrelia	944	5.30E-130
f346.aa	gil1272356	phosphotransferase enzyme II [Borrelia burgdorferi] >gil2688474	828	1.10E-108

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f346.aa	gil145603	PTS enzyme III glc [Escherichia coli] >gil145605 PTS enzyme III glc	385	8.80E-53
f346.aa	gil1314675	glucose-specific component IIA of the PTS system [Escherichia coli]	385	9.30E-53
f346.aa	gil47658	III(Glc) (crr) (AA 1 - 169) [Salmonella typhimurium]	382	2.30E-52
f346.aa	gil1574566	glucose phosphotransferase enzyme III-glc (crr) [Haemophilus]	397	8.70E-50
f346.aa	gil43819	nagE gene product [Klebsiella pneumoniae] >pir1S18607/S18607	349	2.80E-41
f346.aa	gil146913	N-acetylglucosamine transport protein [Escherichia coli]	334	3.20E-39
f346.aa	gil1072418	glcA [Staphylococcus carnosus] >pirS46952/S46952	317	7.20E-37
f346.aa	gil1072419	glcB [Staphylococcus carnosus] >pirS63606/S46953	315	1.40E-36
f346.aa	gil1146177	phosphotransferase system glucose-specific enzyme II [Bacillus]	295	7.30E-36
f346.aa	gil529001	PTS glucose-specific permease [Bacillus stearothermophilus]	294	8.80E-36
f346.aa	gnlPIDle11 82187	alternate gene name: yzfA; similar to phosphotransferase	293	1.40E-33
f346.aa	gil580912	enzyme III-glucose [Bacillus subtilis]	257	1.20E-30
f346.aa	gil602681	phosphocarrier protein (enzyme IIA) [Mycoplasma capricolum]	243	1.00E-28
f346.aa	gil1432153	cellobiose-specific PTS permease [Klebsiella oxytoca]	257	1.20E-28
f352.aa	gil2688482	(AE001157) B. burgdorferi predicted coding region BB0553 [Borrelia]	2547	0
f352.aa	gil2688482	(AE001157) B. burgdorferi predicted coding region BB0553 [Borrelia]	1005	1.30E-132
f363.aa	gil2688468	(AE001156) B. burgdorferi predicted coding region BB0543 [Borrelia]	1109	5.40E-153
f368.aa	gil2688450	(AE001155) conserved hypothetical integral membrane protein	1133	4.10E-157
f368.aa	gil1787004	(AE000181) o234; This 234 aa ORF is 26 pct identical (15 gaps) to	417	1.40E-67
f368.aa	gil2314055	(AE000601) conserved hypothetical integral membrane protein	129	3.50E-16
f368.aa	gnlPIDle12 89272	S1R [Cowpox virus]	135	1.80E-14
f368.aa	gnlPIDid10 03176	24K membrane protein [Pseudomonas aeruginosa]	108	9.00E-13
f368.aa	gil41284	put. 23.5-kd protein [Escherichia coli] >gil1787205 (AE000199)	101	1.00E-11
f371.aa	gil2688452	(AE001155) conserved hypothetical protein [Borrelia burgdorferi]	1066	3.60E-143
f371.aa	gil2196997	Orf256 [Treponema pallidum]	154	1.10E-15
f373.aa	gil2688453	(AE001155) zinc protease, putative [Borrelia burgdorferi]	3663	0
f373.aa	gil1574200	hypothetical [Haemophilus influenzae] >pirE64171/E64171	295	2.70E-67
f373.aa	gil1787770	(AE000246) f931; residues 5-650 are 99 pct identical to YDDC_ECOLI	289	1.10E-57

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f373.aa	gil535004	cds106 gene product [Escherichia coli]	289	3.20E-57
f373.aa	gil799369	metalloendopeptidase [Pisum sativum]	148	7.10E-28
f373.aa	gil2827039	(AF008444) chloroplast processing enzyme [Arabidopsis thaliana]	150	1.70E-26
f373.aa	gil2983709	(AE000732) processing protease [Aquifex aeolicus]	136	4.30E-24
f373.aa	gil2314155	(AE000609) protease (pqgE) [Helicobacter pylori] >pirID64646ID64646	115	5.30E-23
f378.aa	gil2688458	(AE001155) B. burgdorferi predicted coding region BB0531 [Borrelia burgdorferi]	1030	1.30E-136
f384.aa	gil2688435	(AE001154) inositol monophosphatase [Borrelia burgdorferi]	1470	3.80E-201
f4-15.aa	gil2690238	(AE000790) surface lipoprotein P27 [Borrelia burgdorferi]	1400	1.50E-185
f4-15.aa	gil144008	P27 [Borrelia burgdorferi] >pirIS34995IS34995 surface lipoprotein	462	2.40E-96
f4-50.aa	gil2690243	(AE000790) decorin binding protein B (dbpB) [Borrelia burgdorferi]	900	6.30E-117
f4-50.aa	gil2062381	decorin binding protein B [Borrelia burgdorferi]	897	1.60E-116
f4-50.aa	gil2809217	(AF042796) putative decorin-binding protein precursor [Borrelia burgdorferi]	887	3.60E-115
f4-50.aa	gil2809218	(AF042796) decorin-binding protein precursor [Borrelia burgdorferi]	172	2.00E-33
f4-50.aa	gil2690249	(AE000790) decorin binding protein A (dbpA) [Borrelia burgdorferi]	176	9.50E-33
f4-50.aa	gil2062379	decorin binding protein A [Borrelia burgdorferi]	177	6.10E-32
f4-66.aa	gil2690229	(AE000790) chpA protein, putative [Borrelia burgdorferi]	807	1.60E-107
f4.aa	gil2688787	(AE001183) conserved hypothetical integral membrane protein	2408	0
f4.aa	gil2697115	(AF008219) unknown [Borrelia afzelii]	1138	1.90E-305
f4.aa	gil1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	337	2.10E-109
f4.aa	gil1788636	(AE000319) o513; This 513 aa ORF is 31 pct identical (30 gaps) to	327	9.10E-80
f4.aa	gnlPID1d1009571	homologue of hypothetical protein HI0594 of H. influenzae	357	5.40E-69
f42-1.aa	gil2689993	(AE000794) conserved hypothetical protein [Borrelia burgdorferi]	495	2.70E-62
f42-1.aa	gil2689934	(AE000793) conserved hypothetical protein [Borrelia burgdorferi]	312	1.00E-37
f43-3.aa	gil1209843	lipoprotein [Borrelia burgdorferi]	546	1.50E-69
f43-3.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	442	1.80E-55
f43-3.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	365	3.10E-55
f43-3.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	269	5.30E-32
f43-3.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	141	1.70E-13
f43-3.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	140	9.60E-13
f43-3.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	132	1.40E-11

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f43.aa	gil2688752	(AE001179) B. burgdorferi predicted coding region BB0811 [Borrelia]	2337	6.60000000
				084856e-315
f446.aa	gil2688383	(AE001151) B. burgdorferi predicted coding region BB0464 [Borrelia]	920	7.20E-124
f45-2.aa	gil1699017	ErpB2 [Borrelia burgdorferi] >gil1373133 ErpB [Borrelia]	364	7.50E-78
f45-2.aa	gil2627270	ErpJ [Borrelia burgdorferi]	364	2.50E-77
f45-2.aa	gil2627268	ErpM [Borrelia burgdorferi]	452	9.70E-60
f45-2.aa	gil1373144	ErpD [Borrelia burgdorferi]	316	1.60E-58
f45-2.aa	gil2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	380	2.80E-55
f45-2.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	213	7.10E-35
f45-2.aa	gil1663633	ErpK [Borrelia burgdorferi]	152	1.60E-21
f45-2.aa	gnlPIDle32	(AJ000496) cyclic nucleotide-gated channel beta subunit	198	2.80E-16
	9895			
f45-2.aa	gil466482	outer surface protein F [Borrelia burgdorferi] >pir140287/140287	111	5.70E-14
f45-2.aa	gil2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	174	5.90E-14
f45-2.aa	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	169	1.00E-13
f45-2.aa	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	101	2.20E-13
f45-2.aa	gil1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated	175	4.10E-13
f45-2.aa	gnlPIDld10	gene required for phosphorylation of oligosaccharides/ has	166	5.60E-13
	12343			
f45-2.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BB116 [Borrelia]	161	2.70E-12
f457.aa	gil2688369	(AE001150) B. burgdorferi predicted coding region BB0456 [Borrelia]	1021	6.20E-139
f469.aa	gil2688368	(AE001150) Na+/H+ antiporter (napA) [Borrelia burgdorferi]	1544	1.10E-211
f47-2.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	742	2.30E-97
f47-2.aa	gil1209857	lipoprotein [Borrelia burgdorferi]	407	7.80E-86
f47-2.aa	gil1209831	lipoprotein [Borrelia burgdorferi]	393	5.00E-82
f47-2.aa	gnlPIDle26	surface-exposed lipoprotein [Borrelia burgdorferi]	321	2.60E-73
	8245			
f47-2.aa	gil1209874	lipoprotein [Borrelia burgdorferi]	348	1.10E-64
f47-2.aa	gnlPIDle26	surface-exposed lipoprotein [Borrelia garinii]	333	1.40E-57
	8239			
f47-2.aa	gnlPIDle26	surface-exposed lipoprotein [Borrelia afzelii]	292	9.60E-44

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	8244				
f47-2.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]		328	3.80E-40
f47-2.aa	gnlPIDle26 8242	surface-exposed lipoprotein [Borrelia garinii]		320	1.70E-39
f47-2.aa	gil1209837	lipoprotein [Borrelia burgdorferi]		210	4.80E-29
f47-2.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109		205	1.10E-27
f47-2.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]		217	6.30E-25
f47-2.aa	gil1209873	lipoprotein [Borrelia burgdorferi]		113	2.40E-11
f477.aa	gil2688350	(AE001149) fructose-bisphosphate aldolase (fba) [Borrelia]		1506	3.60E-202
f477.aa	gil882454	fructose 1,6-bisphosphate aldolase [Escherichia coli] >gil41423		651	1.10E-131
f477.aa	gil2708661	(AF037440) fructose 1,6-bisphosphate aldolase [Edwardsiella]		593	1.40E-124
f477.aa	gil1573507	fructose-bisphosphate aldolase (fba) [Haemophilus influenzae]		560	8.50E-120
f477.aa	gil671841	fructose 1,6-bisphosphate aldolase [Campylobacter jejuni]		856	3.80E-113
f477.aa	gnlPIDld10 04756	fructose 1,6-bisphosphate aldolase [Schizosaccharomyces]		749	1.70E-98
f477.aa	gil433637	yeast fructose-bisphosphate-aldolase [Saccharomyces cerevisiae] >gil3696		459	1.20E-92
f477.aa	gnlPIDle19 0134	fructose-1,6-bisphosphate aldolase [Euglena gracilis]		701	6.30E-92
f477.aa	gil1334980	fructose 1,6 bisphosphate-aldolase [Neurospora crassa]		647	1.50E-84
f477.aa	gil40495	fructose-bisphosphate aldolase [Corynebacterium glutamicum]		204	6.80E-37
f477.aa	gnlPIDle31 5480	Fba [Mycobacterium tuberculosis]		207	1.50E-35
f477.aa	gil1045692	fructose-bisphosphate aldolase [Mycoplasma genitalium]		108	2.10E-23
f477.aa	gnlPIDld10 03809	hypothetical protein [Bacillus subtilis] >gnlPIDle1184692		102	2.70E-15
f488.aa	gil2688338	(AE001148) DNA gyrase, subunit A (gyrA) [Borrelia burgdorferi]		3222	0
f488.aa	gil1790876	DNA gyrase subunit A [Clostridium acetobutylicum]		822	1.80E-171
f488.aa	gil2650163	(AE001072) DNA gyrase, subunit A (gyrA) [Archaeoglobus fulgidus]		483	1.10E-162
f488.aa	gil40019	ORF 821 (aa 1-821) [Bacillus subtilis] >gnlPIDld1005785 A subunit of		836	6.10E-159
f488.aa	gil459929	gyrase A subunit [Pseudomonas aeruginosa] >splP48372GYRA_PSEAE DNA		418	7.00E-155
f488.aa	gil144206	DNA gyrase A [Campylobacter jejuni] >pirA48902A48902 DNA gyrase		508	7.50E-154

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f488.aa	gil466275	gyrase A [Mycobacterium tuberculosis] >sp Q07702 GYRA_MYCTU DNA	395	3.50E-152
f488.aa	gnllPIDle266924	GyrA [Mycobacterium tuberculosis]	395	2.00E-151
f488.aa	gil43485	DNA gyrase A subunit [Haloferax] >pirIS30571 S30571 DNA topoisomerase	275	6.10E-151
f488.aa	gnllPIDle1025098	(AB010081) A subunit of DNA gyrase [Bacillus sp.]	549	1.20E-150
f488.aa	gnllPIDle214031	DNA gyrase subunit A [Mycobacterium smegmatis]	388	5.90E-150
f488.aa	gil2731385	DNA gyrase [Serratia marcescens]	378	6.00E-148
f488.aa	gnllPIDle137038	DNA topoisomerase (ATP-hydrolysing) [Mycobacterium smegmatis]	388	7.30E-147
f488.aa	gil41634	gyrA gene product (AA 1-875) [Escherichia coli] >gil41636 DNA gyrase	383	2.40E-146
f488.aa	gil497648	DNA gyrase subunit A [Mycoplasma genitalium]	514	5.20E-146
f49-2.aa	gil2039282	putative vls recombination cassette Vls3 [Borrelia burgdorferi]	943	2.30E-120
f49-2.aa	gil2547241	vmp-like sequence protein VlsE [Borrelia burgdorferi]	434	4.10E-106
f49-2.aa	gil2039324	vmp-like sequence protein VlsE [Borrelia burgdorferi]	458	3.00E-104
f49-2.aa	gil2039281	putative vls recombination cassette Vls2 [Borrelia burgdorferi]	793	1.80E-100
f49-2.aa	gil2039283	putative vls recombination cassette Vls4 [Borrelia burgdorferi]	729	4.60E-92
f49-2.aa	gil2039308	vmp-like sequence protein VlsE [Borrelia burgdorferi]	652	1.40E-88
f49-2.aa	gil2039288	putative vls recombination cassette Vls9 [Borrelia burgdorferi]	352	1.80E-88
f49-2.aa	gil2039332	vmp-like sequence protein VlsE [Borrelia burgdorferi]	550	4.40E-88
f49-2.aa	gil2039328	vmp-like sequence protein VlsE [Borrelia burgdorferi]	629	1.50E-85
f49-2.aa	gil2039336	vmp-like sequence protein VlsE [Borrelia burgdorferi]	460	1.40E-82
f49-2.aa	gil2039318	vmp-like sequence protein VlsE [Borrelia burgdorferi]	367	6.20E-82
f49-2.aa	gil2039320	vmp-like sequence protein VlsE [Borrelia burgdorferi]	449	1.80E-77
f49-2.aa	gil2483796	VlsE1 [Borrelia burgdorferi]	497	8.20E-76
f49-2.aa	gil2039326	vmp-like sequence protein VlsE [Borrelia burgdorferi]	427	2.50E-64
f49-2.aa	gil2039291	putative vls recombination cassette Vls13 [Borrelia burgdorferi]	409	1.30E-47
f494.aa	gil2688346	(AE001148) B. burgdorferi predicted coding region BB0428 [Borrelia]	547	8.20E-74
f5-14.aa	gil2627268	ErpM [Borrelia burgdorferi]	1836	2.60E-236

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f5-14.aa	gil1373144	ErpD [Borrelia burgdorferi]	543	4.40E-87
f5-14.aa	gil2627270	ErpJ [Borrelia burgdorferi]	503	4.30E-83
f5-14.aa	gil1699017	ErpB2 [Borrelia burgdorferi] >gil1373133 ErpB [Borrelia burgdorferi]	503	2.60E-82
f5-14.aa	gil2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	399	9.30E-57
f5-14.aa	gnlPIDle32 9895	(AJ000496) cyclic nucleotide-gated channel beta subunit	228	1.50E-20
f5-14.aa	gnlPIDld10 12343	gene required for phosphorylation of oligosaccharides/ has	203	8.70E-18
f5-14.aa	gil2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	197	3.30E-17
f5-14.aa	gil1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated	192	1.20E-16
f5-14.aa	gil3068583	(AF000580) Rep-like [Dictyostelium discoideum]	197	3.60E-16
f5-14.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia	183	2.90E-15
f5-14.aa	gil1825739	No definition line found [Caenorhabditis elegans]	168	1.60E-14
f5-14.aa	gil3044185	(AF056936) mature parasite-infected erythrocyte surface antigen	166	2.00E-14
f5-14.aa	gnlPIDle34 9084	E02A10.2 [Caenorhabditis elegans]	176	2.30E-14
f5-14.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	157	3.30E-12
f5-15.aa	gil2627267	ErpL [Borrelia burgdorferi]	1152	4.40E-147
f5-15.aa	gil197833	Bbk2.11 [Borrelia burgdorferi] >pirS70531S70531 bbk2.11 protein	856	3.30E-108
f5-15.aa	gil896042	OspF [Borrelia burgdorferi] >pirS70532S70532 outer surface protein	325	1.00E-72
f5-15.aa	gil1707281	putative outer membrane protein [Borrelia burgdorferi]	323	1.80E-72
f5-15.aa	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	322	6.60E-70
f5-15.aa	gil466482	outer surface protein F [Borrelia burgdorferi] >pir140287140287	448	6.80E-68
f5-15.aa	gil1707290	putative outer surface protein [Borrelia burgdorferi]	290	1.90E-52
f5-15.aa	gil1663633	ErpK [Borrelia burgdorferi]	172	8.70E-43
f5-15.aa	gil896038	Bbk2.10 precursor [Borrelia burgdorferi] >pirS70534S70534 bbk2.10	153	1.10E-42
f5-15.aa	gil896040	Bbk2.10 precursor [Borrelia burgdorferi] >pirS70533S70533 bbk2.10	124	4.30E-39
f5-15.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	105	3.10E-23
f5-15.aa	gil1373144	ErpD [Borrelia burgdorferi]	103	1.10E-14
f50.aa	gil2688754	(AE001179) B. burgdorferi predicted coding region BB0806 [Borrelia	2651	0
f502.aa	gil2688313	(AF001146) sensory transduction histidine kinase, putative	7570	0



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f502.aa	gnllPID1d10 25877	(AB006363) homologue of histidine kinase [Candida albicans]	296	3.80E-58
f502.aa	gil1354473	Os-1p [Neurospora crassa]	275	3.30E-57
f502.aa	gil1679757	two-component histidine kinase CHK-1 [Glomerella cingulata]	382	4.20E-57
f502.aa	gil1262208	Nik-1 [Neurospora crassa] >gil1262210 Nik-1 [Neurospora crassa]	273	6.30E-57
f502.aa	gil2460283	(AF024654) hybrid histidine kinase DHKB [Dictyostelium discoideum]	273	3.90E-55
f502.aa	gnllPID1d10 17789	sensory transduction histidine kinase [Synechocystis sp.]	288	8.50E-54
f502.aa	gil2623815	(AF030352) two component sensor [Pseudomonas aeruginosa]	252	4.00E-52
f502.aa	gil939724	putative sensor kinase; regulatory protein for production of	252	1.80E-50
f502.aa	gil151329	regulatory protein [Pseudomonas syringae] >spIP48027/LEMA_PSESY	248	1.20E-49
f502.aa	pirB41863 B41863	two-component regulatory protein lemA - Pseudomonas syringae	248	1.30E-49
f502.aa	gnllPID1d10 18725	sensory transduction histidine kinase [Synechocystis sp.]	252	2.10E-49
f502.aa	gnllPID1d10 02185	sensor-regulator protein [Escherichia coli] >gil1789149	262	6.20E-49
f502.aa	gil463195	pectate lyase [Pseudomonas viridiflava]	247	7.50E-49
f502.aa	gnllPID1d10 18731	sensory transduction histidine kinase [Synechocystis sp.]	244	1.00E-48
f51-2.aa	gil2444428	(AF020657) ErpX protein [Borrelia burgdorferi]	1755	2.20E-227
f51-2.aa	gil2627268	ErpM [Borrelia burgdorferi]	399	3.20E-57
f51-2.aa	gil1373144	ErpD [Borrelia burgdorferi]	282	2.20E-50
f51-2.aa	gil2627270	ErpJ [Borrelia burgdorferi]	271	6.00E-34
f51-2.aa	gil1699017	ErpB2 [Borrelia burgdorferi] >gil1373133 ErpB [Borrelia	271	2.50E-33
f51-2.aa	gil1051120	outer surface protein G [Borrelia burgdorferi] >gil1373118 ErpG	109	3.70E-22
f51-2.aa	gnllPID1d10 12343	gene required for phosphorylation of oligosaccharides/ has	203	5.40E-18
f51-2.aa	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	111	7.50E-18
f51-2.aa	gil896042	OspF [Borrelia burgdorferi] >pirS70532/S70532 outer surface protein	111	2.10E-17
f51-2.aa	gil1707281	putative outer membrane protein [Borrelia burgdorferi]	111	7.50E-17
f51-2.aa	gnllPID1e32	(AJ000496) cyclic nucleotide-gated channel beta subunit	198	1.60E-16

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	9895			
f51-2.aa	gil2246532	ORF 73, contains large complex repeat CR 73 [Kaposi's	176	2.30E-14
f51-2.aa	gnllPIDle34 9084	E02A10.2 [Caenorhabditis elegans]	170	2.10E-13
f51-2.aa	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	157	7.30E-12
f516.aa	gil2688326	(AE001146) B. burgdorferi predicted coding region BB0409 [Borrelia	1096	2.00E-150
f517.aa	gil2688320	(AE001146) PTS system, fructose-specific IIBC component (fruA-1)	1637	2.30E-228
f517.aa	gnllPIDle11 83221	similar to fructose phosphotransferase system enzyme II	256	4.00E-88
f517.aa	gil396296	similar to phosphotransferase system enzyme II [Escherichia coli]	305	9.10E-86
f517.aa	gil405893	fructose-specific IIBC component [Escherichia coli] >gil450372	224	4.30E-84
f517.aa	gil151932	fructose enzyme II [Rhodobacter capsulatus] >gil46021 fructose	222	4.70E-79
f517.aa	gil1573422	fructose-permease IIBC component (fruA) [Haemophilus influenzae]	225	6.90E-69
f517.aa	gil2688554	(AE001164) PTS system, fructose-specific IIBC component (fruA-2)	236	8.20E-66
f517.aa	gnllPIDle11 85030	phosphotransferase system (PTS) fructose-specific enzyme IIBC	195	2.80E-65
f517.aa	gil155369	PTS enzyme-II fructose [Xanthomonas campestris] >pirIB40944 B40944	187	8.10E-62
f517.aa	gil305003	similar to fructose-specific phosphotransferase enzyme II	145	1.90E-39
f517.aa	gnllPIDid10 11544	HrsA [Escherichia coli] >gil1786951 (AE0000176)	148	2.80E-39
f517.aa	gil1813488	phosphotransferase enzyme II [Bacillus firmus]	226	3.90E-39
f517.aa	gil757734	fruA gene product [Bacillus amyloliquefaciens] >pirS59965 S59965	177	2.50E-36
f517.aa	gnllPIDid10 16984	PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU)	173	1.10E-34
f517.aa	gil1673731	(AE0000010) Mycoplasma pneumoniae, fructose-permease IIBC component;	143	9.00E-33
f519.aa	gil2688327	(AE001146) B. burgdorferi predicted coding region BB0406 [Borrelia	1060	5.70E-145
f519.aa	gil2688328	(AE001146) B. burgdorferi predicted coding region BB0405 [Borrelia	261	1.20E-47
f520.aa	gil2688328	(AE001146) B. burgdorferi predicted coding region BB0405 [Borrelia	1022	3.90E-138
f520.aa	gil2688327	(AE001146) B. burgdorferi predicted coding region BB0406 [Borrelia	261	4.00E-47
f523.aa	gil2688300	(AE001145) glutamate transporter, putative [Borrelia burgdorferi]	2007	9.90E-284
f526.aa	gil2688309	(AE001145) B. burgdorferi predicted coding region BB0399 [Borrelia	1087	1.60E-145

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f527.aa	gil2688310	(AE001145) B. burgdorferi predicted coding region BB0398 [Borrelia	1814	7.60E-249
f541.aa	gil508421	antigen P39 [Borrelia burgdorferi] >gil2688281 (AE001143) basic	1706	5.40E-230
f541.aa	gil1753225	BmpA protein [Borrelia burgdorferi]	1698	6.80E-229
f541.aa	gnllPIDle11 72833	bmpA(p39,ORF1) [Borrelia burgdorferi]	1695	1.70E-228
f541.aa	gnllPIDle11 72835	membrane protein A [Borrelia burgdorferi] >gil516592 membrane	1642	3.40E-221
f541.aa	gnllPIDle11 72834	membrane protein A [Borrelia burgdorferi]	1638	1.20E-220
f541.aa	gnllPIDle11 72828	bmpA(p39,ORF1) [Borrelia burgdorferi]	1551	1.00E-208
f541.aa	gnllPIDle11 72829	membrane protein A [Borrelia afzelii]	1502	5.60E-202
f541.aa	gnllPIDle11 72831	membrane protein A [Borrelia afzelii]	1499	1.40E-201
f541.aa	gnllPIDle11 72837	membrane protein A [Borrelia garinii]	1496	3.70E-201
f541.aa	gnllPIDle11 72830	membrane protein A [Borrelia afzelii]	1493	9.60E-201
f541.aa	gnllPIDle11 72838	membrane protein A [Borrelia garinii]	1488	4.60E-200
f541.aa	gnllPIDle23 7214	membrane protein A [Borrelia garinii]	1216	1.20E-162
f541.aa	gnllPIDle23 7209	membrane protein A [Borrelia garinii]	1211	5.90E-162
f541.aa	gnllPIDle23 7236	membrane protein A [Borrelia garinii]	1098	2.00E-146
f541.aa	gil2688282	(AE001143) basic membrane protein B (bmpB) [Borrelia burgdorferi]	518	1.20E-123
f542.aa	gil508422	[Borrelia burgdorferi immunodominant antigen P39 gene, complete	711	1.70E-95
f542.aa	gil2688282	(AE001143) basic membrane protein B (bmpB) [Borrelia burgdorferi]	711	1.70E-95
f542.aa	gil551744	membrane lipoprotein [Borrelia burgdorferi]	708	8.60E-95
f542.aa	gnllPIDle11	bmpB(p39,ORF2) [Borrelia burgdorferi]	699	8.20E-94

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	72836				
f542.aa	gnllPIDle11 72832	bmpB(p39,ORF2) [Borrelia afzelii]	634		1.00E-84
f542.aa	gnllPIDle11 72839	bmpB(p39,ORF2) [Borrelia garinii]	613		9.20E-82
f542.aa	gnllPIDle23 7209	membrane protein A [Borrelia garinii]	153		1.70E-32
f542.aa	gnllPIDle11 72828	bmpA(p39,ORF1) [Borrelia burgdorferi]	144		3.80E-32
f542.aa	gnllPIDle23 7214	membrane protein A [Borrelia garinii]	153		2.00E-31
f542.aa	gil1753225	BmpA protein [Borrelia burgdorferi]	155		2.80E-31
f542.aa	gnllPIDle11 72833	bmpA(p39,ORF1) [Borrelia burgdorferi]	155		2.80E-31
f542.aa	gil508421	antigen P39 [Borrelia burgdorferi] >gil2688281 (AE001143) basic	155		2.80E-31
f542.aa	gnllPIDle11 72837	membrane protein A [Borrelia garinii]	156		1.00E-30
f542.aa	gnllPIDle11 72829	membrane protein A [Borrelia afzelii]	144		1.90E-30
f542.aa	gnllPIDle11 72830	membrane protein A [Borrelia afzelii]	144		2.70E-30
f544.aa	gil2688284	(AE001143) Mg2+ transport protein (mgE) [Borrelia burgdorferi]	860		4.20E-119
f544.aa	gil1753228	MgtE [Borrelia burgdorferi]	855		2.20E-118
f544.aa	gil619724	MgtE [Bacillus firmus] >pir140201140201 mgE protein - Bacillus	176		3.70E-37
f544.aa	gil780282	extended ORF of mgE gene; transcription from this start point is	182		1.30E-34
f544.aa	gnllPIDle31 5479	unknown [Mycobacterium tuberculosis]	183		4.50E-31
f544.aa	gnllPIDle10 18132	Mg2+ transporter [Synecocystis sp.] >pir1775521S77552 Mg2+	165		4.60E-31
f544.aa	gnllPIDle11 81529	(AJ002571) YkoK [Bacillus subtilis] >gnllPIDle1183350 similar	142		2.30E-30
f544.aa	gil2621701	(AE000843) Mg2+ transporter [Methanobacterium thermoautotrophicum]	142		3.20E-21

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f545.aa	gil2688284	(AE001143) Mg2+ transport protein (mgE) [Borrelia burgdorferi]	860	4.20E-119
f545.aa	gil1753228	MgtE [Borrelia burgdorferi]	855	2.20E-118
f545.aa	gil619724	MgtE [Bacillus firmus] >pir140201140201 mgE protein - Bacillus	176	3.70E-37
f545.aa	gil780282	extended ORF of mgE gene; transcription from this start point is	182	1.30E-34
f545.aa	gnlPIDle31	unknown [Mycobacterium tuberculosis]	183	4.50E-31
f545.aa	5479			
f545.aa	gnlPIDle10	Mg2+ transporter [Synecocystis sp.] >pir1S77552IS77552 Mg2+	165	4.60E-31
f545.aa	18132			
f545.aa	gnlPIDle11	(AJ002571) YkoK [Bacillus subtilis] >gnlPIDle1183350 similar	142	2.30E-30
f545.aa	81529			
f545.aa	gil2621701	(AE000843) Mg2+ transporter [Methanobacterium thermoautotrophicum]	142	3.20E-21
f561.aa	gil49245	lipoprotein [Borrelia burgdorferi] >gil2688271 (AE001142) lipoprotein	1000	1.30E-132
f561.aa	gil495738	P22 [Borrelia burgdorferi]	982	3.70E-130
f577.aa	gil2688261	(AE001141) B. burgdorferi predicted coding region BB0352 [Borrelia	1930	4.00E-264
f584.aa	gil2688246	(AE001140) B. burgdorferi predicted coding region BB0346 [Borrelia	1094	4.10E-147
f596.aa	gil2688241	(AE001140) P26 [Borrelia burgdorferi] >pir1G7014IG70141 P26	1322	1.20E-180
f596.aa	gil2281465	(AF000366) P26 [Borrelia burgdorferi] >gil2281465 (AF000366) P26	1010	5.90E-137
f598.aa	gil2281462	(AF000366) oligopeptide permease homolog D [Borrelia burgdorferi]	652	1.20E-85
f598.aa	gil143607	sporulation protein [Bacillus subtilis]	372	1.20E-45
f598.aa	gnlPIDle11	oligopeptide ABC transporter (ATP-binding protein) [Bacillus	372	1.20E-45
f598.aa	83166			
f598.aa	gil1574676	oligopeptide transport ATP-binding protein (oppD) [Haemophilus	344	6.70E-42
f598.aa	gil677943	AppD [Bacillus subtilis] >gnlPIDle1183156 oligopeptide ABC	344	8.00E-42
f598.aa	gil1787051	(AE000185) o612; 48 pct identical (33 gaps) to 525 residues from	346	2.50E-41
f598.aa	gil47346	AmiE protein [Streptococcus pneumoniae] >pir1S1152IS1152 amiE	338	1.10E-40
f598.aa	gil47805	Opp D (AA1-335) [Salmonella typhimurium] >sp1P04285IOPPD_SALTY	332	5.70E-40
f598.aa	pir1A034131	oligopeptide transport protein oppD - Salmonella typhimurium	332	5.70E-40
f598.aa	QREBOT			
f598.aa	gil1787499	(AE000223) oligopeptide transport ATP-binding protein OppD	332	5.90E-40
f598.aa	gnlPIDle10	Oligopeptide transport ATP-binding protein OppD. [Escherichia	332	5.90E-40
f598.aa	15494			
f598.aa	gil495177	ATP binding protein [Lactococcus lactis] >sp1P50980IOPPD_LACLC	331	8.40E-40

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f598.aa	gnllPIDle18 7587	oligopeptidpermease [Streptococcus pyogenes]	331	1.10E-39
f598.aa	gil308850	ATP binding protein [Lactococcus lactis] >pirA53290/A53290	329	1.60E-39
f598.aa	gil2313399	(AE000548) dipeptide ABC transporter, ATP-binding protein (dppD)	322	2.30E-39
f6-21.aa	gil2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gil2689891 (AE000792)	565	4.30E-73
f6-21.aa	gil2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	315	1.20E-37
f6-21.aa	gil2688228	(AE001139) oligopeptide ABC transporter, periplasmic	314	1.60E-37
f6-21.aa	gil2809544	(AF043071) oligopeptide permease periplasmic binding protein	314	1.60E-37
f6-21.aa	gil2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	314	1.60E-37
f6-21.aa	gil2688227	(AE001139) oligopeptide ABC transporter, periplasmic	290	3.90E-34
f6-21.aa	gil2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	290	3.90E-34
f6-21.aa	gil2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	279	9.90E-34
f6-21.aa	gil2690261	(AE000790) oligopeptide ABC transporter, periplasmic	282	5.30E-33
f6-21.aa	gil1616644	P30 [Borrelia burgdorferi]	271	6.70E-32
f6-21.aa	gil2688226	(AE001139) oligopeptide ABC transporter, periplasmic	268	5.00E-31
f6-21.aa	gil2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia	268	5.00E-31
f6-21.aa	gil2809546	(AF043071) oligopeptide permease periplasmic binding protein	268	5.00E-31
f6-21.aa	bbs1161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	255	2.90E-30
f6-21.aa	gil2983834	(AE000740) transporter (extracellular solute binding protein family	154	3.50E-14
f6-27.aa	gil2689911	(AE000792) B. burgdorferi predicted coding region BBB09 [Borrelia	1773	7.30E-240
f6-5.aa	gil2689905	(AE000792) B. burgdorferi predicted coding region BBB27 [Borrelia	932	7.50E-126
f600.aa	gil2281461	(AF000366) oligopeptide permease homolog C [Borrelia burgdorferi]	731	1.40E-100
f600.aa	gil2688244	(AE001140) oligopeptide ABC transporter, permease protein (oppC-1)	731	1.40E-100
f600.aa	gil143606	sporulation protein [Bacillus subtilis] >pirC38447/C38447	372	5.00E-48
f600.aa	gil40007	OppC gene product [Bacillus subtilis] >gnllPIDle1183165 oligopeptide	372	5.00E-48
f600.aa	gil1574677	oligopeptide transport system permease protein (oppC)C [Haemophilus	372	7.30E-48
f600.aa	gil47804	Opp C (AA1-301) [Salmonella typhimurium] >pirC29333/QREBOC	366	4.20E-47
f600.aa	gnllPIDId10 15493	Oligopeptide transport system permease protein OppC.	366	4.20E-47
f600.aa	gnllPIDle11 81495	(AJ002571) DppC [Bacillus subtilis] >gnllPIDle1183314	267	1.70E-42

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f600.aa	gil1732315	transport system permease homolog [ <i>Listeria monocytogenes</i> ]	335	5.30E-42
f600.aa	gil580851	dcIAc [ <i>Bacillus subtilis</i> ] >sp126904IDPPC_BACSU DIPEPTIDE TRANSPORT	258	1.50E-40
f600.aa	gnlIPIDId1011164	oligopeptide transport system permease protein [ <i>Synechocystis</i> ]	240	2.50E-39
f600.aa	gil677947	AppC [ <i>Bacillus subtilis</i> ] >gnlIPIDId1183160 oligopeptide ABC	236	2.80E-37
f600.aa	gil1813497	dipeptide transporter protein dppC [ <i>Bacillus firmus</i> ]	281	1.20E-35
f600.aa	spIQ106231Y021_MYC TU	PUTATIVE PEPTIDE TRANSPORT PERMEASE PROTEIN CY373.01C.	290	1.50E-35
f600.aa	gil1532201	BldKA [ <i>Streptomyces coelicolor</i> ]	291	1.60E-35
f603.aa	gil2281460	(AF000366) oligopeptide permease homolog B [ <i>Borrelia burgdorferi</i> ]	1522	5.80E-214
f603.aa	gil1574678	dipeptide transport system permease protein (dppB) [ <i>Haemophilus</i> ]	392	1.30E-100
f603.aa	gnlIPIDId1183164	oligopeptide ABC transporter (permease) [ <i>Bacillus subtilis</i> ]	374	3.40E-96
f603.aa	gil580897	OppB gene product [ <i>Bacillus subtilis</i> ] >pirS15231B38447	373	6.60E-96
f603.aa	gil47803	Opp B (AA1-306) [ <i>Salmonella typhimurium</i> ] >pirB29333QREBOB	371	6.70E-96
f603.aa	gil1787497	(AE000223) oligopeptide transport system permease protein OppB	364	3.50E-95
f603.aa	gnlIPIDId1015492	Oligopeptide transport system permease protein OppB.	357	3.50E-94
f603.aa	gil580850	dcIAb [ <i>Bacillus subtilis</i> ] >gnlIPIDId1181494 (AJ002571) DppB	350	9.10E-90
f603.aa	gil551726	sporulation protein [ <i>Bacillus subtilis</i> ] >gil143605 sporulation	374	2.40E-87
f603.aa	gil349226	transmembrane protein [ <i>Escherichia coli</i> ] >gil466682 dppB	293	9.60E-79
f603.aa	gil1787053	(AE000185) o306; This 306 aa ORF is 46 pct identical (32 gaps) to	284	3.80E-77
f603.aa	gil972895	DppB [ <i>Haemophilus influenzae</i> ] >gil1574114 dipeptide transport system	301	2.50E-76
f603.aa	gil2182646	(AE000098) Y4tP [ <i>Rhizobium</i> sp. NGR234] >spIQ53191Y4TP_RHISN	294	9.10E-74
f603.aa	gil2983140	(AE000692) transporter (OppBC family) [ <i>Aquifex aeolicus</i> ]	169	2.30E-73
f603.aa	gil677946	AppB [ <i>Bacillus subtilis</i> ] >gnlIPIDId1183159 oligopeptide ABC	218	8.70E-73
f604.aa	gil2281459	(AF000366) oligopeptide permease homolog AIII [ <i>Borrelia</i> ]	2818	0
f604.aa	gil2809546	(AF043071) oligopeptide permease periplasmic binding protein	2818	0
f604.aa	gil2688226	(AE001139) oligopeptide ABC transporter, periplasmic	2823	0
f604.aa	gil2688227	(AE001139) oligopeptide ABC transporter, periplasmic	1738	1.40E-234

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f604.aa	gil2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	1731	1.30E-233
f604.aa	gil2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gil2689891 (AE000792)	1675	3.60E-229
f604.aa	gil2688228	(AE001139) oligopeptide ABC transporter, periplasmic	718	1.60E-204
f604.aa	gil2809544	(AF043071) oligopeptide permease periplasmic binding protein	718	3.00E-204
f604.aa	gil2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	718	4.10E-204
f604.aa	gil2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	714	2.00E-203
f604.aa	bbs1161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	704	1.20E-190
f604.aa	gil2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	1402	1.80E-188
f604.aa	gil2690261	(AE000790) oligopeptide ABC transporter, periplasmic	1400	3.40E-188
f604.aa	gil1616644	P30 [Borrelia burgdorferi]	858	4.90E-117
f604.aa	gil47802	Opp A (AA1-542) [Salmonella typhimurium] >gil47808 precursor	296	9.00E-114
f606.aa	gil2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	2762	0
f606.aa	gil2688227	(AE001139) oligopeptide ABC transporter, periplasmic	2774	0
f606.aa	gil2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gil2689891 (AE000792)	1817	6.50E-245
f606.aa	gil2809546	(AF043071) oligopeptide permease periplasmic binding protein	1739	3.10E-234
f606.aa	gil2688226	(AE001139) oligopeptide ABC transporter, periplasmic	1738	4.20E-234
f606.aa	gil2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia	1733	2.00E-233
f606.aa	bbs1161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	762	1.70E-202
f606.aa	gil2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	1456	1.80E-195
f606.aa	gil2690261	(AE000790) oligopeptide ABC transporter, periplasmic	1454	3.30E-195
f606.aa	gil2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	751	2.00E-192
f606.aa	gil2688228	(AE001139) oligopeptide ABC transporter, periplasmic	751	2.70E-192
f606.aa	gil2809544	(AF043071) oligopeptide permease periplasmic binding protein	751	6.90E-192
f606.aa	gil2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	748	2.40E-191
f606.aa	gil1616644	P30 [Borrelia burgdorferi]	1220	7.30E-163
f606.aa	gil47802	Opp A (AA1-542) [Salmonella typhimurium] >gil47808 precursor	285	7.80E-106
f607.aa	gil2281457	(AF000366) oligopeptide permease homolog AI [Borrelia burgdorferi]	2694	0
f607.aa	gil2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	2706	0
f607.aa	gil2809544	(AF043071) oligopeptide permease periplasmic binding protein	2708	0
f607.aa	gil2688228	(AE001139) oligopeptide ABC transporter, periplasmic	2714	0
f607.aa	bbs1161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514	1272	3.80E-242



TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f607.aa	gil2809546	(AF043071) oligopeptide permease periplasmic binding protein	718	1.40E-204
f607.aa	gil2688226	(AE001139) oligopeptide ABC transporter, periplasmic	718	3.60E-204
f607.aa	gil2281459	(AF000366) oligopeptide permease homolog AIII [Borrelia]	713	1.70E-203
f607.aa	gil2688227	(AE001139) oligopeptide ABC transporter, periplasmic	751	2.40E-192
f607.aa	gil2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	751	4.50E-192
f607.aa	gil2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gil2689891 (AE000792)	806	8.40E-189
f607.aa	gil2690261	(AE000790) oligopeptide ABC transporter, periplasmic	601	1.20E-144
f607.aa	gil2281455	(AF000365) oligopeptide permease homolog AV [Borrelia burgdorferi]	600	1.60E-144
f607.aa	gil1616644	P30 [Borrelia burgdorferi]	709	5.40E-103
f607.aa	gil47802	Opp A (AA1-542) [Salmonella typhimurium] >gil47808 precursor	261	8.50E-69
f611.aa	gil2688231	(AE001139) B. burgdorferi predicted coding region BB0325 [Borrelia]	1907	1.10E-261
f617.aa	gil2688213	(AE001138) conserved hypothetical integral membrane protein	1574	2.70E-226
f617.aa	gil2649711	(AE001042) ribose ABC transporter, permease protein (rbsC-1)	109	7.00E-12
f631.aa	gil1165286	FtsW [Borrelia burgdorferi] >gil2688164 (AE001137) cell division	1820	4.00E-259
f631.aa	gnllPIDle22 9592	membrane protein [Borrelia burgdorferi] >gnllPIDle228289 ftsW	1815	2.10E-258
f631.aa	gil146039	cell division protein [Escherichia coli] >gil40857 FtsW protein	362	1.30E-60
f631.aa	gil580938	internal open reading frame (AA 1-290) [Bacillus subtilis]	407	4.90E-55
f631.aa	gnllPIDle31 5953	FtsW [Mycobacterium tuberculosis] >sp10062231FTWH_MYCTU	412	5.40E-55
f631.aa	gil580937	spoVE gene product (AA 1-366) [Bacillus subtilis] >gnllPIDle1185111	410	2.90E-53
f631.aa	gil143657	endospore forming protein [Bacillus subtilis]	405	1.20E-52
f631.aa	gnllPIDle10 19002	rod-shape-determining protein [Synechocystis sp.]	358	3.10E-51
f631.aa	gnllPIDle12 87793	(AL022602) cell division protein FtsW [Mycobacterium leprae]	396	6.70E-51
f631.aa	gil1016213	strong sequence similarity to FtsW, RodA, and SpoV-E [Cyanophora]	349	1.00E-50
f631.aa	gil1574692	cell division protein (ftsW) [Haemophilus influenzae]	304	4.20E-50
f631.aa	gnllPIDle11 85075	similar to cell-division protein [Bacillus subtilis]	281	1.80E-46
f631.aa	gil1469784	putative cell division protein ftsW [Enterococcus hirae]	247	1.60E-38

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f631.aa	gil1572976	rod shape-determining protein (mreB) [Haemophilus influenzae]	196	1.20E-37
f631.aa	gil147695	rod-shape-determining protein [Escherichia coli] >gil1778551	194	5.00E-35
f635.aa	gil1165282	orf7; Method: conceptual translation supplied by author [Borrelia	1166	1.00E-156
f635.aa	gil1448949	ORF 224; The predicted gene product showed weak homology with the	621	2.80E-125
f647.aa	gil2688180	(AE001137) flagellar protein (flhB) [Borrelia burgdorferi]	1032	1.00E-140
f647.aa	gil1196323	putative [Borrelia burgdorferi]	1031	1.50E-140
f647.aa	gil1165270	orf19; Method: conceptual translation supplied by author [Borrelia	1019	7.10E-139
f647.aa	gil2108242	22.5K protein [Treponema pallidum]	200	4.70E-24
f65.aa	gil2688737	(AE001178) B. burgdorferi predicted coding region BB0792 [Borrelia	1095	8.10E-148
f653.aa	gil1165265	MotB [Borrelia burgdorferi] >gil185054 flagellar motor apparatus	1220	1.70E-164
f653.aa	gil1399286	MotB [Treponema phagedenis]	168	5.80E-57
f653.aa	gil2196896	MotB [Treponema pallidum]	179	1.30E-49
f664.aa	gil1185062	flagellar export protein [Borrelia burgdorferi]	1430	1.90E-199
f664.aa	gil1165257	FlhB [Borrelia burgdorferi] >gil2688194 (AE001137) flagellar	1430	1.90E-199
f664.aa	gil1216382	FlhB' [Treponema pallidum] >pirPC4115IPC4115 flagellar protein	272	5.30E-64
f664.aa	gil395390	flagellar biosynthetic protein [Bacillus subtilis]	433	1.30E-61
f664.aa	gnllPIDle11	flagella-associated protein [Bacillus subtilis]	433	1.30E-61
	85229			
f664.aa	gil1147737	third gene in flhQ operon; membrane protein homolog [Caulobacter	353	1.70E-46
f664.aa	gil2313898	(AE000589) flagellar biosynthetic protein (flhB) [Helicobacter	203	1.20E-44
f664.aa	gil2984250	(AE000768) flagellar biosynthetic protein FlhB [Aquifex aeolicus]	319	3.00E-44
f664.aa	gil2459702	FlhB [Agrobacterium tumefaciens]	347	6.20E-44
f664.aa	gil793892	flhB [Yersinia enterocolitica] >pirS54213S54213 flhB protein -	330	1.30E-39
f664.aa	gnllPIDld10	Flagellar biosynthetic protein FlhB. [Escherichia coli]	325	2.20E-39
	16420			
f664.aa	gil475126	yscU [Yersinia pseudotuberculosis] >gil2996233 (AF053946) Yop	309	9.80E-38
f664.aa	gil497216	YscU [Yersinia enterocolitica]	308	1.40E-37
f664.aa	gnllPIDld10	flagellar protein FlhB [Salmonella typhimurium]	312	2.10E-37
	07477			
f664.aa	gnllPIDle28	secretion system apparatus, SsaU [Salmonella typhimurium]	312	8.20E-37
	3684			

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f679.aa	gil2688158	(AE001136) <i>B. burgdorferi</i> predicted coding region BB0259 [Borrelia]	3714	0
f679.aa	gnlPIDd10 11473	soluble lytic transglycosylase [Synechocystis sp.]	180	1.10E-25
f679.aa	gnlPIDe11 83177	similar to lytic transglycosylase [Bacillus subtilis]	108	2.10E-22
f679.aa	gil2984090	(AE000756) hypothetical protein [Aquifex aeolicus]	111	9.30E-17
f680.aa	gil2688153	(AE001136) bacitracin resistance protein (bacA) [Borrelia]	769	3.90E-109
f680.aa	gnlPIDe11 85988	similar to bacitracin resistance protein (undecaprenol)	174	7.30E-18
f680.aa	gil2622542	(AE000905) bacitracin resistance protein [Methanobacterium]	116	3.30E-16
f680.aa	gil2984378	(AE000777) undecaprenol kinase [Aquifex aeolicus]	152	3.90E-15
f680.aa	gil882579	CG Site No. 29739 [Escherichia coli] >gil1789437 (AE000387)	139	2.60E-12
f688.aa	gil2688146	(AE001135) conserved hypothetical integral membrane protein	2497	0
f688.aa	gil2649351	(AE001019) conserved hypothetical protein [Archaeoglobus fulgidus]	110	3.70E-18
f688.aa	gil1592186	<i>M. jannaschii</i> predicted coding region MJ1562 [Methanococcus]	174	1.10E-16
f7-30.aa	gil2690009	(AE000786) conserved hypothetical protein [Borrelia burgdorferi]	682	1.90E-90
f704.aa	gil2688137	(AE001134) glycerol uptake facilitator (glpF) [Borrelia]	1307	4.70E-181
f704.aa	gil142997	glycerol uptake facilitator [Bacillus subtilis] >gnlPIDe1182917	191	1.50E-50
f704.aa	gil521003	C01G6.1 [Caenorhabditis elegans]	152	1.60E-50
f704.aa	gil529582	water channel protein [Rattus norvegicus] >pir1592661I59266 water	142	5.80E-50
f704.aa	dbj1AB0005 07_1	(AB000507) aquaporin 7 [Rattus norvegicus]	155	1.30E-49
f704.aa	pir1A571191 A57119	aquaporin 3 - human	149	4.20E-44
f704.aa	gil1109920	coded for by <i>C. elegans</i> cDNA cml6b11; strong similarity to MIP	168	9.30E-44
f704.aa	gnlPIDd10 19987	(AB001325) aquaporin 3 [Homo sapiens] >sp1Q92482IAQP3_HUMAN	148	5.30E-43
f704.aa	gnlPIDd10 25786	(AB008775) aquaporin 9 [Homo sapiens]	144	1.40E-42
f704.aa	gil146188	glycerol diffusion facilitator [Escherichia coli] >gil305030 CG Site	146	1.30E-40
f704.aa	gil1065485	strong similarity to the MIP family of transmembrane channel	179	1.40E-39
f704.aa	sp1P311401	GLYCEROL UPTAKE FACILITATOR PROTEIN.	146	3.30E-39

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	GLPF_SHI FL			
f704.aa	gil2587035	(AF026270) PduF [Salmonella typhimurium] >spIP37451PDUF_SALTY	168	7.30E-39
f704.aa	gil1399489	glycerol diffusion facilitator [Pseudomonas aeruginosa]	154	7.90E-39
f704.aa	gil2649144	(AE001005) glycerol uptake facilitator, MIP channel (glpF)	150	1.30E-38
f707.aa	gil2688143	(AE001134) B. burgdorferi predicted coding region BB0238 [Borrelia]	1300	3.90E-176
f709.aa	gil2688131	(AE001133) B. burgdorferi predicted coding region BB0236 [Borrelia]	3437	0
f730.aa	gil2688111	(AE001132) gufA protein [Borrelia burgdorferi] >pirC70127IC70127	1376	3.00E-192
f730.aa	gil1707057	coded for by C. elegans cDNA CEES55F; coded for by C. elegans cDNA	235	2.80E-83
f730.aa	gil2621542	(AE000831) conserved protein [Methanobacterium thermoautotrophicum]	259	1.10E-74
f730.aa	gnllPIDle18 3440	gufA gene product [Myxococcus xanthus] >gil49253 orfX gene	175	2.30E-35
f730.aa	gil2984109	(AE000757) hypothetical protein [Aquifex aeolicus]	171	7.00E-28
f736.aa	gil2688115	(AE001132) phosphate ABC transporter, periplasmic phosphate-binding	1403	2.10E-186
f736.aa	gil2622858	(AE000929) phosphate-binding protein PstS [Methanobacterium]	151	4.40E-30
f736.aa	gil2622859	(AE000929) phosphate-binding protein PstS homolog [Methanobacterium]	145	2.80E-24
f736.aa	gnllPIDle10 10224	ORF108 [Bacillus subtilis] >gnllPIDle1185766 alternate gene	120	1.20E-11
f739.aa	gil2688119	(AE001132) B. burgdorferi predicted coding region BB0213 [Borrelia]	1139	1.10E-156
f742.aa	gil2688100	(AE001131) surface-located membrane protein 1 (Imp1) [Borrelia]	5654	0
f742.aa	gil2621120	(AE000799) O-linked GlcNAc transferase [Methanobacterium]	200	9.30E-22
f742.aa	gil2621106	(AE000798) O-linked GlcNAc transferase [Methanobacterium]	180	5.80E-17
f742.aa	pirE69190 E69190	conserved hypothetical protein MTH68 - Methanobacterium	154	1.60E-14
f742.aa	gil1591608	transformation sensitive protein [Methanococcus jannaschii]	109	9.90E-14
f742.aa	gil1589778	SPINDLY [Arabidopsis thaliana]	101	1.40E-13
f742.aa	gil2984175	(AE000762) hypothetical protein [Aquifex aeolicus]	132	7.30E-13
f742.aa	gil3037137	(AF056198) Hsp70/Hsp90 organizing protein homolog [Drosophila]	105	5.40E-11
f743.aa	gil2688104	(AE001131) B. burgdorferi predicted coding region BB0209 [Borrelia]	1299	1.70E-174
f748.aa	gil2688089	(AE001130) Lambda CII stability-governing protein (hflC) [Borrelia]	1615	5.10E-220

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f748.aa	gil436158	putative integral membrane protease required for high frequency	191	4.80E-35
f748.aa	gil1573107	Lambda CII stability-governing protein (hfIC) [Haemophilus	193	4.90E-33
f748.aa	gil507735	HfIC [Vibrio parahaemolyticus] >spIP40606HFLC_VIBPA HFLC PROTEIN	212	6.10E-26
f752.aa	gil2688092	(AE001130)	2585	0
f752.aa	gil2984050	(AE000754) UDP-MurNac-tripeptide synthetase [Aquifex aeolicus]	202	9.10E-74
f752.aa	gil40162	murE gene product [Bacillus subtilis] >gnlPIDle1185108	157	6.40E-70
f752.aa	gnlPIDle110 11466	UDP-MurNac-tripeptide synthetase [Synecocystis sp.]	166	5.20E-57
f752.aa	gnlPIDle30 7808	UDP-MurNac-tripeptide synthetase [Rickettsia prowazekii]	108	2.30E-51
f752.aa	gil1574688	UDP-MurNac-tripeptide synthetase (murE) [Haemophilus influenzae]	166	3.20E-50
f752.aa	gnlPIDle12 87797	(AL022602) udp-n-acetylmuramoylalanyl-d-glutamate	183	3.20E-50
f752.aa	gnlPIDle31 6022	MurE [Mycobacterium tuberculosis]	181	4.10E-46
f752.aa	gil581032	UDP-MurNac-tripeptide synthetase (MurE) [Escherichia coli]	175	1.30E-41
f752.aa	gil2177098	UDP-MurNac-Dipeptide: meso-diaminopimelate ligase [Escherichia	172	3.70E-41
f752.aa	gil2314673	(AE000648) UDP-MurNac-tripeptide synthetase (murE) [Helicobacter	137	9.80E-41
f752.aa	gil840843	UDP-N-acetylmuramoylalanyl-D-glutamate-- 2,6-diaminopimelate ligase	135	1.70E-20
f76-1.aa	gil1209837	lipoprotein [Borrelia burgdorferi]	395	2.80E-49
f76-1.aa	gil1209873	lipoprotein [Borrelia burgdorferi]	250	7.00E-37
f76-1.aa	gil1209843	lipoprotein [Borrelia burgdorferi]	267	7.30E-32
f76-1.aa	gil2121280	(AF000270) lipoprotein [Borrelia burgdorferi] >gil3095109	258	1.20E-30
f76-1.aa	gnlPIDle26 8244	surface-exposed lipoprotein [Borrelia afzelii]	116	2.40E-18
f76-1.aa	gil1209849	lipoprotein [Borrelia burgdorferi]	146	8.30E-17
f76-1.aa	gil3095105	(AF046998) 2.9-8 lipoprotein [Borrelia burgdorferi]	148	5.80E-14
f76-1.aa	gil3095107	(AF046999) 2.9-9 lipoprotein [Borrelia burgdorferi]	127	7.20E-11
f764.aa	gil2688084	(AE001129) B. burgdorferi predicted coding region BB0193 [Borrelia	1218	1.20E-164
f770.aa	gil2688077	(AE001129) conserved hypothetical protein [Borrelia burgdorferi]	646	7.60E-87
f790.aa	gil2688065	(AE001128) outer membrane protein (ipn50) [Borrelia burgdorferi]	2013	2.50E-271

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f790.aa	gil458015	TpN50 precursor [Treponema pallidum]	134	4.30E-33
f790.aa	spiP38369IT P50_TREP A	OUTER MEMBRANE PROTEIN TPN50 PRECURSOR.	134	4.30E-33
f790.aa	gil532658	antigen [Treponema pallidum] >pirIS61867IS61867 antigen tpp57 -	139	4.30E-31
f792.aa	gil2688052	(AE001127) B. burgdorferi predicted coding region BB0165 [Borrelia]	3185	0
f797.aa	gil2688056	(AE001127) B. burgdorferi predicted coding region BB0159 [Borrelia]	1116	5.30E-148
f798.aa	gil2688051	(AE001127) antigen, S2, putative [Borrelia burgdorferi]	1223	9.70E-164
f798.aa	gil1063419	S2 gene product [Borrelia burgdorferi]	116	4.70E-23
f798.aa	gil2690227	(AE000790) antigen, S2 [Borrelia burgdorferi] >pirID70207ID70207	116	1.50E-22
f798.aa	gil2690128	(AE000788) protein p23 [Borrelia burgdorferi] >pirC70257IC70257	110	1.40E-19
f798.aa	gil2689956	(AE000785) protein p23 [Borrelia burgdorferi] >pirID70225ID70225	104	2.70E-15
f799.aa	gil2688043	(AE001126) B. burgdorferi predicted coding region BB0156 [Borrelia]	632	1.40E-83
f8-10.aa	gil2690052	(AE000784) antigen, P35, putative [Borrelia burgdorferi]	1241	1.10E-167
f8-10.aa	gil2689955	(AE000785) antigen, P35, putative [Borrelia burgdorferi]	298	1.70E-57
f8-10.aa	gil2690120	(AE000789) B. burgdorferi predicted coding region BBI34 [Borrelia]	254	3.80E-54
f8-10.aa	gil2690100	(AE000789) B. burgdorferi predicted coding region BBI16 [Borrelia]	182	2.90E-31
f8-10.aa	gil2690207	(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia]	196	1.50E-20
f8-10.aa	gil2690116	(AE000789) B. burgdorferi predicted coding region BBI29 [Borrelia]	192	5.50E-20
f8-10.aa	gil2690125	(AE000788) antigen, P35, putative [Borrelia burgdorferi]	129	5.80E-14
f8-10.aa	gil2690206	(AE000787) B. burgdorferi predicted coding region BBJ01 [Borrelia]	103	1.10E-13
f8-10.aa	gil2690099	(AE000789) B. burgdorferi predicted coding region BBI15 [Borrelia]	142	8.50E-13
f8-10.aa	gil2690115	(AE000789) B. burgdorferi predicted coding region BBI28 [Borrelia]	130	3.30E-12
f8-14.aa	gil2690074	(AE000784) B. burgdorferi predicted coding region BBH37 [Borrelia]	1560	2.60E-206
f8-14.aa	gil2690188	(AE000787) B. burgdorferi predicted coding region BBJ08 [Borrelia]	599	3.50E-123
f8-14.aa	gil2690030	(AE000786) B. burgdorferi predicted coding region BBG01 [Borrelia]	337	4.40E-106
f8-14.aa	gil2690139	(AE000788) B. burgdorferi predicted coding region BBK01 [Borrelia]	173	8.00E-91
f8.aa	gil2688783	(AE001182) B. burgdorferi predicted coding region BB0840 [Borrelia]	2765	0
f8.aa	gil2697112	(AF008219) unknown [Borrelia afzelii]	1494	2.80E-205
f800.aa	gil2688044	(AE001126) B. burgdorferi predicted coding region BB0155 [Borrelia]	1936	1.00E-262
f805.aa	gil2688039	(AE001126) N-acetylglucosamine-6-phosphate deacetylase (nagA)	641	6.30E-85

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f810.aa	gil2688024	(AE001125) glycine betaine, L-proline ABC transporter,	1527	4.20E-207
f810.aa	gil984805	glycine betaine-binding protein precursor [Bacillus subtilis]	179	6.80E-21
f810.aa	gil1850605	ProX [Streptococcus mutans]	181	2.30E-18
f814.aa	pirD701171 D70117	acriflavine resistance protein (acrB) homolog - Lyme disease	5105	0
f814.aa	gil2688027	(AE001125) acriflavine resistance protein (acrB) [Borrelia]	5111	0
f814.aa	gil2983346	(AE000707) cation efflux (AcrB/AcrD/AcrF family) [Aquifex aeolicus]	325	4.80E-119
f814.aa	gil2313726	(AE000574) acriflavine resistance protein (acrB) [Helicobacter]	327	4.50E-111
f814.aa	gil3068786	(AF059041) RND pump protein [Helicobacter pylori]	297	1.70E-110
f814.aa	gnlPIDle11 82651	similar to acriflavine resistance protein [Bacillus subtilis]	257	8.90E-100
f814.aa	gil1573914	acriflavine resistance protein (acrB) [Haemophilus influenzae]	294	2.10E-97
f814.aa	gnlPIDle25 6815	mexF [Pseudomonas aeruginosa]	300	2.00E-88
f814.aa	gnlPIDld10 19295	cation efflux system protein CzcA [Synechocystis sp.]	198	1.30E-87
f814.aa	gnlPIDle28 5274	membrane-bound cation-proton-antiporter [Ralstonia eutropha]	283	2.20E-87
f814.aa	gil438854	envD homologue; ORFB [Pseudomonas aeruginosa] >pirS39630IS39630	290	6.50E-87
f814.aa	gnlPIDld10 11721	CzcA [Alcaligenes sp.] >pirJC4700JC4700 cadmium, zinc,	275	8.20E-87
f814.aa	gil2314107	(AE000605) cation efflux system protein (czcA) [Helicobacter]	266	2.30E-86
f814.aa	pirA33830 A33830	cation efflux system membrane protein czcA - Alcaligenes	275	3.10E-86
f814.aa	gnlPIDld10 17073	envD gene product homolog [Escherichia coli] >gil1788814	283	8.30E-86
f818.aa	gil2688032	(AE001125) B. burgdorferi predicted coding region BB0139 [Borrelia]	664	3.00E-87
f82.aa	gil2688729	(AE001177) B. burgdorferi predicted coding region BB0776 [Borrelia]	991	2.20E-132
f820.aa	gil2688029	(AE001125) penicillin-binding protein (pbp-1) [Borrelia]	3171	0
f820.aa	gil580936	SpoVD [Bacillus subtilis] >gnlPIDle1185107 penicillin-binding	149	3.00E-49
f820.aa	gil150283	penicillin-binding protein 2 [Neisseria meningitidis]	154	6.90E-43
f820.aa	gnlPIDle12	(AL022602) penicillin binding protein 2 [Mycobacterium]	182	4.20E-42

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f820 aa	87798				
gil509190		penicillin-binding protein 2 [Neisseria meningitidis]		158	1.70E-41
f820 aa	gil509118	penicillin-binding protein 2 [Neisseria meningitidis]		151	7.10E-41
f820 aa	gil840842	penicillin-binding protein 3 [Pseudomonas aeruginosa]		177	1.20E-40
f820 aa	gil509065	penicillin-binding protein 2 [Neisseria meningitidis]		152	1.40E-40
f820 aa	gil509043	penicillin-binding protein 2 [Neisseria meningitidis]		150	2.70E-40
f820 aa	gil509159	penicillin-binding protein 2 [Neisseria meningitidis]		147	2.80E-40
f820 aa	gil509120	penicillin-binding protein 2 [Neisseria meningitidis]		155	1.60E-39
f820 aa	gil509157	penicillin-binding protein 2 [Neisseria meningitidis]		155	1.60E-39
f820 aa	gil509126	penicillin-binding protein 2 [Neisseria meningitidis]		158	1.70E-39
f820 aa	gil45178	penicillin-binding protein 2 (AA 1 - 581) [Neisseria meningitidis]		155	2.30E-38
f820 aa	gil150279	penicillin binding protein 2 [Neisseria gonorrhoeae]		154	8.70E-38
f831 aa	gil2688018	(AE001124) B. burgdorferi predicted coding region BB0126 [Borrelia burgdorferi]		994	1.20E-133
f843 aa	gil2688014	(AE001124) PTS system, maltose and glucose-specific IIABC component		2590	0
f843 aa	gil2688579	(AE001166) PTS system, glucose-specific IIBC component (ptsG)		594	1.80E-129
f843 aa	gil1072418	glcA [Staphylococcus carnosus] >pirS46952IS46952		283	1.00E-72
f843 aa	gil1072419	glcB [Staphylococcus carnosus] >pirS63606IS46953		248	1.00E-66
f843 aa	dbj1D86417	YnfF [Bacillus subtilis] >gnlPIDle1182760 similar to		215	7.90E-65
f843 aa	gil2197104	(AF003742) MalX homolog [Escherichia coli]		182	8.90E-64
f843 aa	gil43819	nagE gene product [Klebsiella pneumoniae] >pirS18607IS18607		264	8.50E-63
f843 aa	gil146913	N-acetylglucosamine transport protein [Escherichia coli]		256	1.10E-62
f843 aa	gil39956	IIIGlc [Bacillus subtilis] >gnlPIDle1184979 phosphotransferase system		315	5.20E-62
f843 aa	dbj1D87820	NagE [Vibrio cholerae non-O1] >pirIC5651IIC5651		263	3.80E-61
f843 aa	gil2689888	(AE000792) PTS system, maltose and glucose-specific IIABC component		198	1.10E-60
f843 aa	gil397363	enzyme II-glc [Salmonella typhimurium] >pirS36620IS36620		227	1.20E-58
f843 aa	gil147393	glucose-specific enzyme II of phosphotransferase system [Escherichia coli]		226	3.90E-57
f843 aa	gnlPIDle1182187	alternate gene name: yzfA; similar to phosphotransferase		180	9.00E-56
f843 aa	gil1732194	PTS permease for glucose [Vibrio furnissii]		349	4.30E-50



TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f850.aa	gil2687999	(AE001123) B. burgdorferi predicted coding region BB0110 [Borrelia burgdorferi]	2374	0
f853.aa	gil2687994	(AE001123) basic membrane protein [Borrelia burgdorferi]	1672	2.20E-224
f853.aa	gil155055	basic membrane protein precursor [Treponema pallidum]	130	3.60E-24
f859.aa	gil2688002	(AE001123) B. burgdorferi predicted coding region BB0102 [Borrelia burgdorferi]	888	1.80E-115
f86.aa	gil2688725	(AE001177) flagellar P-ring protein (flgI) [Borrelia burgdorferi]	1647	1.50E-217
f86.aa	gil2920802	(AF019213) FlgI [Vibrio cholerae]	143	3.50E-14
f86.aa	gil405550	flagellar P-ring protein [Pseudomonas putida] >spQ52082 FLGI_PSEPU	102	3.70E-13
f86.aa	gil144241	flagellin [Caulobacter crescentus] >pirA41891 A41891 basal body	110	6.70E-13
f860.aa	gil2687998	(AE001123) asparaginyl-tRNA synthetase (asnS) [Borrelia burgdorferi]	1110	2.40E-149
f860.aa	gil1574761	asparaginyl-tRNA synthetase (asnS) [Haemophilus influenzae]	634	1.30E-83
f860.aa	gil147935	asparaginyl-tRNA synthetase (asnS) [Escherichia coli] >gil41000	622	6.10E-82
f860.aa	gnlPIDle1202698	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]	404	2.40E-80
f860.aa	gnlPIDle1011495	asparaginyl-tRNA synthetase [Synechocystis sp.]	618	4.50E-80
f860.aa	gil530408	Asn-tRNA synthetase [Mycoplasma capricolum] >pirS77842 S77842	439	1.60E-65
f860.aa	gil1045792	asparaginyl-tRNA synthetase [Mycoplasma genitalium]	365	2.20E-62
f860.aa	gil1674281	(AE000057) Mycoplasma pneumoniae, asparaginyl-tRNA synthetase;	338	3.10E-61
f860.aa	gnlPIDle1202700	(AJ222645) asparaginyl-tRNA synthetase [Arabidopsis thaliana]	364	3.90E-59
f860.aa	gnlPIDle264488	YCR024c, len:492 [Saccharomyces cerevisiae] >pirS19435 S19435	150	3.90E-47
f860.aa	gnlPIDle254305	asparaginyl-tRNA synthetase [Salmonella typhi]	370	1.70E-46
f860.aa	gnlPIDle188505	asparagine--tRNA ligase [Lactobacillus delbrueckii]	224	1.30E-44
f860.aa	pirS71072 S71072	asparagine--tRNA ligase (EC 6.1.1.22) asnS1 - Lactobacillus	224	1.30E-44
f860.aa	gnlPIDle188572	asparagine--tRNA ligase [Lactobacillus delbrueckii]	224	2.40E-44
f860.aa	gil146247	asparaginyl-tRNA synthetase [Bacillus subtilis] >gnlPIDle1183681	234	6.10E-44
f861.aa	gil2687975	(AE001122) glutamate racemase (murl) [Borrelia burgdorferi]	1354	2.90E-186

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f861.aa	gil396314	glutamate synthase [Escherichia coli] >gil290428 glutamate synthase	168	1.20E-16
f861.aa	gnlPIDle11 65353	glutamate racemase [Bacillus subtilis] >gnlPIDle1184088	120	1.80E-13
f861.aa	pirJC5587IJ C5587	glutamate racemase (EC 5.1.1.3) - Bacillus pumilus	122	1.80E-13
f861.aa	spiP52973I MURI_HA EIN	PROBABLE GLUTAMATE RACEMASE (EC 5.1.1.3).	114	8.10E-13
f867.aa	gil2687979	(AE001122) V-type ATPase, subunit A (atpA) [Borrelia burgdorferi]	2826	0
f867.aa	pirJC5532IJ C5532	vacuolar-type ATPase (EC 3.-.-) A chain - Desulfurococcus	594	2.20E-162
f867.aa	gil2104726	V-ATPase A subunit [Desulfurococcus sp. SY]	594	3.10E-162
f867.aa	gil2605627	ATPase alpha subunit [Thermococcus sp.]	592	7.10E-161
f867.aa	gnlPIDId10 03475	Na+ -ATPase alpha subunit [Enterococcus hirae]	601	1.60E-153
f867.aa	gil1590955	H+-transporting ATP synthase, subunit A (atpA) [Methanococcus	585	6.00E-147
f867.aa	gil496904	membrane ATPase [Haloflex volcanii] >pirS55895IS45144	728	6.00E-147
f867.aa	gil152927	ATPase alpha subunit [Sulfolobus acidocaldarius] >pirA28652IA28652	548	5.00E-163
f867.aa	gil2649416	(AE001023) H+-transporting ATP synthase, subunit A (atpA)	748	2.00E-146
f867.aa	gil2622052	(AE000869) ATP synthase, subunit A [Methanobacterium	607	9.40E-146
f867.aa	gil168926	vacuolar ATPase vma-1 [Neurospora crassa] >pirA30799IPXNCV7	302	9.00E-145
f867.aa	gil149820	ATPase alpha subunit [Methanosarcina barkeri] >pirA34283IA34283	743	1.40E-143
f867.aa	gil160736	vacuolar ATPase [Plasmodium falciparum] >pirA48582IA48582 vacuolar	305	9.40E-140
f867.aa	gnlPIDId10 09732	adenosine triphosphatase A subunit [Acetabularia acetabulum]	307	9.00E-137
f867.aa	gil49048	ATPase alpha-subunit [Thermus aquaticus thermophilus]	684	4.80E-136
f868.aa	gil2687980	(AE001122) V-type ATPase, subunit B (atpB) [Borrelia burgdorferi]	2205	1.80E-298
f868.aa	gil1590954	H+-transporting ATP synthase, subunit B (atpB) [Methanococcus	156	2.00E-114
f868.aa	gil2605628	ATPase beta subunit [Thermococcus sp.]	151	3.30E-108
f868.aa	gil2104727	V-ATPase B subunit [Desulfurococcus sp. SY]	151	1.10E-107
f868.aa	gil43641	ATP synthase subunit [Halobacterium salinarum] >pirS14733IS14733	150	1.80E-107
f868.aa	gil149821	ATPase beta subunit [Methanosarcina barkeri] >pirB34283IB34283	172	1.00E-105

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f868.aa	gnlPIDd10 03476	Na+ -ATPase beta subunit [Enterococcus hirae]	151	1.40E-105
f868.aa	gil2649415	(AE001023) H+-transporting ATP synthase, subunit B (atpB)	151	1.70E-103
f868.aa	gil496905	membrane ATPase [Haloferax volcanii] >pirS55896[S45145]	153	5.80E-103
f868.aa	gil1199639	A1AO H+ ATPase, subunit B [Methanosarcina mazei]	173	2.20E-102
f868.aa	gil2622051	(AE000869) ATP synthase, subunit B [Methanobacterium]	155	1.00E-101
f868.aa	gnlPIDd10 09734	adenosine triphosphatase B subunit [Acetabularia acetabulum]	159	1.30E-101
f868.aa	gil1086645	Similar to vacuolar ATP synthase (strong). [Caenorhabditis elegans]	163	1.30E-101
f868.aa	gil459198	vacuolar H+-ATPase subunit B [Gossypium hirsutum]	164	4.60E-101
f868.aa	gil167108	vacuolar ATPase B subunit [Hordeum vulgare] >spIQ40078[VAT1_HORVU]	164	4.60E-101
f872.aa	gil2687986	(AE001122) B. burgdorferi predicted coding region BB0089 [Borrelia]	1684	1.60E-230
f874.aa	gil2687965	(AE001121) L-lactate dehydrogenase (ldh) [Borrelia burgdorferi]	1603	2.80E-217
f874.aa	gil39758	L- lactate dehydrogenase [Bacillus psychrosaccharolyticus]	520	3.10E-109
f874.aa	pirS081831 S08183	L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus	515	4.30E-109
f874.aa	pirA258051 A25805	L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis	520	1.00E-107
f874.aa	gil143136	L-lactate dehydrogenase [Bacillus megaterium] >pirS00133[DEBSLM]	430	5.20E-107
f874.aa	gil143138	lactate dehydrogenase (EC 1.1.1.27) [Bacillus stearothermophilus]	514	6.60E-107
f874.aa	gnlPIDd10 09574	L-lactate dehydrogenase [Bacillus subtilis] >gnlPIDe1182257	512	8.90E-107
f874.aa	gil143134	lactate dehydrogenase (EC 1.1.1.27) [Bacillus caldotenax]	516	1.70E-106
f874.aa	gil143132	lactate dehydrogenase (AC 1.1.1.27) [Bacillus caldolyticus]	506	2.30E-106
f874.aa	gil412392	NAD-dependent dehydrogenase [unidentified]	508	4.40E-106
f874.aa	gil143130	L-lactate dehydrogenase [Bacillus caldotenax] >pirS00019[S00019]	510	1.10E-105
f874.aa	gil642256	L-lactate dehydrogenase [Pedococcus acidilactici]	560	1.70E-91
f874.aa	gil847956	L-lactate dehydrogenase [Lactobacillus sake] >spIP50934[LDH_LACSK]	381	2.30E-91
f874.aa	gil581305	L-lactate dehydrogenase [Lactobacillus plantarum] >pirA36957[A36957]	547	2.30E-91
f874.aa	gil149575	L(+)-lactate dehydrogenase [Lactobacillus casei]	386	3.20E-91
f886.aa	gil2687958	(AE001120) B. burgdorferi predicted coding region BB0077 [Borrelia]	1792	9.50E-237

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f888.aa	gi2687959	(AE001120) B. burgdorferi predicted coding region BB0075 [Borrelia]	2351	3.59999944
f893.aa	gi2687962	(AE001120) B. burgdorferi predicted coding region BB0071 [Borrelia]	2514	710933e-318
f895.aa	gi2687954	(AE001120) conserved hypothetical protein [Borrelia burgdorferi]	747	3.60E-100
f895.aa	gnllPIDle1184285	similar to hypothetical proteins [Bacillus subtilis]	103	2.50E-35
f899.aa	gi2687946	(AE001119) B. burgdorferi predicted coding region BB0066 [Borrelia]	1161	4.30E-158
f924.aa	gi2687934	(AE001118) B. burgdorferi predicted coding region BB0044 [Borrelia]	692	3.90E-93
f925.aa	gi2687935	(AE001118) B. burgdorferi predicted coding region BB0043 [Borrelia]	1771	7.50E-242
f929.aa	gi2687916	(AE001117) B. burgdorferi predicted coding region BB0038 [Borrelia]	2589	0
f93.aa	gi2688703	(AE001176) pyridoxal kinase (pdxK) [Borrelia burgdorferi]	1334	6.60E-181
f933.aa	gi2687917	(AE001117) B. burgdorferi predicted coding region BB0034 [Borrelia]	902	1.90E-122
f933.aa	gi2690091	(AE000789) conserved hypothetical protein [Borrelia burgdorferi]	136	3.10E-37
f933.aa	gi2690225	(AE000790) conserved hypothetical protein [Borrelia burgdorferi]	149	4.50E-37
f933.aa	gi2690045	(AE000784) conserved hypothetical protein [Borrelia burgdorferi]	126	5.70E-28
f933.aa	gi2239281	No definition line found [Borrelia burgdorferi]	148	2.40E-14
f939.aa	gi2687919	(AE001117) B. burgdorferi predicted coding region BB0028 [Borrelia]	1796	7.50E-241
f940.aa	gi2687920	(AE001117) B. burgdorferi predicted coding region BB0027 [Borrelia]	1109	1.20E-152
f943.aa	gi2687905	(AE001116) B. burgdorferi predicted coding region BB0024 [Borrelia]	2001	5.00E-273
f943.aa	gi411592	L-sorbose dehydrogenase [unidentified]	175	2.30E-15
f943.aa	gnllPIDd1006418	L-sorbose dehydrogenase [Acetobacter liquefaciens]	173	4.40E-15
f952.aa	gi2687880	(AE001115) glpE protein (glpE) [Borrelia burgdorferi]	628	2.90E-84
Query	GenSeq Access No.	GenSeq Gene Description	BLAST Score	BLAST P-Value
f07A.aa	R33279	43 kD endoflagellum sheath protein.	120	6.10E-25
f142.aa	R95044	Apoptosis participating protein.	103	4.70E-18
f147.aa	W18209	Staphylococcus aureus Coenzyme A disulphide reductase (CoADR).	194	4.80E-91

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f147.aa	W06425	Water-forming NADH oxidase.	369	8.00E-86
f147.aa	R32089	Benzene dioxygenase polypeptide V.	104	4.70E-11
f147.aa	R66733	Aromatic dihydrodiol/catechol deoxygenase #5.	105	9.00E-11
f152.aa	R81549	High affinity potassium uptake transporter HKT1.	137	3.70E-18
f157.aa	W15192	Staphylococcus aureus cell surface protein.	239	3.40E-37
f17-6.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	178	5.20E-16
f17-6.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	145	1.30E-11
f17-6.aa	W03626	Human thyrotropin GPR N-terminal sequence.	144	1.90E-11
f17-6.aa	W21591	Antibiotic potentiating peptide #3.	141	5.10E-11
f196.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	183	2.70E-18
f196.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	180	3.60E-17
f196.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	169	6.50E-15
f196.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	169	1.40E-14
f196.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	140	6.10E-14
f197.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	190	2.30E-19
f197.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	190	2.00E-18
f197.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	179	4.00E-16
f197.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	182	6.30E-16
f197.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	150	1.10E-12
f21-4.aa	R69629	B. burgdorferi OspF operon.	321	7.00E-39
f21-4.aa	R89476	B. burgdorferi OspG lipoprotein.	107	6.10E-34
f24-1.aa	W22676	Borrelia variable major protein (VMP)-like protein VlsE.	412	4.60E-72
f291.aa	W20152	H. pylori transporter protein, 1464715.aa.	336	1.70E-41
f291.aa	W24682	Helicobacter pylori transporter protein 4882763.aa.	234	8.20E-27
f291.aa	W20528	H. pylori cell envelope transporter protein 4882763.aa.	234	8.20E-27
f291.aa	W20592	H. pylori transporter protein, 01cel1513orf21.	168	7.60E-17
f301.aa	W20287	H. pylori inner membrane protein, 24132293.aa.	158	1.60E-13
f301.aa	W20916	H. pylori inner membrane protein 14gp12015orf12.	158	1.90E-13
f301.aa	W20769	H. pylori inner membrane protein, 07ee20513orf28.	158	2.40E-13
f301.aa	W05196	Helicobacter pylori 50 kDa protective antigen G3.8.	157	2.80E-13
f301.aa	W20767	H. pylori cytoplasmic protein, 07ee20513orf1.	138	4.30E-11

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f320.aa	R24300	Glycopeptide resistance protein VanY from <i>E. faecium</i> .	142	2.90E-14
f328.aa	R15642	CTP synthetase.	274	3.00E-50
f328.aa	W20778	<i>H. pylori</i> cytoplasmic protein, 07ge20415orf6.	122	1.90E-34
f352.aa	W03626	Human thyrotropin GPR N-terminal sequence.	153	4.70E-12
f352.aa	W21591	Antibiotic potentiating peptide #3.	152	6.60E-12
f352.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	145	5.30E-11
f4-50.aa	W07187	<i>B. garinii</i> IP90 decorin binding protein.	305	1.30E-41
f4-50.aa	W07186	<i>B. afzelii</i> strain pGau decorin binding protein.	161	1.60E-34
f4-50.aa	W07185	<i>B. burgdorferi</i> HB-19 decorin binding protein.	173	2.80E-34
f4-50.aa	W07183	<i>B. burgdorferi</i> B31 decorin binding protein.	176	1.80E-33
f4-50.aa	W07190	<i>B. burgdorferi</i> JDI decorin binding protein.	177	1.80E-33
f4-50.aa	W07182	<i>B. burgdorferi</i> 297 decorin binding protein.	177	1.10E-32
f4-50.aa	W07189	<i>B. burgdorferi</i> LP7 decorin binding protein.	177	1.10E-32
f4-50.aa	W07188	<i>B. burgdorferi</i> LP4 decorin binding protein.	177	3.90E-32
f4-50.aa	W07184	<i>B. burgdorferi</i> Sh.2.82 decorin binding protein.	177	1.30E-31
f45-2.aa	R89476	<i>B. burgdorferi</i> OspG lipoprotein.	213	1.30E-35
f45-2.aa	R70491	Leucocytozoan protozoa structural protein epitope.	206	2.10E-20
f45-2.aa	W03626	Human thyrotropin GPR N-terminal sequence.	211	6.10E-20
f45-2.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	202	8.90E-19
f45-2.aa	R69629	<i>B. burgdorferi</i> OspF operon.	111	1.10E-14
f45-2.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	166	1.00E-13
f45-2.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	154	7.10E-12
f488.aa	W15078	<i>M. leprae</i> gyrA precursor.	390	2.70E-143
f488.aa	R88733	<i>S. aureus</i> mutant grIA protein.	698	6.70E-122
f488.aa	R88731	<i>S. aureus</i> topoisomerase IV grIA subunit.	698	6.70E-122
f49-2.aa	W22676	<i>Borrelia</i> variable major protein (VMP)-like protein VIsE.	497	2.70E-75
f5-14.aa	W03626	Human thyrotropin GPR N-terminal sequence.	234	6.60E-23
f5-14.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	231	1.40E-22
f5-14.aa	R70491	Leucocytozoan protozoa structural protein epitope.	221	1.00E-20
f5-14.aa	W30763	Mannose-1-phosphate transferase protein MNN4.	203	1.60E-18
f5-14.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	187	2.10E-15

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f5-14.aa	W21591	Antibiotic potentiating peptide #3.	176	4.60E-15
f5-14.aa	R69629	B. burgdorferi OspF operon.	106	3.50E-13
f5-14.aa	R89476	B. burgdorferi OspG lipoprotein.	157	6.20E-13
f5-14.aa	W26536	Trypanosoma cruzi antigen.	143	5.00E-11
f5-15.aa	R69629	B. burgdorferi OspF operon.	448	1.30E-68
f5-15.aa	R89476	B. burgdorferi OspG lipoprotein.	105	5.80E-24
f502.aa	R69852	Ethylene response (ETR) mutant protein etr1-3.	191	1.90E-35
f502.aa	R69849	Ethylene response (ETR) gene product.	191	2.70E-35
f502.aa	R69853	Ethylene response (ETR) mutant protein etr1-4.	191	2.70E-35
f502.aa	R69850	Ethylene response (ETR) mutant protein etr1-1.	191	3.60E-35
f502.aa	R69851	Ethylene response (ETR) mutant protein etr1-2.	191	3.60E-35
f502.aa	R74632	QETR ethylene response (ETR) protein from Arabidopsis thaliana.	190	5.20E-26
f502.aa	R74629	Tomato ethylene response (TETR) protein.	171	6.50E-23
f502.aa	R74633	Nr (never ripe) tomato ethylene response (ETR) protein.	171	6.50E-23
f502.aa	R74630	Tomato TGETR1 ethylene response protein.	123	1.20E-19
f51-2.aa	W03626	Human thyrotropin GPR N-terminal sequence.	235	2.90E-23
f51-2.aa	R89476	B. burgdorferi OspG lipoprotein.	109	6.90E-23
f51-2.aa	W03627	Human follicle stimulating hormone GPR N-terminal sequence.	228	2.20E-22
f51-2.aa	W30763	Mannose-1-phosphate transferase protein MN4.	203	1.00E-18
f51-2.aa	R70491	Leucocytozoan protozoa structural protein epitope.	191	7.50E-18
f51-2.aa	R97866	Chicken leucocytozoan immunogenic protein for use in vaccines.	183	4.80E-16
f51-2.aa	W21591	Antibiotic potentiating peptide #3.	159	6.20E-13
f51-2.aa	R68838	Plasmodium falciparum ABRA gene protein.	142	1.10E-12
f51-2.aa	R27530	Plasmodium falciparum bloodand liver stage ABRA antigen.	142	2.80E-12
f51-2.aa	W31186	Human p160 polypeptide 160.2.	148	2.30E-11
f51-2.aa	W31185	Human p160 polypeptide 160.1.	148	2.40E-11
f517.aa	W24296	Staphylococcus aureus Gene #1 polypeptide sequence 2.	237	6.80E-30
f541.aa	R31013	P39-alpha.	1253	3.80E-229
f541.aa	R33280	P39-beta.	504	1.90E-117
f542.aa	R33280	P39-beta.	711	3.20E-96
f542.aa	R31013	P39-alpha.	101	7.90E-16

TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f561.aa	R69631	B. burgdorferi T5 protein.	982	6.90E-131
f598.aa	W20289	H. pylori transporter protein, 24218968.aa.	264	9.90E-33
f598.aa	W20640	H. pylori transporter protein, 02ce11022orf8.	264	1.00E-30
f598.aa	W20101	H. pylori transporter protein 1132778.aa.	233	8.50E-27
f598.aa	W20861	H. pylori cell envelope transporter protein, 12ge10305orf16.	233	9.60E-27
f598.aa	W34202	Streptomyces efflux pump protein (frenolicin gene D product).	196	2.80E-21
f598.aa	R71091	C. jejuni PEB1A antigen from ORF3.	168	1.20E-17
f600.aa	W25527	Staphylococcus aureus Gene #20 polypeptide sequence 2.	209	3.40E-26
f600.aa	W34201	Streptomyces efflux pump protein (frenolicin gene C product).	169	6.50E-19
f600.aa	W20639	H. pylori transporter protein, 02ce11022orf7.	127	1.10E-14
f603.aa	W34200	Streptomyces efflux pump protein (frenolicin gene B product).	155	7.40E-32
f604.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	110	2.30E-20
f606.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	116	1.20E-25
f607.aa	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	141	1.50E-26
f631.aa	W15192	Staphylococcus aureus cell surface protein.	160	7.30E-29
f664.aa	W20105	H. pylori flagella-associated protein, 1171928.aa.	202	3.20E-46
f664.aa	W20688	H. pylori flagella-associated protein 04ge11713orf5.	202	2.60E-45
f664.aa	R97245	Virulence gene cluster polypeptide product.	158	3.90E-13
f704.aa	R60153	Nematode-inducible transmembrane pore protein.	104	2.50E-18
f704.aa	R33913	Sequence encoded by TobRB7-5A which encodes a membrane channel	104	2.50E-18
f704.aa	R77082	Tobacco root specific promoter RB7 from clone lambda5A (TobRB7-5A).	104	2.50E-18
f742.aa	W46499	Amino acid sequence of the spindly (SPY) protein of Arabidopsis.	101	2.50E-14
f752.aa	W20733	H. pylori cell envelope protein, 06cp11722orf15.	141	3.00E-37
f752.aa	W20358	H. pylori cell envelope protein 26366312.aa.	110	4.20E-18
f814.aa	W20753	H. pylori transporter protein, 06gp11202orf7.	178	7.90E-35
f814.aa	W20420	H. pylori cell envelope transporter protein 33399142.aa.	160	2.30E-21
f843.aa	R14319	Human T-cell immunosuppressive factor.	167	1.20E-19
f860.aa	W21894	Asparaginyl-tRNA synthetase from Staphylococcus aureus.	245	2.30E-38
f860.aa	W33903	Streptococcus pneumoniae asparaginyl tRNA synthetase.	177	1.10E-22
f867.aa	W34261	An alpha subunit of a thermostable ATPase.	592	1.30E-161
f867.aa	R10098	Alpha subunit of ATP-synthase.	741	4.90E-144



TABLE 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

f867.aa	R31522	Carrot reverse transcriptase.	311	4.60E-130
f867.aa	R10099	Beta subunit of ATP-synthase.	121	7.90E-14
f867.aa	W34262	A beta subunit of a thermostable ATPase.	116	1.00E-12
f868.aa	W34262	A beta subunit of a thermostable ATPase.	151	6.10E-109
f868.aa	R10099	Beta subunit of ATP-synthase.	172	1.90E-106
f868.aa	W34261	An alpha subunit of a thermostable ATPase.	117	3.10E-19
f868.aa	R10098	Alpha subunit of ATP-synthase.	113	2.00E-18
f868.aa	R31522	Carrot reverse transcriptase.	101	7.10E-15
f874.aa	R10591	L-lactic acid dehydrogenase.	538	7.20E-109
f874.aa	R08355	Recombinant thermophilic NAD-dependant dehydrogenase.	455	9.80E-99
f874.aa	R09295	Recombinant thermophilic NAD-dependant dehydrogenase.	455	9.80E-99
f874.aa	R15736	L-lactic acid dehydrogenase.	426	1.60E-85
f874.aa	P91948	Pig H4 isoenzyme.	393	2.00E-82
f874.aa	W33108	Chicken lactic acid dehydrogenase type B subunit.	390	2.20E-80
f874.aa	W33107	Chicken lactic acid dehydrogenase type B subunit.	385	1.10E-79
f874.aa	P80891	Testis-specific lactate dehydrogenase subunit LDH-C4.	339	5.50E-74
f874.aa	R94013	Heat resistant maleate dehydrogenase.	255	1.30E-55
f874.aa	R11119	Recombinant L-2-hydroxyisocaproic acid dehydrogenase.	224	7.90E-49
f874.aa	R62605	P. falciparum lactate dehydrogenase.	255	2.00E-44
f874.aa	W11476	Eimeria lactate dehydrogenase.	203	1.10E-25
f943.aa	P91223	Coenzyme-independent L-sorbose dehydrogenase from Gluconobacter	175	4.30E-16

TABLE 3. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

TABLE 4. Residues Comprising Epito-Bearing Fragments

Query	Residues Comprising Epito-Bearing Fragments
f101.aa	from about Lys-62 to about Gly-64, from about Ser-111 to about Asp-113, from about Arg-136 to about Arg-139, from about Pro-189 to about Asn-193.
f11.aa	from about Pro-38 to about Lys-40, from about Glu-92 to about Lys-96.
f12.aa	from about Pro-288 to about Asp-290, from about Asn-336 to about Gly-338, from about Tyr-410 to about Gly-413, from about Asp-418 to about Arg-420, from about Pro-552 to about Val-555, from
	about Gln-643 to about Asp-645, from about Gln-1061 to about Arg-1063, from about Asn-1130 to about Lys-1132.
f129.aa	from about Glu-76 to about Arg-81, from about Lys-144 to about Asn-146.
f147.aa	from about Gln-94 to about Thr-96.
f152.aa	from about Gly-35 to about Gly-37, from about Gln-321 to about Gly-323.
f154.aa	from about Asn-39 to about Lys-41, from about Ser-74 to about Lys-77, from about Ser-213 to about Gly-215, from about Ser-303 to about Asp-306, from about Asp-422 to about Asn-424.
f157.aa	from about Lys-21 to about Asp-24, from about Ser-45 to about Tyr-47.
f17.aa	from about Arg-17 to about Asn-20, from about Thr-94 to about Gly-96.
f186.aa	from about Lys-305 to about Tyr-308.
f196.aa	from about Lys-121 to about Asn-123, from about Pro-278 to about Lys-282, from about Glu-576 to about Tyr-578.
f899.aa	from about Asn-174 to about Asp-177.
f925.aa	from about Lys-201 to about Asp-204, from about Phe-291 to about Lys-294.
f929.aa	from about Pro-139 to about Asn-141, from about Arg-211 to about Glu-214, from about Thr-370 to about Asn-375.
f933.aa	from about Ser-139 to about Lys-143.
f940.aa	from about Gly-143 to about Asn-148.
f943.aa	from about Asp-58 to about Asp-60, from about Lys-157 to about Asn-159, from about Asp-217 to about Asp-221, from about Lys-250 to about Asn-254, from about Pro-262 to about Asn-264, from about Gly-305 to about Trp-307.
f952.aa	from about Ser-52 to about Ser-54.
f4.aa	from about Arg-64 to about Arg-67.
f43.aa	from about Ser-84 to about Gln-87, from about Asp-231 to about Tyr-233, from about Arg-296 to about Asp-300.
f50.aa	from about Glu-136 to about Gly-138, from about Asp-153 to about Lys-155, from about Asp-289 to about Asp-291, from about Glu-458 to about Asn-461.
f65.aa	from about Glu-120 to about Asp-122, from about Pro-204 to about Tyr-206.
f8.aa	from about Pro-263 to about Arg-265, from about Asp-274 to about Lys-278.
f82.aa	from about Tyr-66 to about Gly-68, from about Ser-116 to about Lys-119, from about Asp-121 to about Gly-123, from about Pro-128 to about Gly-131.

TABLE 4. Residues Comprising Epito-Bearing Fragments

f86.aa	from about Asn-179 to about Asn-181, from about Lys-192 to about Asn-194, from about Lys-270 to about Asn-272, from about Lys-279 to about Lys-282, from about Asp-331 to about Asn-333.
f477.aa	from about Pro-250 to about Lys-253.
f488.aa	from about Lys-76 to about Lys-79, from about Asn-486 to about Asp-489, from about Lys-508 to about Gly-510, from about Asn-559 to about Gly-562.
f494.aa	from about Lys-76 to about Asn-78.
f516.aa	from about Lys-32 to about Asp-34.
f523.aa	from about Pro-202 to about Asn-206, from about Lys-255 to about Tyr-258.
f526.aa	from about Asn-85 to about Lys-88, from about Asp-136 to about Gly-138.
f577.aa	from about Cys-18 to about Lys-22, from about Asn-297 to about Gln-300.
f584.aa	from about Pro-131 to about Lys-133, from about Pro-200 to about Ser-202.
f596.aa	from about Arg-42 to about Asp-44, from about Asp-117 to about Tyr-119, from about Pro-205 to about Asp-207.
f600.aa	from about Pro-143 to about Asp-145.
f603.aa	from about Phe-35 to about Ser-37.
f607.aa	from about Gln-67 to about Lys-70, from about Asp-273 to about Tyr-275, from about Asp-333 to about Gly-338, from about Pro-359 to about Lys-362, from about Arg-409 to about Gly-411.
f611.aa	from about Arg-133 to about Gly-135.
f631.aa	from about Pro-132 to about Asn-136, from about Asn-159 to about Tyr-161, from about Pro-216 to about Asp-218, from about Pro-220 to about Lys-223.
f688.aa	from about Lys-266 to about Asp-268, from about Lys-271 to about Asn-273, from about Lys-315 to about Lys-318.
f704.aa	from about Lys-250 to about Lys-253.
f707.aa	from about Lys-131 to about Asp-134, from about Asp-246 to about Asn-249.
f709.aa	from about Tyr-39 to about Gly-42, from about Lys-148 to about Gly-150, from about Arg-269 to about Gly-272, from about Ser-466 to about Tyr-468, from about Asn-489 to about Asn-491, from about Lys-575 to about Asp-578, from about Pro-642 to about Lys-644.
f197.aa	from about Pro-217 to about Asp-219, from about Glu-675 to about Asp-678, from about Pro-687 to about Asn-689, from about Glu-694 to about Gln-696.
f200.aa	from about Arg-174 to about Phe-179.
f208.aa	from about Arg-326 to about Ser-328.
f210.aa	from about Pro-191 to about Ile-194.
f221.aa	from about Asn-133 to about Asn-135.
f253.aa	from about Arg-191 to about Gly-194.
f269.aa	from about Ser-271 to about Thr-273, from about Asp-284 to about Gly-286.
f29.aa	from about Pro-159 to about Ser-161.
f290.aa	from about Pro-240 to about Gly-244.
f291.aa	from about Gln-267 to about Lys-269.

TABLE 4. Residues Comprising Epitope-Bearing Fragments

f296.aa	from about Glu-98 to about Lys-101.
f3.aa	from about Asn-241 to about Lys-245.
f30.aa	from about Asn-156 to about Tyr-159, from about Asn-178 to about Lys-180.
f939.aa	from about Ser-245 to about Asn-249.
f739.aa	from about Asn-80 to about Tyr-82, from about Lys-208 to about Ser-210.
f742.aa	from about Ser-141 to about Asp-145, from about Asn-222 to about Gln-225, from about Asp-243 to about Tyr-247, from about Asn-249 to about Asn-251.
f743.aa	from about Arg-111 to about Gly-114, from about Pro-131 to about Asp-134.
f790.aa	from about Thr-40 to about Asn-42, from about Ser-53 to about Ser-55, from about Lys-215 to about Asp-218, from about Asn-274 to about Gly-277.
f792.aa	from about Val-82 to about Ser-84, from about Ser-102 to about Asn-104, from about Gln-127 to about Tyr-130, from about Lys-309 to about Asn-314, from about Lys-375 to about Thr-377, from about Pro-511 to about His-513, from about Thr-515 to about Asp-517.
f797.aa	from about Pro-119 to about Gly-122, from about Lys-166 to about Asn-169.
f799.aa	from about Asn-31 to about Asn-34, from about Gln-44 to about Asn-47, from about Pro-123 to about Gly-125.
f814.aa	from about Ser-120 to about Ser-122, from about Arg-636 to about Asn-638, from about Cys-967 to about Ser-969.
f820.aa	from about Thr-563 to about Tyr-565.
f850.aa	from about Tyr-159 to about Tyr-164, from about Gln-375 to about Asp-379.
f853.aa	from about Thr-180 to about Lys-184, from about Arg-231 to about Asp-233, from about Asn-252 to about Gly-254.
f859.aa	from about Lys-46 to about Ser-52, from about Pro-88 to about Asn-91, from about Asn-117 to about Asp-120.
f861.aa	from about Asp-38 to about Lys-40, from about Lys-219 to about Asn-225.
f368.aa	from about Gln-228 to about Asn-231.
f371.aa	from about Tyr-109 to about Asn-111, from about Asn-162 to about Gln-164.
f502.aa	from about Asn-118 to about Lys-122, from about Ser-269 to about Gly-271, from about Lys-370 to about Asp-373, from about Asn-509 to about Lys-511, from about Lys-705 to about Arg-707, from about Thr-912 to about Gly-914, from about Pro-1213 to about Asp-1216, from about Asn-1491 to about Arg-1493.
f527.aa	from about Cys-20 to about Gln-22, from about Asn-38 to about Asn-40, from about Phe-112 to about Asp-114, from about Lys-160 to about Asn-162, from about Ser-199 to about Asp-201, from about Gln-258 to about Gly-261, from about Arg-282 to about Asn-284, from about Ser-297 to about Asp-299.
f541.aa	from about Ser-68 to about Asn-71.
f604.aa	from about Lys-77 to about Gly-79, from about Lys-201 to about Asn-203, from about Asp-252 to about Asp-254, from about Tyr-

TABLE 4. Residues Comprising Epito-Bearing Fragments

	347 to about Gly-350, from about Asp-514 to about Trp-516.
f736.aa	from about Lys-20 to about Asn-24, from about Arg-147 to about Ser-153, from about Ser-231 to about Lys-233.
f752.aa	from about Thr-119 to about Lys-122, from about Pro-420 to about Gly-422.
f798.aa	from about Asp-33 to about Thr-36, from about Lys-180 to about His-183.
f635.aa	from about Pro-100 to about Asn-102, from about Asp-145 to about Phe-147.
f32.aa	from about Lys-18 to about Asn-20.
f320.aa	from about Asn-193 to about Leu-195, from about Gln-248 to about Lys-250.
f352.aa	from about Ser-46 to about Asn-49.
f301.aa	from about Lys-178 to about Lys-180, from about Ser-401 to about Tyr-404.
f373.aa	from about Gly-88 to about Lys-90, from about Asn-539 to about Lys-542, from about Glu-654 to about Ser-657.
f384.aa	from about Pro-250 to about Asn-252, from about Asp-266 to about Lys-268.
f446.aa	from about Asp-20 to about Ser-26, from about Asn-146 to about Lys-149.
f542.aa	from about Arg-86 to about Gly-88, from about Arg-163 to about Asn-165.
f93.aa	from about Asn-152 to about Asp-155.
f105.aa	from about Asp-48 to about Phe-50.
f150.aa	from about Thr-214 to about Asp-218, from about Asp-256 to about Asp-259.
f219.aa	from about Asn-77 to about Asn-81, from about Asp-111 to about Asn-115.
f229.aa	from about Gln-61 to about Asn-63.
f32.aa	from about Lys-18 to about Asn-20.
f186.aa	from about Lys-305 to about Tyr-308.
f216.aa	from about Ser-105 to about Asn-107.
f328.aa	from about Asn-105 to about Asp-107.
f352.aa	from about Ser-46 to about Asn-49.
f867.aa	from about Thr-3 to about Gly-5, from about Lys-156 to about Ser-159.
f868.aa	from about Arg-94 to about Gly-96, from about Pro-257 to about Gly-261, from about Pro-295 to about Asp-297, from about Arg-340 to about Asp-342.
f872.aa	from about Ser-19 to about Lys-23, from about Thr-139 to about Asp-142, from about Ser-282 to about Tyr-286, from about Ser-311 to about Ser-313.
f886.aa	from about Thr-83 to about Asp-85, from about Asp-106 to about Lys-108, from about Lys-143 to about Gly-147, from about Asp-186 to about Asn-191.
f888.aa	from about Asn-65 to about Asp-67.
f893.aa	from about Asn-203 to about Asn-207, from about Thr-446 to about Asn-450.
f605.aa	from about Arg-31 to about Asp-33.
f606.aa	from about Asn-68 to about Gly-71, from about Asn-136 to about

TABLE 4. Residues Comprising Epito-Bearing Fragments

	Lys-139, from about Asn-223 to about Tyr-226, from about Ser-276 to about Tyr-279, from about Pro-362 to about Asn-365, from about Arg-503 to about Trp-507.
f679.aa	from about Lys-154 to about Asp-156, from about Lys-224 to about Arg-226, from about Asn-260 to about Asp-264, from about Glu-363 to about Lys-366, from about Asp-387 to about Gly-389, from
	about Tyr-441 to about Lys-443, from about Arg-501 to about Tyr-504.
f11-12.aa	from about Pro-91 to about Asn-93, from about Pro-181 to about Asp-186, from about Lys-244 to about Ser-248.
f11-4.aa	from about Asn-160 to about Lys-163.
f14-8.aa	from about Pro-92 to about Gln-95, from about Lys-123 to about Thr-125, from about Lys-215 to about Asp-219.
f17-6.aa	from about Pro-36 to about Glu-38.
f19-2.aa	from about Ser-104 to about Ser-106, from about Gln-230 to about Asn-232.
f19-4.aa	from about Val-79 to about Thr-82, from about Pro-195 to about Gly-201.
f19-6.aa	from about Asp-24 to about Lys-30, from about Pro-36 to about Glu-38.
f21-4.aa	from about Cys-24 to about Asn-26.
f28-2.aa	from about Ser-77 to about Lys-80, from about Tyr-274 to about Asn-277.
f28-3.aa	from about Glu-53 to about Arg-57, from about Gln-82 to about Asn-85, from about Gln-157 to about Asn-159.
f31-2.aa	from about Arg-95 to about Arg-97, from about Asn-297 to about Asn-299.
f4-15.aa	from about Pro-182 to about Asp-184, from about Lys-220 to about Asp-222.
f4-50.aa	from about Thr-109 to about Asn-111.
f42-1.aa	from about Asn-55 to about Asn-57, from about Arg-81 to about Ser-84, from about Asp-94 to about Asn-97.
f45-2.aa	from about Asn-83 to about Gly-86.
f47-2.aa	from about Ser-29 to about Asp-33, from about Asn-94 to about Lys-99, from about Pro-152 to about Lys-157.
f49-2.aa	from about Asn-452 to about Gly-454.
f5-14.aa	from about Glu-102 to about Asp-106, from about Thr-272 to about Asn-275, from about Glu-313 to about Asn-315, from about Ser-370 to about Ser-372.
f5-15.aa	from about Lys-170 to about Gly-173, from about Asn-194 to about Gly-196.
f51-2.aa	from about Asp-302 to about Lys-304.
f6-21.aa	from about Glu-38 to about Asn-42, from about Arg-84 to about Gly-87.
f6-27.aa	from about Asp-67 to about Asn-69, from about Arg-85 to about Asn-89, from about Lys-168 to about Gly-171, from about Lys-179 to about Asn-181, from about Ser-380 to about His-382.
f6-5.aa	from about Ser-67 to about Asn-71.
f7-30.aa	from about Pro-94 to about Asp-96, from about Lys-144 to about Arg-147.
f76-1.aa	from about Asn-30 to about Lys-35, from about Lys-113 to about

TABLE 4. Residues Comprising Epito-Bearing Fragments

	Gly-116, from about Glu-119 to about Lys-121.
f8-10.aa	from about Pro-25 to about Lys-32, from about Ser-168 to about Thr-172.
f01a.aa_bb001	from about Pro-123 to about Asp-125, from about Ser-179 to about Asp-181, from about Lys-255 to about Gly-259.
_bb0011	from about Ala8 about Arg 17, from about Tyr31 to about Gly40, from about Ser65 to about Lys78, from about Val93 to about Asp102, from about Ser120 to about Ile129, from about Pro156 to about Glu170, from about Lys187 to about Asn 196, from about His205 to about Lys214, from about Gly226 to about Glu235, from about Gln253 to about Asn266, from about Glu283 to about Glu293, from about Leu311 to about Ile320, from about Arg326 to about Gly335, from about Pro340 to about Ala349
f02a.aa_bb002	from about Tyr-169 to about Asn-171, from about Tyr-242 to about Asn-245, from about Lys-264 to about Asp-267.
_bb9	from about Met7 to about Lys16, from about Lys47 to about Ser57, from about Asn80 to about Ser89, from about Gly103 to about Glu113, from about Lys125 to about Pro133, from about Lys138 to about Ala147
f03a.aa_bb006	from about Asp-54 to about Thr-57, from about Lys-201 to about His-204.
_bb014	from about Pro23 to about Gln31, from about Ser37 to about Asp45, from about Leu76 to about Asn84, from about Leu76 to about Val84, from about Ser89 to about Asn97, from about Ser105 to about Lys113, from about Asn120 to about Met128, from about Asn159 to about Gly 167, from about Lys173 to about Bal181
_bb023	from about Asp17 to about Gly27, from about Arg40 to about Asp48, from about Val64 to about Asp72, from about Glu105 to about Thr113, from about Ser141 to about Gly150, from about Asp155 to about Ile163, from about Asn184 to about Lys198, from about Ile219 to about Pro227, from about Ser230 to about Phe238, from about Ser241 to about Asn250, from about Asp270 to about Val278, from about Ser285 to about Leu293, from about Gly307 to about Ser315, from about Lys327 to about Asn335
f08a.aa_bb024	from about Asn-30 to about Asp-33, from about Ser-116 to about Asn-118, from about Asn-154 to about Gly-156.
f09a.aa_bb025	from about Asn-30 to about Ser-35, from about Thr-145 to about Asn-148.



Applicant's or agent's file reference number	PB370PCT2	International application No.	Unassigned
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>8</u> , line <u>8</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <b>American Type Culture Collection</b>	
Address of depositary institution (including postal code and country) <b>10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</b>	
Date of deposit <b>August 8, 1998</b>	Accession Number <b>202012</b>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	
<b>F r receiving Office use only</b> <input type="checkbox"/> This sheet was received with the international application  Authorized officer	<b>F r International Bureau use only</b> <input type="checkbox"/> This sheet was received by the International Bureau on:  Authorized officer

***What Is Claimed Is:***

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:
  - (a) a nucleotide sequence encoding any one of the amino acid sequences of the polypeptides shown in Table 1; or
  - (b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).
  - (c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences shown in Table 1; or,
  - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.
4. The isolated nucleic acid molecule of claim 3, wherein said epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 4.
5. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
  - (a) growing the host cell of claim 7 such that the protein is expressed by the cell; and
  - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:

- (a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
- (b) a polypeptide consisting of one the complete amino acid sequences of Table 1 except the N-terminal residue;
- (c) a fragment of the polypeptide of (a) having biological activity; and
- (d) a fragment of the polypeptide of (a) which binds to an antibody specific for the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *B. burgdorferi* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A hybridoma which produces an antibody of claim 10.

16. A vaccine, comprising:

- (1) one or more *B. burgdorferi* polypeptides selected from the group consisting of a polypeptide of claim 9; and
  - (2) a pharmaceutically acceptable diluent, carrier, or excipient;
- wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Borrelia* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Borrelia* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Borrelia* nucleic acids in a biological sample comprising:

- (a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and
- (b) detecting hybridization of said nucleic acids to the one or more *Borrelia* nucleic acid

sequences present in the biological sample.

19. A method of detecting *Borrelia* nucleic acids in a biological sample obtained from an animal, comprising:

- (a) amplifying one or more *Borrelia* nucleic acid sequences in said sample using polymerase chain reaction, and
- (b) detecting said amplified *Borrelia* nucleic acid.

20. A kit for detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

- (a) a polypeptide of claim 9 attached to a solid support; and
- (b) detecting means.

21. A method of detecting *Borrelia* antibodies in a biological sample obtained from an animal, comprising

- (a) contacting the sample with a polypeptide of claim 9; and
- (b) detecting antibody-antigen complexes.